

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: April 6, 2005, 16:53:22 ; Search time 190 Seconds

(without alignments)
695.350 Million cell updates/sec

Title: US-09-646-835-1_COPY_384_641

Perfect score: 1314

Sequence: 1 KSENVQILLDVLAPLSGL.....FGAQGPKGSGSGPTIEVD 258

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database : UniProt_03.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Query Length	ID	Description
1	1314	100.0	641	1 HS71_HUMAN	P08107 homo sapien
2	1296	98.6	641	2 Q6S4R2	Q6S4R2 sus scrofa
3	1295	98.6	641	1 HS71_BOVIN	Q27975 bos taurus
4	1295	98.6	641	1 HS71_BOVIN	Q27965 bos taurus
5	1295	98.6	641	2 Q6DLW1	Q6DLW1 bos taurus
6	1295	98.6	641	2 Q7YQF7	Q7YQF7 bos taurus
7	1291	98.2	641	2 Q7YQ66	Q7YQ66 canis fami
8	1279.5	97.4	638	1 HS71_CERAB	Q28222 cercopithec
9	1279	97.3	641	1 HS71_PIG	P34930 sus scrofa
10	1258.5	95.8	640	2 Q8WNS9	Q8WNS9 canis fami
11	1258	95.7	641	1 HS71_RAT	Q07439 rattus norv
12	1258	95.7	641	2 Q63256	Q63256 rattus norv
13	1239	94.3	641	2 Q9QWU5	Q9QWU5 mus musculu
14	1236	94.1	641	2 Q7TQD8	Q7TQD8 mus musculu
15	1228.5	93.5	642	1 HS71_MOUSE	P17879 mus musculu
16	1216	92.5	420	1 HS1A_MOUSE	Q61696 mus musculu
17	1109	84.4	641	1 HS7H_HUMAN	P34931 homo sapien
18	1108.5	84.4	650	2 Q6Q154	Q6Q154 pimephales
19	1108	84.3	649	2 Q804B6	Q804B6 carassius a
20	1102.5	83.9	646	2 Q7ZTK6	Q7ZTK6 xenopus lae
21	1101	83.8	649	1 HS7C_BRARE	Q20473 brachydanio
22	1101	83.8	649	2 Q6NYR4	Q6NYR4 brachydanio
23	1100.5	83.8	646	1 HS7C_CRIGR	P34931 cricetus
24	1100.5	83.8	646	1 HS7C_MOUSE	P63017 mus musculu
25	1100.5	83.8	646	1 HS7C_RAT	P63018 rattus norv
26	1100.5	83.8	646	2 Q75P34	Q75P34 numida mele
27	1098	83.6	653	2 Q6TDU0	Q6TDU0 dicentrarch
28	1097.5	83.5	269	2 Q96BE0	Q96BE0 homo sapien
29	1097.5	83.5	586	2 Q961S6	Q961S6 homo sapien
30	1097.5	83.5	646	1 HS7C_HUMAN	P11142 homo sapien
31	1097.5	83.5	646	1 HS7C_SAGOE	Q71U34 saguinus oe

ALIGNMENTS

32	1097	83.5	649	2	Q7ZVU1	Q7ZVU1 brachydanio
33	1096.5	83.4	646	2	Q6NZD0	Q6NZD0 mus musculu
34	1096.5	83.4	650	2	Q8AVE2	Q8AVE2 xenopus lae
35	1095	83.3	641	2	Q8NE72	Q8NE72 homo sapien
36	1094	83.3	631	2	Q801X8	Q801X8 carassius a
37	1092	83.1	282	2	Q91ZU5	Q91ZU5 mus musculu
38	1092	83.1	461	2	Q91ZU4	Q91ZU4 mus musculu
39	1092	83.1	552	2	Q9QWU1	Q9QWU1 mus musculu
40	1091.5	83.1	650	1	HS7C_BOVIN	P19120 bos taurus
41	1091	83.0	649	2	Q6TEQ5	Q6TEQ5 brachydanio
42	1090.5	83.0	655	2	Q6XVG4	Q6XVG4 chlamsy far
43	1089.5	82.9	650	2	Q76N60	Q76N60 paralichthy
44	1089	82.9	641	2	Q6MG67	Q6MG67 rattus norv
45	1088	82.8	649	1	HS7C_ICTPU	P47773 ictalurus p
46	1088	82.8	651	2	Q8UV14	Q8UV14 ambystoma m
47	1087	82.7	641	1	HS1A_RAT	P55063 rattus norv
48	1087	82.7	641	2	Q886B6	Q886B6 mus musculu
49	1086	82.6	644	2	Q7SZM7	Q7SZM7 cyprinus ca
50	1086	82.6	659	2	Q6RYT8	Q6RYT8 aequipecten
51	1085	82.6	641	1	HS7T_MOUSE	P16627 mus musculu
52	1084	82.5	651	1	HS70_ONCMY	P08108 oncorhynch
53	1078.5	82.1	646	2	Q738B5	Q738B5 gallus gall
54	1077	82.0	659	2	Q9XZJ2	Q9XZJ2 crassostrea
55	1074	81.7	345	2	Q23954	Q23954 dirofilaria
56	1073.5	81.7	650	2	Q73788	Q73788 paralichthy
57	1073.5	81.7	652	2	Q6AZH8	Q6AZH8 xenopus lae
58	1070	81.4	654	2	Q86QM8	Q86QM8 locusta mig
59	1070	81.4	655	2	Q6WAW3	Q6WAW3 locusta mig
60	1069	81.4	643	2	Q6PH56	Q6PH56 brachydanio
61	1067	81.2	658	2	Q7Z1W9	Q7Z1W9 crassostrea
62	1066	81.1	490	2	Q6QAN5	Q6QAN5 megachile r
63	1066	81.1	647	2	Q6PGX4	Q6PGX4 brachydanio
64	1064.5	81.0	656	2	Q81S62	Q81S62 cotesia rub
65	1064	81.0	634	2	Q7SX63	Q7SX63 gallus gall
66	1064	81.0	645	2	Q9NGK9	Q9NGK9 wuchereria
67	1064	81.0	649	2	P79984	P79984 brachydanio
68	1063.5	80.9	652	2	Q6GUA8	Q6GUA8 penaeus van
69	1063.5	80.9	652	2	Q71KW5	Q71KW5 penaeus mon
70	1063	80.9	335	2	Q17267	Q17267 brugia paha
71	1063	80.9	644	1	HS70_BRUMA	P27541 brugia mala
72	1060	80.7	583	2	Q6QAN4	Q6QAN4 megachile r
73	1059.5	80.6	639	1	HS72_HUMAN	P54652 homo sapien
74	1059.5	80.6	658	2	Q271Z1	Q271Z1 urechis cau
75	1058	80.5	645	1	HS70_PLEWA	Q1291 pleurodeles
76	1057.5	80.5	657	2	Q6RYT7	Q6RYT7 patinopecte
77	1056	80.4	228	2	Q61698	Q61698 mus musculu
78	1056	80.4	645	2	Q96541	Q96541 setaria dig
79	1055	80.3	649	2	Q6S4R6	Q6S4R6 macrobrachi
80	1054.5	80.3	633	1	HS72_MOUSE	P17156 mus musculu
81	1054.5	80.3	633	2	Q99KD7	Q99KD7 mus musculu
82	1054.5	80.3	633	2	Q66HL1	Q66HL1 rattus norv
83	1054	80.2	645	2	Q9NJB7	Q9NJB7 wuchereria
84	1052.5	80.1	646	2	Q94614	Q94614 mesocostoid
85	1052.5	80.1	650	2	Q81860	Q81860 heterodera
86	1052.5	80.1	650	2	Q9GFK0	Q9GFK0 heterodera
87	1051	80.0	636	2	Q9TUG3	Q9TUG3 capra hircu
88	1050	79.9	623	2	Q801X9	Q801X9 carassius a
89	1050	79.9	634	1	HS70_CHICK	P08106 gallus gall
90	1049.5	79.9	640	2	Q93240	Q93240 paralichthy
91	1049	79.8	634	2	Q8AYL6	Q8AYL6 numida mele
92	1048	79.8	649	2	Q86MC3	Q86MC3 balanus amp
93	1047.5	79.7	633	1	HS72_RAT	P14659 rattus norv
94	1045.5	79.6	656	2	Q7PYR5	Q7PYR5 anopheles g
95	1043.5	79.4	652	1	HS7D_MANSE	Q96339 manduca sex
96	1043	79.4	631	1	HS73_BOVIN	P34933 bos taurus
97	1042.5	79.3	639	2	Q73922	Q73922 oreochromis
98	1042.5	79.3	644	1	HS70_ONCTS	Q12333 oncorhynch
99	1042	79.3	653	2	Q17310	Q17310 ceratitis c
100	1041.5	79.3	650	2	Q8ITL5	Q8ITL5 chironomus

RESULT 1

HS71_HUMAN STANDARD; PRT; 641 AA.

AC P08107; P19790; Q9UOL9; Q9UQW0;

DT 01-AUG-1988 (Rel. 08, Created)

DT 01-FEB-1994 (Rel. 28, Last sequence update)

DT 25-OCT-2004 (Rel. 45, Last annotation update)

DE Heat shock 70 kDa protein 1 (HSP70.1) (HSP70-1/HSP70-2).

GN Name=HSPA1A; Synonyms=HSPAL;

GN and

GN Name=HSPA1B;

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A. (HSPA1A AND HSPA1B).

RX MEDLINE=91055806; PubMed=1700760;

RA Milner C.M., Campbell R.D.;

RT "Structure and expression of the three MHC-linked HSP70 genes.";

RL Immunogenetics 32:242-251(1990).

RN [2]

RP SEQUENCE FROM N.A.

RX MEDLINE=86016721; PubMed=3931075;

RA Hunt C., Morimoto R.I.;

RT "Conserved features of eukaryotic hsp70 genes revealed by comparison with the nucleotide sequence of human hsp70.";

RL Proc. Natl. Acad. Sci. U.S.A. 82:6455-6459(1985).

RN [3]

RP SEQUENCE FROM N.A. (HSPA1A AND HSPA1B).

RA Rowen L., Madan A., Qin S., Shaffer T., James R., Ratcliffe A.,

RA Abbasi N., Dickhoff R., Loretz C., Madan A., Dors M., Young J.,

RA Laskey S., Hood L.;

RT "Sequence of the human major histocompatibility complex class III region.";

RL Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.

RN [4]

RP SEQUENCE FROM N.A. (HSPA1A AND HSPA1B).

RA Shiina S., Tamiya G., Oka A., Inoko H.;

RT "Homo sapiens 2,229,817bp genomic DNA of 6p21.3 HLA class I region.";

RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.

RN [5]

RP SEQUENCE FROM N.A.

RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

RA Stapleton M., Soares M.B., Donald M.F., Casavant T.L., Scheetz T.E.,

RA Brownstein M.J., Udwin T.B., Toshiyuki S., Carninci P., Frange C.,

RA Raha S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,

RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

RA Fahey J., Heiton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,

RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

RA Blakesley R.W., Truchman J.W., Green E.D., Dickson M.C.,

RA Rodriguez A.C., Glickman J.J., Schmutz J., Myers R.M.,

RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalilus D.E.,

RA Schnurch A., Schein J.E., Jones S.J.M., Marra M.A.;

RT "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences.";

RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).

RN [6]

RP SEQUENCE OF 1-36 AND 360-424 FROM N.A.

RX MEDLINE=89184548; PubMed=2538825;

RA Sargent C.A., Dunham I., Trowsdale J., Campbell R.D.;

RT "Human major histocompatibility complex contains genes for the major heat shock protein HSP70.";

RL Proc. Natl. Acad. Sci. U.S.A. 86:1968-1972(1989).

RN [7]

RP SEQUENCE OF 1-22 AND 618-641 FROM N.A.

RX MEDLINE=87066768; PubMed=3786141;

RA Drabant B., Genthe A., Beneske B.-J.;

RT "In vitro transcription of a human hsp 70 heat shock gene by extracts prepared from heat-shocked and non-heat-shocked human cells.";

RL Nucleic Acids Res. 14:8933-8948(1986).

RN [8]

RP X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS) OF 1-382.

RX MEDLINE=99234376; PubMed=10216320; DOI=10.1107/S0907444999002103;

RA Osipiuk J., Walsh M.A., Freeman B.C., Morimoto R.I., Joachimiak A.;

RT "Structure of a new crystal form of human hsp70 ATPase domain.";

RL Acta Crystallogr. D 55:1105-1107(1999).

CC -I- FUNCTION: In cooperation with other chaperones, HSP70s stabilize preexistent proteins against aggregation and mediate the folding of newly translated polypeptides in the cytosol as well as within organelles. The HSP70s in mitochondria and the endoplasmic reticulum play an additional role by providing a driving force for protein translocation. They are involved in signal transduction pathways in cooperation with HSP90. They participate in all these processes through their ability to recognize nonnative conformations of other proteins. They bind extended peptide segments with a net hydrophobic character exposed by polypeptides during translation and membrane translocation, or following stress-induced damage.

CC -I- INDUCTION: By heat shock.

CC -I- SIMILARITY: Belongs to the heat shock protein 70 family.

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DR EMBL; M59828; AAA63226.1; -

DR EMBL; M59830; AAA63227.1; -

DR EMBL; AF134726; AAD21816.1; -

DR EMBL; AF134726; AAD21815.1; -

DR EMBL; AP000503; BAB63300.1; -

DR EMBL; AP000503; BAB63299.1; -

DR EMBL; M11717; AAA52697.1; -

DR EMBL; BC002453; AAH02453.1; -

DR EMBL; BC009322; AAH09322.1; -

DR EMBL; BC018740; AAH18740.1; -

DR EMBL; M24743; AAA59844.1; -

DR EMBL; M24744; AAA59845.1; -

DR EMBL; X04676; CAA28381.1; -

DR EMBL; X04677; CAA28382.1; -

DR PIR; A29160; A29160.

DR PIR; A45871; A45871.

DR PIR; I59139; I59139.

DR PIR; I79540; I79540.

DR PDB; 1H3O; X-ray; A=3-382.

DR PDB; 1S3X; X-ray; A=1-382.

DR SWISS-2DPAGE; P08107; HUMAN.

DR OGP; P08107; -

DR Genew; HGNC:5232; HSPA1A.

DR Genew; HGNC:5233; HSPA1B.

DR H-InvDB; HIX0005733; -

DR H-InvDB; HIX0005734; -

DR MIM; 140550; -

DR GO; GO:0005737; C:cytoplasm; TAS.

DR GO; GO:0005634; C:nucleus; TAS.

DR GO; GO:0003773; F:heat shock protein activity; TAS.

DR GO; GO:0006402; P:mRNA catabolism; TAS.

DR InterPro; IPR001023; Hsp70.

DR Pfam; PF00012; Hsp70; 1.

DR PRINTS; PR00301; HEATSHOCK70.

DR ProDom; PD000089; Hsp70; 1.

DR TIGRFAMs; TIGR01991; HscA; 1.

DR PROSITE; PS00297; HSP70_1; 1.
DR PROSITE; PS00329; HSP70_2; 1.
DR PROSITE; PS01036; HSP70_3; 1.
KW 3D-structure; ATP-binding; Chapterone; Heat shock; Multigene family.
FT CONFLICT 7 7
FT CONFLICT 110 110
FT CONFLICT 370 370
FT CONFLICT 469 469
FT CONFLICT 499 499
FT STRAND 7 11
FT STRAND 15 22
FT TURN 23 24
FT STRAND 25 28
FT TURN 32 33
FT STRAND 38 39
FT STRAND 42 44
FT STRAND 49 51
FT TURN 52 52
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FT TURN 58 58
FT HELIX 59 61
FT HELIX 63 65
FT STRAND 66 67
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FT TURN 74 75
FT TURN 78 79
FT HELIX 81 87
FT TURN 88 89
FT STRAND 93 97
FT TURN 98 99
FT STRAND 100 107
FT TURN 108 109
FT STRAND 110 114
FT HELIX 116 135
FT STRAND 141 146
FT TURN 148 149
FT HELIX 152 164
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FT TURN 226 227
FT HELIX 230 248
FT TURN 254 255
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FT TURN 274 276
FT STRAND 279 288
FT TURN 289 290
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FT HELIX 299 312
FT TURN 313 313
FT HELIX 314 323

Query Match 100.0%; Score 1314; DB 1; Length 641;
Best Local Similarity 100.0%; Pred. No. 3.9e-73;
Matches 258; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KSENVQDLLLDVAPLSGLGTAGVMTALIKRNSTIPTKTQITFTTYSNQPGLIQVY 60
Db 384 KSENVQDLLLDVAPLSGLGTAGVMTALIKRNSTIPTKTQITFTTYSNQPGLIQVY 443

Qy 61 EGERAMTKNNLLGRFELSGIPAPRGVPOIEVTFDIDANGILNVTATDKSTGKANKITI 120
Db 444 EGERAMTKNNLLGRFELSGIPAPRGVPOIEVTFDIDANGILNVTATDKSTGKANKITI 503

Qy 121 TNDKGRLSKEEIERMVQEAKEYKAEDVQRRVSAKNALESYAFNMKSAVEDEGLKGKIS 180
Db 504 TNDKGRLSKEEIERMVQEAKEYKAEDVQRRVSAKNALESYAFNMKSAVEDEGLKGKIS 563

Qy 181 EADKKKVLDCQEVISWLDANTLAEKDFEHHKKELEQVCNPIISGLYQAGGPGGFG 240
Db 564 EADKKKVLDCQEVISWLDANTLAEKDFEHHKKELEQVCNPIISGLYQAGGPGGFG 623

Qy 241 AQPCKGSGSGPTIEVD 258
Db 624 AQPCKGSGSGPTIEVD 641

RESULT 2
Q6S4N2 ID Q6S4N2 PRELIMINARY; PRT; 641 AA.
AC Q6S4N2;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Heat shock protein 70.2.
GN Name=hsp70.2;
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE FROM N.A.
RA Chen M.Y., Lee W.C.;
RL Submitted (NOV-2003) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: Belongs to the heat shock protein 70 family.
DR EMBL; AY466608; AAR30953.1; -.
DR HSP; P19120; IBA1.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0006457; P:protein folding; IEA.
DR GO; GO:0006986; P:response to unfolded protein; IEA.
DR InterPro; IPR001023; Hsp70.
DR Pfam; PF00012; HSP70; 1.
DR PRINTS; PR00301; HEATSHOCK70.
DR ProDom; PD000089; Hsp70; 1.
DR PROSITE; PS00297; HSP70_1; 1.
DR PROSITE; PS00329; HSP70_2; 1.
DR PROSITE; PS01036; HSP70_3; 1.
KW ATP-binding; Heat shock;
SQ SEQUENCE 641 AA; 70098 MW; 9B49BF380AF0E2A CRC64;

Query Match 98.6%; Score 1296; DB 2; Length 641;
Best Local Similarity 98.4%; Pred. No. 5.1e-72;
Matches 254; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 1 KSENVQDLLLDVAPLSGLGTAGVMTALIKRNSTIPTKTQITFTTYSNQPGLIQVY 60
Db 384 KSENVQDLLLDVAPLSGLGTAGVMTALIKRNSTIPTKTQITFTTYSNQPGLIQVY 443

Qy 61 EGERAMTKNNLLGRFELSGIPAPRGVPOIEVTFDIDANGILNVTATDKSTGKANKITI 120
Db 444 EGERAMTKNNLLGRFELSGIPAPRGVPOIEVTFDIDANGILNVTATDKSTGKANKITI 503

Qy 121 TNDKGRLSKEEIERMVQEAKEYKAEDVQRRVSAKNALESYAFNMKSAVEDEGLKGKIS 180
Db 504 TNDKGRLSKEEIERMVQEAKEYKAEDVQRRVSAKNALESYAFNMKSAVEDEGLKGKIS 563

Qy 181 EADKKKVLDCQEVISWLDANTLAEKDFEHHKKELEQVCNPIISGLYQAGGPGGFG 240
Db 564 EADKKKVLDCQEVISWLDANTLAEKDFEHHKKELEQVCNPIISGLYQAGGPGGFG 623

Qy 241 AQPCKGSGSGPTIEVD 258
Db 624 AQPCKGSGSGPTIEVD 641

RESULT 3
HS71_BOVIN
ID HS71_BOVIN STANDARD; PRT; 641 AA.
AC Q27975; Q27964;
DT 01-NOV-1997 (Rel. 35, Created)


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DR ProDom; PD000089; Hsp70; 1.
DR TIGRFAMs; TIGR01991; Hsca; 1.
DR PROSITE; PS00297; HSP70_1; 1.
DR PROSITE; PS00329; HSP70_2; 1.
DR PROSITE; PS01036; HSP70_3; 1.
KW ATP-binding; Chaperone; Heat shock; Multigene family.
SQ SEQUENCE 641 AA; 70228 MW; 229C19EBBFBF610DF CRC64;

Query Match          98.6%; Score 1295; DB 1; Length 641;
Best Local Similarity 98.8%; Pred. No. 5.9e-72;
Matches 255; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 KSENVQDLLLDVAPLSGLGLETAGGVMTALIKRNSTIPTKTQTQFTTYSNQPGLVLIQVY 60
Db KSENVQDLLLDVAPLSGLGLETAGGVMTALIKRNSTIPTKTQTQFTTYSNQPGLVLIQVY 443

Qy 61 EGERAMTKONLLGRFELSGIPAPRGVPOIEVTFDIDANGILNVTATDKSTGKANKITI 120
Db EGERAMTRDNNLLGRFELSGIPAPRGVPOIEVTFDIDANGILNVTATDKSTGKANKITI 503

Qy 121 TNDKGRLSKEEIERMWQEAERYKAEDVQERVSAKNALESYAFNMKSAYEDELGLKGKIS 180
Db TNDKGRLSKEEIERMWQEAERYKAEDVQERVSAKNALESYAFNMKSAYEDELGLKGKIS 563

Qy 181 EADKKVKLDKQCVISWLDANTLAEDKDEFEHKKELQVNCNPIISGLYQAGGPGGPGFG 240
Db EADKKVKLDKQCVISWLDANTLAEDKDEFEHKKELQVNCNPIISGLYQAGGPGGPGFG 623

Qy 241 AQPGKGGSGSGPTIEEVD 258
Db AQPGKGGSGSGPTIEEVD 641

RESULT 5
Q6DLW1 PRELIMINARY; PRT; 641 AA.
AC Q6DLW1
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DE 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Heat shock protein 70 kDa.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Cardiac muscle;
RA LakshmiKuttyamma A., Selvakumar P., Anderson D.H., Datla R.S.,
RA Sharma R.K.;
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: Belongs to the heat shock protein 70 family.
DR EMBL; AY662497; AAT75223.1; -.
DR GO; GO:0006457; P:protein folding; IEA.
DR GO; GO:0006986; P:response to unfolded protein; IEA.
DR InterPro; IPR001023; Hsp70.
DR Pfam; PF00012; HSP70; 1.
DR PRINTS; PR00301; HEATSHOCK70.
DR ProDom; PD000089; Hsp70; 1.
DR PROSITE; PS00297; HSP70_1; 1.
DR PROSITE; PS00329; HSP70_2; 1.
DR PROSITE; PS01036; HSP70_3; 1.
KW ATP-binding; Heat shock.
SQ SEQUENCE 641 AA; 70231 MW; 6B3F9E6B8E8FDFB0 CRC64;

Query Match          98.6%; Score 1295; DB 2; Length 641;
Best Local Similarity 98.8%; Pred. No. 5.9e-72;
Matches 255; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 KSENVQDLLLDVAPLSGLGLETAGGVMTALIKRNSTIPTKTQTQFTTYSNQPGLVLIQVY 60
Db KSENVQDLLLDVAPLSGLGLETAGGVMTALIKRNSTIPTKTQTQFTTYSNQPGLVLIQVY 443

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Qy 61 EGERAMTKONLLGRFELSGIPAPRGVPOIEVTFDIDANGILNVTATDKSTGKANKITI 120
Db EGERAMTRDNNLLGRFELSGIPAPRGVPOIEVTFDIDANGILNVTATDKSTGKANKITI 503

Qy 121 TNDKGRLSKEEIERMWQEAERYKAEDVQERVSAKNALESYAFNMKSAYEDELGLKGKIS 180
Db TNDKGRLSKEEIERMWQEAERYKAEDVQERVSAKNALESYAFNMKSAYEDELGLKGKIS 563

Qy 181 EADKKVKLDKQCVISWLDANTLAEDKDEFEHKKELQVNCNPIISGLYQAGGPGGPGFG 240
Db EADKKVKLDKQCVISWLDANTLAEDKDEFEHKKELQVNCNPIISGLYQAGGPGGPGFG 623

Qy 241 AQPGKGGSGSGPTIEEVD 258
Db AQPGKGGSGSGPTIEEVD 641

RESULT 6
Q7YQF7 PRELIMINARY; PRT; 641 AA.
AC Q7YQF7
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Heat-shock 70-kilodalton protein 1A.
GN Names=HSPA1A;
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22640451; PubMed=12755819;
RA Sugimoto M., Furuoka H., Sugimoto Y.;
RT "Deletion of one of the duplicated Hsp70 genes causes hereditary
RL myopathy of diaphragmatic muscles in Holstein-Friesian cattle.";
RL Anim. Genet. 34:191-197(2003).
CC -1- SIMILARITY: Belongs to the heat shock protein 70 family.
DR EMBL; AY149618; AAN78092.1; -.
DR EMBL; AY149619; AAN78094.1; -.
DR HSP; P08107; IS3X.
DR GO; GO:0005524; F:ATP binding; IEA.
DR InterPro; IPR001023; Hsp70.
DR Pfam; PF00012; HSP70; 1.
DR ProDom; PD000089; Hsp70; 1.
DR PROSITE; PS00297; HSP70_1; 1.
DR PROSITE; PS00329; HSP70_2; 1.
DR PROSITE; PS01036; HSP70_3; 1.
KW ATP-binding.
SQ SEQUENCE 641 AA; 70258 MW; 6FAC1F30540E80F9 CRC64;

Query Match          98.6%; Score 1295; DB 2; Length 641;
Best Local Similarity 98.8%; Pred. No. 5.9e-72;
Matches 255; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 KSENVQDLLLDVAPLSGLGLETAGGVMTALIKRNSTIPTKTQTQFTTYSNQPGLVLIQVY 60
Db KSENVQDLLLDVAPLSGLGLETAGGVMTALIKRNSTIPTKTQTQFTTYSNQPGLVLIQVY 443

Qy 61 EGERAMTKONLLGRFELSGIPAPRGVPOIEVTFDIDANGILNVTATDKSTGKANKITI 120
Db EGERAMTRDNNLLGRFELSGIPAPRGVPOIEVTFDIDANGILNVTATDKSTGKANKITI 503

Qy 121 TNDKGRLSKEEIERMWQEAERYKAEDVQERVSAKNALESYAFNMKSAYEDELGLKGKIS 180
Db TNDKGRLSKEEIERMWQEAERYKAEDVQERVSAKNALESYAFNMKSAYEDELGLKGKIS 563

Qy 181 EADKKVKLDKQCVISWLDANTLAEDKDEFEHKKELQVNCNPIISGLYQAGGPGGPGFG 240
Db EADKKVKLDKQCVISWLDANTLAEDKDEFEHKKELQVNCNPIISGLYQAGGPGGPGFG 623

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Qy 241 AQP6GSGSGPTIEVD 258
Db 624 AQP6GSGSGPTIEVD 641

RESULT 7
Q7YQC6 PRELIMINARY; PRT; 641 AA.
AC Q7YQC6;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Heat shock protein 70.
GN Name=hsp70;
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OX NCBI_TaxID=9615;
RN [1]
RP SEQUENCE FROM N.A.
RA Yamasaki M., Tajima M., Yamato O., Jeong J., Maede Y.;
RL Submitted (JUL-2003) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: Belongs to the heat shock protein 70 family.
DR EMBL; AB114672; BAC79353.1; -
DR EMBL; AB114673; BAC79354.1; -
DR EMBL; AB114674; BAC79355.1; -
DR EMBL; AB114675; BAC79356.1; -
DR HSP; P08107; I53X.
DR GO; GO:000524; F:ATP binding; IEA.
DR GO; GO:0006457; P:protein folding; IEA.
DR GO; GO:0006986; P:response to unfolded protein; IEA.
DR InterPro; IPR001023; Hsp70.
DR Pfam; PF00012; HSP70_1.
DR ProDom; PD000089; Hsp70_1.
DR PROSITE; PS00297; HSP70_1; 1.
DR PROSITE; PS00329; HSP70_2; 1.
DR PROSITE; PS01036; HSP70_3; 1.
DR ATP-binding; Heat shock.
KW ATP-binding; Heat shock.
SQ SEQUENCE 641 AA; 70070 MW; DID80C3689346C88 CRC64;

Query Match 98.2%; Score 1291; DB 2; Length 641;
Best Local Similarity 98.1%; Pred. No. 1e-71;
Matches 253; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 1 KSENVQDLLLDVAPLSGLGTAGVMTALIKRNSTIPTKTQITFTYSDNQPGVLIQVY 60
Db 384 KSENVQDLLLDVAPLSGLGTAGVMTALIKRNSTIPTKTQITFTYSDNQPGVLIQVY 443

Qy 61 EGERAMTKDNNLGRFELSGIPPPAPRGVPOIEVTFDIDANGILNVATDKSTGKANKITI 120
Db 444 EGERAMTRDNNLGRFELSGIPPPAPRGVPOIEVTFDIDANGILNVATDKSTGKANKITI 503

Qy 121 TNDKGRLSKEEIERMWQAEKKAEDVQERVSAKNALESYAFNMKSAVEDEGLKGKIS 180
Db 504 TNDKGRLSKEEIERMWQAEKKAEDVQERVSAKNALESYAFNMKSAVEDEGLKGKIS 563

Qy 181 EADKKVKLDKQEVISWLDANTLAEKDFEHRKELEQVNCNPIISGLYQAGGPGPGFG 240
Db 564 EADKKVKLDKQEVISWLDANTLAEKDFEHRKELEQVNCNPIISGLYQAGGPGPGFG 623

Qy 241 AQP6GSGSGPTIEVD 258
Db 624 AQP6GSGSGPTIEVD 641

RESULT 8
HS71_CERAE STANDARD; PRT; 638 AA.
AC HS71_CERAE
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Heat shock 70 kDa protein 1.

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GN Name=HSPAL;
OS Cercopithecus aethiops (Green monkey) (Grivet);
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
OC Cercopithecinae; Cercopithecus.
OX NCBI_TaxID=9534;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Kidney;
RX MEDLINE=95080396; PubMed=7988690; DOI=10.1016/0014-5793(94)01210-5;
RA Sains I., Angelidis C., Pagoulatos G., Lazaridis I.;
RT "The hsc70 gene which is slightly induced by heat is the main virus
RL inducible member of the hsp70 gene family.";
PBBS Lett. 355:282-286(1994).
CC -1- FUNCTION: In cooperation with other chaperones, HSP70s stabilize
CC preexistent proteins against aggregation and mediate the folding
CC of newly translated polypeptides in the cytosol as well as within
CC organelles. The HSP70s in mitochondria and the endoplasmic
CC reticulum play an additional role by providing a driving force for
CC protein translocation. They are involved in signal transduction
CC pathways in cooperation with HSP90. They participate in all these
CC processes through their ability to recognize nonnative
CC conformations of other proteins. They bind extended peptide
CC segments with a net hydrophobic character exposed by polypeptides
CC during translation and membrane translocation, or following
CC stress-induced damage.
CC -1- INDUCTION: By heat shock.
CC -1- SIMILARITY: Belongs to the heat shock protein 70 family.
CC
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CC
CC EMBL; X70684; CAA50019.1; -
CC PIR; S31766; S31766.
CC HSP; P08107; IHJO.
CC InterPro; IPR001023; Hsp70.
CC Pfam; PF00012; HSP70_1.
CC PRINTS; PR00301; HEATSHOCK70.
CC ProDom; PD000089; Hsp70_1.
CC TIGRfams; TIGR01991; Hsca; 1.
CC PROSITE; PS00297; HSP70_1; 1.
CC PROSITE; PS00329; HSP70_2; 1.
CC PROSITE; PS01036; HSP70_3; 1.
CC ATP-binding; Chaperone; Heat shock; Multigene family.
KW ATP-binding; Chaperone; Heat shock; Multigene family.
SQ SEQUENCE 638 AA; 69920 MW; D5076A0FFAB6AB3 CRC64;

Query Match 97.4%; Score 1279.5; DB 1; Length 638;
Best Local Similarity 98.1%; Pred. No. 5.3e-71;
Matches 253; Conservative 1; Mismatches 3; Indels 1; Gaps 1;

Qy 1 KSENVQDLLLDVAPLSGLGTAGVMTALIKRNSTIPTKTQITFTYSDNQPGVLIQVY 60
Db 382 KSENVQDLLLDVAPLSGLGTAGVMTALIKRNSTIPTKTQITFTYSDNQPGVLIQVY 441

Qy 61 EGERAMTKDNNLGRFELSGIPPPAPRGVPOIEVTFDIDANGILNVATDKSTGKANKITI 120
Db 442 EGERAMTKDNNLGRFELSGIPPPAPRGVPOIEVTFDIDANGILNVATDKSTGKANKITI 500

Qy 121 TNDKGRLSKEEIERMWQAEKKAEDVQERVSAKNALESYAFNMKSAVEDEGLKGKIS 180
Db 501 TNDKGRLSKEEIERMWQAEKKAEDVQERVSAKNALESYAFNMKSAVEDEGLKGKIS 560

Qy 181 EADKKVKLDKQEVISWLDANTLAEKDFEHRKELEQVNCNPIISGLYQAGGPGPGFG 240
Db 561 EADKKVKLDKQEVISWLDANTLAEKDFEHRKELEQVNCNPIISGLYQAGGPGPGFG 620

Qy 241 AQP6GSGSGPTIEVD 258
Db 624 AQP6GSGSGPTIEVD 258

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Db 621 AQGPKGGSGSGPTIEVD 638
RESULT 9
HS71_PIG
ID HS71_PIG STANDARD; PRT; 641 AA.
AC P34930;
DT 01-FEB-1994 (Rel. 28, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Heat shock 70 kDa protein 1 (HSP70.1).
GN Name=HSPAL;
OS Sus scrofa (pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=92175874; PubMed=1339404;
RA Peelman L.J., de Weghe A.R., Coppieters W.R., van Zeveren A.J.,
RT Bouquet Y.H.;
RL Immunogenetics 35:286-289(1992).
CC -1- FUNCTION: In cooperation with other chaperones, Hsp70s stabilize
CC of newly translated polypeptides in the cytosol as well as within
CC organelles. These chaperones participate in all these processes
CC through their ability to recognize nonnative conformations of
CC other proteins. They bind extended peptide segments with a net
CC hydrophobic character exposed by polypeptides during translation
CC and membrane translocation, or following stress-induced damage.
CC -1- SIMILARITY: Belongs to the heat shock protein 70 family.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; M69100; -; NOT_ANNOTATED_CDS.
DR PIR; S35718; S35718.
DR HSP; P08107; 1HJO.
DR InterPro; IPR001023; Hsp70.
DR Pfam; PF00012; HSP70; 1.
DR PRINTS; P00301; HEATSHOCK70.
DR PRODOM; PD000089; Hsp70; 1.
DR TIGRFAMs; TIGR01991; HscA; 1.
DR PROSITE; PS00297; HSP70_1; 1.
DR PROSITE; PS00329; HSP70_2; 1.
DR PROSITE; PS01036; HSP70_3; 1.
KW ATP-binding; Chaperone; Heat shock; Multigene family.
SQ SEQUENCE 641 AA; 70083 MW; FE77BE20A03E0A33 CRC64;

Query Match 97.3%; Score 1279; DB 1; Length 641;
Best Local Similarity 97.3%; Pred. No. 5.7e-71;
Matches 251; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

Qy 1 KSENVQDLLLDVAPLSLGLETAGVMTALIKRSTIPTKTQITFTTYSNQPGLIQVY 60
Db 384 KSENVQDLLLDVAPLSLGLETAGVMTALIKRSTIPTKTQITFTTYSNQPGLIQVY 443
Qy 61 EGERAMTKNNLLGRFELSGIPPPAPRGVQIEVTFDIDANGILNVTATDKSTGKANKITI 120
Db 444 EGERAMTKNNLLGRFELSGIPPPAPRGVQIEVTFDIDANGILNVTATDKSTGKANKITI 503
Qy 121 TNDKGRLSKEIERMVOEAEKYKAEDVQERVSNAKNALESYAFNMKSAVEDEGLKGKIS 180
Db 504 TNDKGRLSKEIERMVOEAEKYKAEDVQERVSNAKNALESYAFNMKSAVEDEGLKGKIS 563
Qy 181 EADKKKVLDCQEVISWLDANTLAEKDFEHRKLEQVNCNPIISGLYQAGGPGGFG 240
Db 181 EADKKKVLDCQEVISWLDANTLAEKDFEHRKLEQVNCNPIISGLYQAGGPGGFG 240
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Db 564 EADKKKVLDCQEVISWLDANTLAEKDFEHRKLEQVNCNPIISGLYQAGGPGGFG 623
Qy 241 AQGPKGGSGSGPTIEVD 258
Db 624 APDLKGGSGSGPTIEVD 641
RESULT 10
Q8WNS9
ID Q8WNS9 PRELIMINARY; PRT; 640 AA.
AC Q8WNS9;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Heat shock protein 70.
GN Name=hsp70;
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OX NCBI_TaxID=9615;
RN [1]
RP SEQUENCE FROM N.A.
RA Abe K., Kano R., Hasegawa A.;
RL Submitted (NOV-2001) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: Belongs to the heat shock protein 70 family.
DR EMBL; AB075027; BAB78505.1; -.
DR HSP; P08107; 1S3X.
DR GO; GO:0005524; P:ATP binding; IEA.
DR GO; GO:0006457; P:protein folding; IEA.
DR GO; GO:0006986; P:response to unfolded protein; IEA.
DR Pfam; PF00012; HSP70; 1.
DR PRINTS; PR00301; HEATSHOCK70.
DR PRODOM; PD000089; Hsp70; 1.
DR PROSITE; PS00297; HSP70_1; 1.
DR PROSITE; PS00329; HSP70_2; 1.
DR PROSITE; PS01036; HSP70_3; 1.
KW ATP-binding; Heat shock.
SQ SEQUENCE 640 AA; 69934 MW; 402F3E91871BF87F CRC64;

Query Match 95.8%; Score 1258.5; DB 2; Length 640;
Best Local Similarity 96.5%; Pred. No. 1.1e-69;
Matches 249; Conservative 3; Mismatches 5; Indels 1; Gaps 1;

Qy 1 KSENVQDLLLDVAPLSLGLETAGVMTALIKRSTIPTKTQITFTTYSNQPGLIQVY 60
Db 384 KSENVQDLLLDVAPLSLGLETAGVMTAL-SRNSTIPTKTQITFTTYSNQPGLIQVY 442
Qy 61 EGERAMTKNNLLGRFELSGIPPPAPRGVQIEVTFDIDANGILNVTATDKSTGKANKITI 120
Db 443 EGERAMTKNNLLGRFELSGIPPPAPRGVQIEVTFDIDANGILNVTATDKSTGKANKITI 502
Qy 121 TNDKGRLSKEIERMVOEAEKYKAEDVQERVSNAKNALESYAFNMKSAVEDEGLKGKIS 180
Db 503 TNDKGRLSKEIERMVOEAEKYKAEDVQERVSNAKNALESYAFNMKSAVEDEGLKGKIS 562
Qy 181 EADKKKVLDCQEVISWLDANTLAEKDFEHRKLEQVNCNPIISGLYQAGGPGGFG 240
Db 563 EADKKKVLDCQEVISWLDGFTLAEKDFEHRKLEQVNCNPIITGLYQAGGPGGFG 622
Qy 241 AQGPKGGSGSGPTIEVD 258
Db 623 AQAPKGGSGSGPTIEVD 640
RESULT 11
HS71_RAT
ID HS71_RAT STANDARD; PRT; 641 AA.
AC Q07439; P42853;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Heat shock 70 kDa protein 1/2 (HSP70.1/2).
GN Name=Hsp70-1;
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GN and
 OS Name=Hsp70-2;
 OC Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OC NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Brain;
 RX MEDLINE=94096443; PubMed=8271311;
 RA Longo F.M., Wang S., Narasimhan P., Zhang J.S., Chen J., Massa S.M.,
 RA Sharp F.R.;
 RT "cDNA cloning and expression of stress-inducible rat hsp70 in normal
 RT and injured rat brain.";
 RL J. Neurosci. Res. 36:325-335 (1993).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=LEW.1W/GUN;
 RX MEDLINE=95012453; PubMed=7927536;
 RA Walter L., Rauh P., Guenther E.;
 RT "Comparative analysis of the three major histocompatibility complex-
 RT linked heat shock protein 70 (Hsp70) genes of the rat.";
 RL Immunogenetics 40:325-330 (1994).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Sprague-Dawley; TISSUE=Liver;
 RX MEDLINE=94368874; PubMed=8086479; DOI=10.1016/0167-4781(94)90247-X;
 RA Lisowska K., Krawczyk Z., Widiak W., Wolniczek P., Wisniewski J.;
 RT "Cloning, nucleotide sequence and expression of rat heat inducible
 RT hsp70 gene.";
 RL Biochim. Biophys. Acta 1219:64-72 (1994).
 CC -1- FUNCTION: In cooperation with other chaperones, Hsp70s stabilize
 CC preexistent proteins against aggregation and mediate the folding
 CC of newly translated polypeptides in the cytosol as well as within
 CC organelles. These chaperones participate in all these processes
 CC through their ability to recognize nonnative conformations of
 CC other proteins. They bind extended peptide segments with a net
 CC hydrophobic character exposed by polypeptides during translation
 CC and membrane translocation, or following stress-induced damage.
 CC -1- INDUCTION: By heat shock.
 CC -1- SIMILARITY: Belongs to the heat shock protein 70 family.
 CC
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 DR EMBL; L16764; AAA17441.1; -;
 DR EMBL; X77208; CAA54423.1; -;
 DR EMBL; X77207; CAA54422.1; -;
 DR EMBL; X74271; CAA52328.1; -;
 DR PIR; I54542; I54542.
 DR HSP; P08107; IHQO.
 DR InterPro; IPR001023; Hsp70.
 DR Pfam; PF00012; HSP70; 1.
 DR PRINTS; PR00301; HEATSHOCK70.
 DR ProDom; PD000089; Hsp70; 1.
 DR TIGRFAMs; TIGR01991; Hsca; 1.
 DR PROSITE; PS00297; HSP70_1; 1.
 DR PROSITE; PS00329; HSP70_2; 1.
 DR PROSITE; PS01036; HSP70_3; 1.
 DR ATP-binding; Chaperone; Heat shock; Multigene family.
 KW CONFLICT 71 72 KR -> NG (in Ref. 3).
 FT CONFLICT 227 227 D -> H (in Ref. 2 and 3).
 FT CONFLICT 408 408 G -> A (in Ref. 3).
 SQ SEQUENCE 641 AA; 70163 NW; D02D96751C868583 CRC64;
 Query Match 95.7%; Score 1258; DB 1; Length 641;
 Best Local Similarity 95.3%; Pred. No. 1.le-69;
 Matches 246; Conservative 7; Mismatches 5; Indels 0; Gaps 0;

QY 1 KSENVQDLLLLDVAPLSLGLETAGGVMTALIKRNSTIPTKTQTOIFTTYSNQPGLIQVY 60
 DB |||||
 384 KSENVQDLLLLDVAPLSLGLETAGGVMTALIKRNSTIPTKTQTOIFTTYSNQPGLIQVY 443
 QY 61 EGERAMTKDNLLGRFELSGIPAPRGVPOIEVTFDIDANGILNVATDKSTGKANKITI 120
 DB |||||
 444 EGERAMTRNNLLGRFELSGIPAPRGVPOIEVTFDIDANGILNVATDKSTGKANKITI 503
 QY 121 TNDKGRLSKEIERMVOEAKYKAEDVQERVSAKNALESYAFNMKSAVEDGLGKGIS 180
 DB |||||
 504 TNDKGRLSKEIERMVOEAKYKAEDVQERVSAKNALESYAFNMKSAVEDGLGKGIS 563
 QY 181 EADKKVKLDKQEVISWLDANTLAEKDEFEHKKRKELEQVCNPTIISGLYQAGGPGGFG 240
 DB |||||
 564 EADKKVKLDKQEVISWLDANTLAEKDEFEHKKRKELEQVCNPTIISGLYQAGGPGGFG 623
 QY 241 AQPKGSGSGGPTIERVD 258
 DB |||||
 624 AQPKGSGSGGPTIERVD 641
 RESULT 12
 Q63256 PRELIMINARY; PRT; 641 AA.
 ID Q63256 AC Q63256;
 DT 01-NOV-1996 (T-EMBLrel. 01, Created)
 DT 01-NOV-1996 (T-EMBLrel. 01, Last sequence update)
 DT 01-MAR-2004 (T-EMBLrel. 26, Last annotation update)
 DE Heat shock protein 70.
 GN Name=hsp 70;
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OC NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=wistar; TISSUE=Spleen;
 RX MEDLINE=94190258; PubMed=8141767;
 RA Mestril R., Chi S.H., Sayen M.R., Dillmann W.H.;
 RT "Isolation of a novel inducible rat heat shock protein (HSP70) gene
 RT and its expression during ischaemia/hypoxia and heat shock.";
 RL Biochem. J. 298:561-569 (1994).
 CC -1- SIMILARITY: Belongs to the heat shock protein 70 family.
 DR EMBL; X75357; CAA53140.1; -;
 DR PIR; I54542; I54542.
 DR HSP; P08107; I53X.
 DR GO; GO:0005524; P:ATP binding; IEA.
 DR GO; GO:0006457; P:protein folding; IEA.
 DR GO; GO:0006986; P:response to unfolded protein; IEA.
 DR InterPro; IPR001023; Hsp70.
 DR Pfam; PF00012; HSP70; 1.
 DR PRINTS; PR00301; HEATSHOCK70.
 DR ProDom; PD000089; Hsp70; 1.
 DR PROSITE; PS00297; HSP70_1; 1.
 DR PROSITE; PS01036; HSP70_3; 1.
 KW ATP-binding; Heat shock.
 SQ SEQUENCE 641 AA; 69977 MW; A3A1223439AB2D03 CRC64;
 Query Match 95.7%; Score 1258; DB 2; Length 641;
 Best Local Similarity 95.3%; Pred. No. 1.le-69;
 Matches 246; Conservative 7; Mismatches 5; Indels 0; Gaps 0;

QY 1 KSENVQDLLLLDVAPLSLGLETAGGVMTALIKRNSTIPTKTQTOIFTTYSNQPGLIQVY 60
 DB |||||
 384 KSENVQDLLLLDVAPLSLGLETAGGVMTALIKRNSTIPTKTQTOIFTTYSNQPGLIQVY 443
 QY 61 EGERAMTKDNLLGRFELSGIPAPRGVPOIEVTFDIDANGILNVATDKSTGKANKITI 120
 DB |||||
 444 EGERAMTRNNLLGRFELSGIPAPRGVPOIEVTFDIDANGILNVATDKSTGKANKITI 503
 QY 121 TNDKGRLSKEIERMVOEAKYKAEDVQERVSAKNALESYAFNMKSAVEDGLGKGIS 180
 DB |||||

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Db 504 TNDKGRLSKEIERMVOEAERYKAEDVQVRRVAAKNALAESYAFNMKSAVEDEGLKGKIS 563
Qy 181 EADKKVKLDKQOEIVSWLDANTLAEKORFEHKKRKELEQVCNPIISGLYQGAGGPGGFG 240
Db 564 EADKKVKLDKQOEIVSWLDNSNTLAEKEEFVHKREBELRVCNPIISGLYQGAGGPGGFG 623
Qy 241 AQGPKGSGSGPTTIEVD 258
Db 624 AQAPKGSAGSGPTTIEVD 641

RESULT 13
Q9QWJ5 PRELIMINARY; PRT; 641 AA.
ID Q9QWJ5;
AC Q9QWJ5;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DE 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
DE HSP70.
GN Name=H2-Bf;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_taxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=129;
RX PubMed=14656967; DOI=10.1101/gr.1736803;
RA Xie T., Rowen L., Aguado B., Ahearn M.E., Madan A., Qin S.,
RA Campbell R.D., Hood L.;
RT "Analysis of the gene-dense major histocompatibility complex class III
RL region and its comparison to mouse.";
CC Genome Res. 13:2621-2636(2003).
-1- SIMILARITY: Belongs to the heat shock protein 70 family.
DR EMBL; AF109906; AAC84169.1; --
DR HSP; P08107; IHJO.
DR MGP; MGI:105975; H2-Bf.
DR GO; GO:0005524; F:ATP binding; IEA.
DR InterPro; IPR001023; Hsp70.
DR Pfam; PF00012; Hsp70; 1.
DR PRINTS; PR00301; HEATSHOCK70.
DR ProDom; PD000089; Hsp70; 1.
DR PROSITE; PS00297; Hsp70_1; 1.
DR PROSITE; PS00329; Hsp70_2; 1.
DR PROSITE; PS01036; Hsp70_3; 1.
KW ATP-binding.
SQ SEQUENCE 641 AA; 70079 MW; F49C333E602EAE334 CRC64;

Query Match 94.3%; Score 1239; DB 2; Length 641;
Best Local Similarity 93.4%; Pred. No. 1.7e-68;
Matches 241; Conservative 11; Mismatches 6; Indels 0; Gaps 0;

Qy 1 KSENVQDLLLDVAPLSGLTAGVMTALIKRNSTIPTKTQTFTTYSNDQPGVLIQVY 60
Db 384 KSENVQDLLLDVAPLSGLTAGVMTALIKRNSTIPTKTQTFTTYSNDQPGVLIQVY 443

Qy 61 EGERAMTKDNLLGRFELSGIPPPAPRGVPQIEVTFDIDANGILNVATDKSTGKANKITI 120
Db 444 EGERAMTFDNNLLGRFELSGIPPPAPRGVPQIEVTFDIDANGILNVATDKSTGKANKITI 503

Qy 121 TNDKGRLSKEIERMVOEAERYKAEDVQVRRVAAKNALAESYAFNMKSAVEDEGLKGKIS 180
Db 504 TNDKGRLSKEIERMVOEAERYKAEDVQVRRVAAKNALAESYAFNMKSAVEDEGLKGKIS 563

Qy 181 EADKKVKLDKQOEIVSWLDANTLAEKORFEHKKRKELEQVCNPIISGLYQGAGGPGGFG 240
Db 564 EADKKVKLDKQOEIVSWLDNSNTLAEKEEFVHKREBELRVCNPIISGLYQGAGGPGGFG 623
Qy 241 AQGPKGSGSGPTTIEVD 258
Db 624 AQAPKGSAGSGPTTIEVD 641
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RESULT 14
Q7TQD8 PRELIMINARY; PRT; 641 AA.
ID Q7TQD8;
AC Q7TQD8;
DT 01-OCT-2003 (TREMBLrel. 25, Created)
DT 01-OCT-2003 (TREMBLrel. 25, Last sequence update)
DE 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
DE Heat shock protein 1A.
GN Name=Hspalpa;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_taxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6; TISSUE=Brain;
RX MEDLINE=22389257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heideh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullihy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Greenwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
[2]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6; TISSUE=Brain;
RA Strausberg R.;
RL Submitted (JUL-2003) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: Belongs to the heat shock protein 70 family.
DR EMBL; BC054782; AAH54782.1; -.
DR HSSP; P08107; IHJO.
DR GO; GO:0006281; P:DNA repair; IMP.
DR GO; GO:0009408; P:response to heat; IMP.
DR GO; GO:0000723; P:telomere maintenance; IMP.
DR InterPro; IPR001023; Hsp70.
DR Pfam; PF00012; Hsp70; 1.
DR ProDom; PD000089; Hsp70; 1.
DR PROSITE; PS00297; Hsp70_1; 1.
DR PROSITE; PS00329; Hsp70_2; 1.
DR PROSITE; PS01036; Hsp70_3; 1.
KW ATP-binding; Heat shock.
SQ SEQUENCE 641 AA; 70093 MW; F49B439372C8E364 CRC64;

Query Match 94.1%; Score 1236; DB 2; Length 641;
Best Local Similarity 93.0%; Pred. No. 2.6e-68;
Matches 240; Conservative 12; Mismatches 6; Indels 0; Gaps 0;

Qy 1 KSENVQDLLLDVAPLSGLTAGVMTALIKRNSTIPTKTQTFTTYSNDQPGVLIQVY 60
Db 384 KSENVQDLLLDVAPLSGLTAGVMTALIKRNSTIPTKTQTFTTYSNDQPGVLIQVY 443

Qy 61 EGERAMTKDNLLGRFELSGIPPPAPRGVPQIEVTFDIDANGILNVATDKSTGKANKITI 120
Db 444 EGERAMTRDNNLLGRFELSGIPPPAPRGVPQIEVTFDIDANGILNVATDKTGTGKANKITI 503

Qy 121 TNDKGRLSKEIERMVOEAERYKAEDVQVRRVAAKNALAESYAFNMKSAVEDEGLKGKIS 180
Db 504 TNDKGRLSKEIERMVOEAERYKAEDVQVRRVAAKNALAESYAFNMKSAVEDEGLKGKIS 563
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QY 181 EADKKVLDKQEVISWLDANTLAELKDFEHKRELBOVCNPIISGLYQAGAGPGGFG 240
DB 564 EADKKVLDKQEVISWLDNTLADKEEFVHKRELERVCSPISGLYQAGAGPGGFG 623
QY 241 AQGPKGSGSGPTIEVD 258
DB 624 AQAPKGSGSGPTIEVD 641

RESULT 15
HS71_MOUSE
ID HS71_MOUSE STANDARD; PRT; 642 AA.
AC P17879; Q61689; Q925V6;
DT 01-AUG-1990 (Rel. 15, Created)
DT 29-MAR-2004 (Rel. 43, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Heat shock 70 kDa protein 1 (HSP70.1) (HSP70-1/HSP70-2).
GN Name=Hspal; Synonyms=Hsp70.1, Hsp70-1, Hsp70a1;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=90236310; PubMed=2332169; DOI=10.1016/0378-1119(90)90302-8;
RA Hunt C., Calderwood S.;
RT "Characterization and sequence of a mouse hsp70 gene and its
expression in mouse cell lines.";
RL Gene 87:199-204(1990).
RN [2]
RP SEQUENCE FROM N.A.
RX TISSUE=Liver;
RX MEDLINE=94357449; PubMed=8076831; DOI=10.1016/0378-1119(94)90305-0;
RA Perry M.D., Aujame L., Shtang S., Moran L.A.;
RT "Structure and expression of an inducible HSP70-encoding gene from Mus
musculus.";
RL Gene 146:273-278(1994).
RN [3]
RP SEQUENCE FROM N.A.
RX STRAIN=129;
RA Rowen L., Madan A., Qin S., Hall J., Dahl T., James R., Dickhoff R.,
Schaffer T., Ratcliffe A., Abbasi N., Loretz C., Lasky S., Hood L.;
RT "Sequence of the mouse MHC class III region.";
RL Submitted (NOV-1998) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: In cooperation with other chaperones, Hsp70s stabilize
of newly translated polypeptides in the cytosol as well as within
other proteins. They bind extended peptide segments with a net
hydrophobic character exposed by polypeptides during translation
and membrane translocation, or following stress-induced damage.
CC -!- SIMILARITY: Belongs to the heat shock protein 70 family.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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or send an email to license@isb-sib.ch).
CC -----
CC EMBL; M35021; AAA37864.1; -
CC EMBL; W76613; AAA57233.1; -
CC EMBL; AF103906; AAC84168.1; -
CC HSSP; P08107; IHJ0.
CC MGD; MGI:99517; Hsp70-1.
CC GO; GO:0001719; P:inhibition of caspase activation; IDA.
CC InterPro; IPR001023; Hsp70.
CC Pfam; PF00012; HSP70; 1.
CC PRINTS; PR00301; HEATSHOCK70.
CC ProDom; PD000089; Hsp70; 1.
CC TIGRFAMs; TIGR01991; HSCA; 1.

DR PROSITE; PS00297; HSP70_1; 1.
DR PROSITE; PS00329; HSP70_2; 1.
DR PROSITE; PS01036; HSP70_3; 1.
KW ATP-binding; Chaperone; Heat shock; Multigene family.
FT CONFLICT 342 R->A (in Ref. 2).
FT CONFLICT 628 Missing (in Ref. 2).
SQ SEQUENCE 642 AA; 70176 MW; 4BB9B0B130C23D8B CRC64;

Query Match 93.5%; Score 1228.5; DB 1; Length 642;
Best Local Similarity 93.1%; Pred. No. 7.6e-68;
Matches 241; Conservative 11; Mismatches 6; Indels 1; Gaps 1;

QY 1 KSENVQDLLLDVAPLSGLGLETAGGVMTALIKRNPSTPTKQTFITYSDNPGVLIQVY 60
DB 384 KSENVQDLLLDVAPLSGLGLETAGGVMTALIKRNPSTPTKQTFITYSDNPGVLIQVY 443
QY 61 EGERATMKNNLLGRFELSGIPAPRGVQIETVFDIDANGILNVTTATDKSTGKANKITI 120
DB 444 EGERATMKNNLLGRFELSGIPAPRGVQIETVFDIDANGILNVTTATDKSTGKANKITI 503
QY 121 TNDKGRLSKEEIERMVOEAEKYKAEDVQERVSNAKNALESYAFNMKSAVEDGLKGKIS 180
DB 504 TNDKGRLSKEEIERMVOEAEKYKAEDVQERVSNAKNALESYAFNMKSAVEDGLKGKIS 563
QY 181 EADKKVLDKQEVISWLDANTLAELKDFEHKRELBOVCNPIISGLYQAGAGPGGFG 240
DB 564 EADKKVLDKQEVISWLDNTLADKEEFVHKRELERVCSPISGLYQAGAGPGGFG 623
QY 241 AQGPKGSGSGPTIEVD 258
DB 624 AQAPKGSGSGPTIEVD 642

RESULT 16
HS1A_MOUSE
ID HS1A_MOUSE STANDARD; PRT; 420 AA.
AC Q61696; Q61697;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Heat shock protein 1A (Heat shock 70 kDa protein 3) (HSP70.3)
DE (Fragment).
GN Name=Hspal; Synonyms=Hsp70-3, Hsp70a1;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=86111900; PubMed=2868009;
RA Lowe D.G., Moran L.A.;
RT "Molecular cloning and analysis of DNA complementary to three mouse Mr
= 68,000 heat shock protein mRNAs.";
RL J. Biol. Chem. 261:2102-2112(1986).
RN [2]
RP SEQUENCE OF 155-420 FROM N.A.
RX MEDLINE=94357449; PubMed=8076831; DOI=10.1016/0378-1119(94)90305-0;
RA Perry M.D., Aujame L., Shtang S., Moran L.A.;
RT "Structure and expression of an inducible HSP70-encoding gene from Mus
musculus.";
RL Gene 146:273-278(1994).
CC -!- FUNCTION: In cooperation with other chaperones, Hsp70s stabilize
of newly translated polypeptides in the cytosol as well as within
other proteins. These chaperones participate in all these processes
through their ability to recognize nonnative conformations of
other proteins. They bind extended peptide segments with a net
hydrophobic character exposed by polypeptides during translation
and membrane translocation, or following stress-induced damage.
CC -!- INDUCTION: By heat shock.
CC -!- SIMILARITY: Belongs to the heat shock protein 70 family.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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Qy 181 EADKKVLDKQEVISWLDANTLAEKDFEHRKLEQVNCNPIISGLYQAGGPGGFG 240
Db 566 ESDKNKILDKCNELLSWLVNQLAEKDFEHRKLEQVNCNPIITKLYQG-----G 616

Qy 241 AQPCKGSG-----SGPTIEEVD 258
Db 617 CTGPACGTGYVPRPATGPTIEEVD 641

RESULT 18
Q6Q1S4 PRELIMINARY; PRT; 650 AA.
AC Q6Q1S4;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Heat shock cognate 70 kDa protein.
GN Name=HSP70;
OS Pimphales promelas.
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Pimphales.
OX NCB1_TaxID=90988;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RA Lynn S.G., Scholik A.R., Yan H.Y., Shepherd B.S.;
RL Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: Belongs to the heat shock protein 70 family.
DR EMBL; AY538777; AAS46619.1; -.
DR HSP; P19120; IATR.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0006457; P:protein folding; IEA.
DR GO; GO:0006986; P:response to unfolded protein; IEA.
DR InterPro; IPR001023; Hsp70.
DR Pfam; PF00012; HSP70; 1.
DR PRINTS; PR00301; HEATSHOCK70.
DR PRODOM; PD000089; Hsp70; 1.
DR PROSITE; PS00297; HSP70_1; 1.
DR PROSITE; PS00329; HSP70_2; 1.
DR PROSITE; PS01036; HSP70_3; 1.
DR ATP-binding; Heat shock.
KW ATP-binding; Heat shock.
SQ SEQUENCE 650 AA; 71316 MW; 60D538BA36A2EEF4 CRC64;

Query Match 84.4%; Score 1108.5; DB 2; Length 650;
Best Local Similarity 82.8%; Pred. No. 2e-60;
Matches 221; Conservative 17; Mismatches 20; Indels 9; Gaps 4;

Qy 1 KSENVQDLLLDVAPLSGLGTAGGVTALIKRNSTIPTKTQTFTTYSNQPGVLIQVY 60
Db 384 KSENVQDLLLDVTPLSGLGTAGGVTALIKRNTTPTKTQTFTTYSNQPGVLIQVY 443

Qy 61 EGERAMTKDNLGRFELSGTPAPRGVPQIEVTFDIDANGILNVTATDKSTGKANKITI 120
Db 444 EGERAMTKDNLGLGKFLTGTPAPRGVPQIEVTFDIDANGIMNVSAVDKSTGKANKITI 503

Qy 121 TNDKGRLSKEIERMVOEAEKYKAEDVQERVSANALSYAFNMKSATVEDEGLKGKIS 180
Db 504 TNDKGRLSKEDIERMVOEAEKYKSEDDVQREKVSANGLSEYAFNMKSTVEDEKLKGKIS 563

Qy 181 EADKKVLDKQEVISWLDANTLAEKDFEHRKLEQVNCNPIISGLYQAGG-PG---- 235
Db 564 EEDKQKILDKCNELLSWLVNQLAEKDFEHRKLEQVNCNPIITKLYQAGGMPGGMPE 623

Qy 236 --PGGF-GAQG-PKGGSGSGPTIEEVD 258
Db 624 GMPGFFGAGAPGSGSGSGPTIEEVD 650

RESULT 19
Q804B6 PRELIMINARY; PRT; 649 AA.
ID Q804B6
AC Q804B6;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Heat shock cognate 70 kDa protein.
GN Name=HSP70;
OS Pimphales promelas.
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Pimphales.
OX NCB1_TaxID=90988;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RA Lynn S.G., Scholik A.R., Yan H.Y., Shepherd B.S.;
RL Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: Belongs to the heat shock protein 70 family.
DR EMBL; AY538777; AAS46619.1; -.
DR HSP; P19120; IATR.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0006457; P:protein folding; IEA.
DR GO; GO:0006986; P:response to unfolded protein; IEA.
DR InterPro; IPR001023; Hsp70.
DR Pfam; PF00012; HSP70; 1.
DR PRINTS; PR00301; HEATSHOCK70.
DR PRODOM; PD000089; Hsp70; 1.
DR PROSITE; PS00297; HSP70_1; 1.
DR PROSITE; PS00329; HSP70_2; 1.
DR PROSITE; PS01036; HSP70_3; 1.
DR ATP-binding; Heat shock.
KW ATP-binding; Heat shock.
SQ SEQUENCE 650 AA; 71316 MW; 60D538BA36A2EEF4 CRC64;

Query Match 84.4%; Score 1108.5; DB 2; Length 650;
Best Local Similarity 82.8%; Pred. No. 2e-60;
Matches 221; Conservative 17; Mismatches 20; Indels 9; Gaps 4;

Qy 1 KSENVQDLLLDVAPLSGLGTAGGVTALIKRNSTIPTKTQTFTTYSNQPGVLIQVY 60
Db 384 KSENVQDLLLDVTPLSGLGTAGGVTALIKRNTTPTKTQTFTTYSNQPGVLIQVY 443

Qy 61 EGERAMTKDNLGRFELSGTPAPRGVPQIEVTFDIDANGILNVTATDKSTGKANKITI 120
Db 444 EGERAMTKDNLGLGKFLTGTPAPRGVPQIEVTFDIDANGIMNVSAVDKSTGKANKITI 503

Qy 121 TNDKGRLSKEIERMVOEAEKYKAEDVQERVSANALSYAFNMKSATVEDEGLKGKIS 180
Db 504 TNDKGRLSKEDIERMVOEAEKYKSEDDVQREKVSANGLSEYAFNMKSTVEDEKLKGKIS 563

Qy 181 EADKKVLDKQEVISWLDANTLAEKDFEHRKLEQVNCNPIISGLYQAGG-PG---- 235
Db 564 EEDKQKILDKCNELLSWLVNQLAEKDFEHRKLEQVNCNPIITKLYQAGGMPGGMPE 623

Qy 236 --PGGF-GAQG-PKGGSGSGPTIEEVD 258
Db 624 GMPGFFGAGAPGSGSGSGPTIEEVD 650

RESULT 19
Q804B6 PRELIMINARY; PRT; 649 AA.
ID Q804B6
AC Q804B6;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Heat shock cognate 70 kDa protein.
GN Name=HSP70;
OS Pimphales promelas.
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Pimphales.
OX NCB1_TaxID=90988;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RA Lynn S.G., Scholik A.R., Yan H.Y., Shepherd B.S.;
RL Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: Belongs to the heat shock protein 70 family.
DR EMBL; AY538777; AAS46619.1; -.
DR HSP; P19120; IATR.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0006457; P:protein folding; IEA.
DR GO; GO:0006986; P:response to unfolded protein; IEA.
DR InterPro; IPR001023; Hsp70.
DR Pfam; PF00012; HSP70; 1.
DR PRINTS; PR00301; HEATSHOCK70.
DR PRODOM; PD000089; Hsp70; 1.
DR PROSITE; PS00297; HSP70_1; 1.
DR PROSITE; PS00329; HSP70_2; 1.
DR PROSITE; PS01036; HSP70_3; 1.
DR ATP-binding; Heat shock.
KW ATP-binding; Heat shock.
SQ SEQUENCE 650 AA; 71316 MW; 60D538BA36A2EEF4 CRC64;

Query Match 84.3%; Score 1108; DB 2; Length 649;
Best Local Similarity 82.3%; Pred. No. 2.2e-60;
Matches 219; Conservative 18; Mismatches 21; Indels 8; Gaps 3;

Qy 1 KSENVQDLLLDVAPLSGLGTAGGVTALIKRNSTIPTKTQTFTTYSNQPGVLIQVY 60
Db 384 KSENVQDLLLDVTPLSGLGTAGGVTALIKRNTTPTKTQTFTTYSNQPGVLIQVY 443

Qy 61 EGERAMTKDNLGRFELSGTPAPRGVPQIEVTFDIDANGILNVTATDKSTGKANKITI 120
Db 444 EGERAMTKDNLGLGKFLTGTPAPRGVPQIEVTFDIDANGIMNVSAVDKSTGKANKITI 503

Qy 121 TNDKGRLSKEIERMVOEAEKYKAEDVQERVSANALSYAFNMKSATVEDEGLKGKIS 180
Db 504 TNDKGRLSKEDIERMVOEAEKYKSEDDVQREKVSANGLSEYAFNMKSTVEDEKLKGKIS 563

Qy 181 EADKKVLDKQEVISWLDANTLAEKDFEHRKLEQVNCNPIISGLYQAGG-PG---- 235
Db 564 EEDKQKILDKCNELLSWLVNQLAEKDFEHRKLEQVNCNPIITKLYQAGGMPGGMPE 623

Qy 236 --PGGF-GAQG-PKGGSGSGPTIEEVD 258
Db 624 GMPGFFGAGAPGSGSGSGPTIEEVD 649

RESULT 20
Q7ZTK6 PRELIMINARY; PRT; 646 AA.
ID Q7ZTK6
AC Q7ZTK6;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE MGC53952 protein.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae;
OC Xenopodinae; Xenopus.
OX NCB1_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Embryo;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
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RA Altachul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Lequellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.G., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smalios D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE-Embryo;
RX MEDLINE=22341132; PubMed=12454917; DOI=10.1002/dvdy.10174;
RA Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,
RA Richardson P.;
RT "Genetic and genomic tools for Xenopus research: The NIH Xenopus
initiative.";
RL Dev. Dyn. 225:384-391(2002).
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE-Embryo;
RX Klein S., Strausberg R.;
RL Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: Belongs to the heat shock protein 70 family.
DR EMBL; BC046262; AAH46262.1; -.
DR HSSP; P19120; IATR.
DR GO; GO:0005524; P:ATP binding; IEA.
DR InterPro; IPR001023; Hsp70.
DR Pfam; PF00012; HSP70; 1.
DR PRINTS; PR00301; HEATSHOCK70.
DR ProDom; PD000089; Hsp70; 1.
DR PROSITE; PS00297; HSP70_1; 1.
DR PROSITE; PS00329; HSP70_2; 1.
DR PROSITE; PS01036; HSP70_3; 1.
KW ATP-binding.
SQ SEQUENCE 646 AA; 70791 MW; 08F72BEDD2C4D58D CRC64;

Query Match 83.9%; Score 1102.5; DB 2; Length 646;
Best Local Similarity 82.1%; Pred. No. 4.8e-60;
Matches 216; Conservative 22; Mismatches 20; Indels 5; Gaps 3;

Qy 1 KSENVQDLLLLDVAPLSIGLETAGVMTALIKRNSTIPTKTQITFTTYSNDQPGVLIQVY 60
Db 384 KSENVQDLLLLDVTPLSIGLETAGVMTVLKRNVTITPTKTQITFTTYSNDQPGVLIQVY 443

Qy 61 EGERAMTKDNNLLGRFELSGIPPPAPRGVQPIEVTFDIDANGILNVTATDKSTGKANKITI 120
Db 444 EGERAMTKDNNLLGKGFELTGIPPPAPRGVQPIEVTFDIDANGILNVTATDKSTGKANKITI 503

Qy 121 TNDKGRLSKEIERMVOEAEKYKAEDVQERVSNAKNALESYAFNMKSAVEDEGLKGIS 180
Db 504 TNDKGRLSKEDIERMVOEAEKYKAEDVQERVSNAKNALESYAFNMKSTVDEKLGKIS 563

Qy 181 EADKKVLDKQCVISWLDANTLAEKDFEHRKLEQVNCNPIISGLYQAGG-PG--PG 237
Db 504 TNDKGRLSKEDIERMVOEAEKYKAEDVQERVSNAKNALESYAFNMKSTVDEKLGKIS 563

Qy 181 EADKKVLDKQCVISWLDANTLAEKDFEHRKLEQVNCNPIISGLYQAGG-PG--PG 237
Db 564 DEDKQKILEKNEVSWLDKNQTAEREFHQKELEKVCNPIITKLYQAGGPGGMPG 623

Qy 238 GFAGAG--PKGSGSGGPTIEVD 258
Db 624 GFPGAGAPSGGASGSGPTIEVD 646

RESULT 21
HS7C_BRARE

HS7C_BRARE STANDARD; PRT; 649 AA.
AC Q90473;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Heat shock cognate 71 kDa protein.
GN Name=hsc70;
OS Brachydanio rerio (Zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97348566; PubMed=9204550;
RA Graser R.T., Mainar-Dragojevic D., Vincsek V.;
RT "Cloning and characterization of a 70 kd heat shock cognate (hsc70)
gene from the zebrafish (Danio rerio).";
RL Genetica 98:273-276(1996).
CC -!- SIMILARITY: Belongs to the heat shock protein 70 family.
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or send an email to license@isb-sib.ch).
CC -----
DR EMBL; L77146; AB03704.1; -.
DR HSSP; P08109; ICKR.
DR ZFIN; ZDB-GENE-990415-92; hsc70.
DR InterPro; IPR001023; Hsp70.
DR Pfam; PF00012; HSP70; 1.
DR PRINTS; PR00301; HEATSHOCK70.
DR ProDom; PD000089; Hsp70; 1.
DR TIGRFAMs; TIGR01991; HscA; 1.
DR PROSITE; PS00297; HSP70_1; 1.
DR PROSITE; PS00329; HSP70_2; 1.
DR PROSITE; PS01036; HSP70_3; 1.
KW ATP-binding; Heat shock; Multigene family.
SQ SEQUENCE 649 AA; 70974 MW; D486B85CA8E8938C CRC64;

Query Match 83.8%; Score 1101; DB 1; Length 649;
Best Local Similarity 81.6%; Pred. No. 5.9e-60;
Matches 217; Conservative 19; Mismatches 22; Indels 8; Gaps 3;

Qy 1 KSENVQDLLLLDVAPLSIGLETAGVMTALIKRNSTIPTKTQITFTTYSNDQPGVLIQVY 60
Db 384 KSENVQDLLLLDVTPLSIGLETAGVMTVLKRNVTITPTKTQITFTTYSNDQPGVLIQVY 443

Qy 61 EGERAMTKDNNLLGRFELSGIPPPAPRGVQPIEVTFDIDANGILNVTATDKSTGKANKITI 120
Db 444 EGERAMTKDNNLLGKGFELTGIPPPAPRGVQPIEVTFDIDANGIMVSAVDKSTGKANKITI 503

Qy 121 TNDKGRLSKEIERMVOEAEKYKAEDVQERVSNAKNALESYAFNMKSAVEDEGLKGIS 180
Db 504 TNDKGRLSKEDIERMVOEAEKYKAEDVQERVSNAKNALESYAFNMKSTVDEKLGKIS 563

Qy 181 EADKKVLDKQCVISWLDANTLAEKDFEHRKLEQVNCNPIISGLYQAGG-PG----- 235
Db 564 DEDKQKILDKNEVSWLDKNQTAEREFHQKELEKVCNPIITKLYQAGGPGGMPG 623

Qy 236 --PGGF--GAQPGKSGSGGPTIEVD 258
Db 624 GMPGPGFAGAPSGGSGSGGPTIEVD 649

RESULT 22
Q6NYR4
ID Q6NYR4 PRELIMINARY; PRT; 649 AA.
AC Q6NYR4;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)

05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
 Hsp88 protein.
 Name=hsp88;
 Brachydanio rerio (Zebrafish) (Danio rerio).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
 OC Cyprinidae; Danio.
 OX NCBI_TaxID=7955;
 [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Kidney, and Whole;
 RX MEDLINE=2238257; PubMed=12477932; DOI=10.1073/pnas.242603999;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haie H.F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Udell T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Wuzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahy J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Greenwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
 RA Krzywinski M.I., Skalska U., Smalios D.E., Schnerch A., Schein J.E.,
 RA Jones S.J., Marra M.A.;
 RA "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
 [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Kidney;
 RA Strausberg R.;
 RL Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.
 [3]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Whole;
 RA Strausberg R.;
 RL Submitted (DEC-2003) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: belongs to the heat shock protein 70 family.
 CC EMBL; BC066491; AA66491.1; -;
 CC EMBL; BC063228; AA63228.1; -;
 CC HSP; P19120; IATR.
 CC ZFIN; ZDB-GENE-990415-92; hsp88.
 CC GO; GO:0005524; F:ATP binding; IEA.
 CC InterPro; IPR001023; Hsp70.
 CC Pfam; PF00012; HSP70_1.
 CC PRINTS; PR00301; HEATSHOCK70.
 CC ProDom; PD000089; Hsp70_1.
 CC PROSITE; PS00297; HSP70_1; 1.
 CC PROSITE; PS00329; HSP70_2; 1.
 CC PROSITE; PS01036; HSP70_3; 1.
 KW ATP-binding; Chaperone; Heat shock; Multigene family; Nuclear protein.
 SQ SEQUENCE 649 AA; 71180 MW; 18454BE693C838A9 CRC64;
 Query Match 83.8%; Score 1101; DB 2; Length 649;
 Best Local Similarity 81.6%; Pred. No. 5.9e-60;
 Matches 217; Conservative 19; Mismatches 22; Indels 8; Gaps 3;
 QY 1 KSNVQDLLLDVAPLSGLGTAGGVTALIKRNSTIPTKQTQIFTYSDNPGVLIQVY 60
 DB 384 KSNVQDLLLDVAPLSGLGTAGGVTALIKRNSTIPTKQTQIFTYSDNPGVLIQVY 443
 QY 61 EGERAMTKNNLLGRFELSGIPPPAPRGVPQIEVTFDIDANGILNVATDKSTGKANKITI 120
 DB 444 EGERAMTKNNLLGRFELSGIPPPAPRGVPQIEVTFDIDANGILNVATDKSTGKANKITI 503
 QY 121 TNDKGRLSKEDIERMVQEAKEYKAEDVDQVQDKVSARNGLESYAFNMKSTVEDKLGKIS 180

504 TNDKGRLSKEDIERMVQEAKEYKAEDVDQVQDKVSARNGLESYAFNMKSTVEDKLGKIS 563
 181 EADKKVLDKCOEVIWLDANTLAKRPFHKRKELEQVCNPIISGLYQAGG-PG----- 235
 564 DEDQKILDKNEVIGWLDKNTQABEEFEHQKLEKVCNPIITKLYQSAGMGGMPE 623
 236 --PGGF-GAQQPGKGGSGGPTTIEVD 258
 624 GMPGFPAGAAAPGGSSGPTTIEVD 649

RESULT 23
 HS7C CRIGR STANDARD; PRT; 646 AA.
 ID HS7C CRIGR
 AC P19378;
 DT 01-NOV-1990 (Rel. 16, Created)
 DT 01-NOV-1990 (Rel. 16, Last sequence update)
 DT 25-OCT-2004 (Rel. 45, Last annotation update)
 DE Heat shock cognate 71 kDa protein.
 GN Name=HSP88; Synonyms=HSC70;
 OS Cricetus griseus (Chinese hamster).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Theria; Rodentia; Sciurognathi; Muridae; Cricetinae;
 OC Cricetulus.
 OX NCBI_TaxID=10029;
 [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=90377205; PubMed=1975944; Gupta R.S.;
 RA Ahmad S., Ahuja R., Venner T.J., Gupta R.S.;
 RT "Identification of a protein altered in mutants resistant to
 RT microtubule inhibitors as a member of the major heat shock protein
 RL (hsp70) family.";
 RL Mol. Cell. Biol. 10:5160-5165 (1990).
 CC -1- FUNCTION: Chaperone.
 CC -1- SUBCELLULAR LOCATION: Translocates rapidly from the cytoplasm to
 CC the nuclei, and especially to the nucleoli, upon heat shock (By
 CC similarity).
 CC -1- INDUCTION: Constitutively synthesized.
 CC -1- SIMILARITY: Belongs to the heat shock protein 70 family.
 CC
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 CC
 CC EMBL; M34561; AAA36991.1; -;
 CC PIR; A35922; A35922.
 CC HSP; P08109; 1CKR.
 CC InterPro; IPR001023; Hsp70.
 CC Pfam; PF00012; HSP70_1.
 CC PRINTS; PR00301; HEATSHOCK70.
 CC ProDom; PD000089; Hsp70_1.
 CC TIGRFAMs; TIGR01991; HscA; 1.
 CC PROSITE; PS00297; HSP70_1; 1.
 CC PROSITE; PS00329; HSP70_2; 1.
 CC PROSITE; PS01036; HSP70_3; 1.
 KW ATP-binding; Chaperone; Heat shock; Multigene family; Nuclear protein.
 SQ SEQUENCE 646 AA; 70805 MW; FC65A2DC5095AD1C CRC64;
 Query Match 83.8%; Score 1100.5; DB 1; Length 646;
 Best Local Similarity 81.7%; Pred. No. 6.3e-60;
 Matches 215; Conservative 23; Mismatches 20; Indels 5; Gaps 3;
 QY 1 KSNVQDLLLDVAPLSGLGTAGGVTALIKRNSTIPTKQTQIFTYSDNPGVLIQVY 60
 DB 384 KSNVQDLLLDVAPLSGLGTAGGVTALIKRNSTIPTKQTQIFTYSDNPGVLIQVY 443
 QY 61 EGERAMTKNNLLGRFELSGIPPPAPRGVPQIEVTFDIDANGILNVATDKSTGKANKITI 120
 DB 444 EGERAMTKNNLLGRFELSGIPPPAPRGVPQIEVTFDIDANGILNVATDKSTGKANKITI 503

KW ATP-binding; Chaperone; Heat shock; Multigene family; Nuclear protein.
 FT CONFLICT 428 428 F -> L (in Ref. 2 and 3).
 SQ SEQUENCE 646 AA; 70871 MW; 03A27B30B6C076ED CRC64;

Query Match 83.8%; Score 1100.5; DB 1; Length 646;
 Best Local Similarity 81.7%; Pred. No. 6.3e-60;
 Matches 215; Conservative 23; Mismatches 20; Indels 5; Gaps 3;

Qy 1 KSENVQDLLLLLDVAPLSGLGTAGVMTALIKRNTSTPTKQTQTFYSDNQPGVLIQVY 60
 Db 384 KSENVQDLLLLLDVAPLSGLGTAGVMTALIKRNTSTPTKQTQTFYSDNQPGVLIQVY 443

Qy 61 EGERAMTKDNNLLGRFELSGIPPPAPRGVPOLEVTFDIDANGILNVATDKSTGKANKITI 120
 Db 444 EGERAMTKDNNLLGKFELTGIPPPAPRGVPOLEVTFDIDANGILNVATDKSTGKANKITI 503

Qy 121 TNDKGRSLKKEIERMVOEAEKYKAEDVQRRVSAKNALSAVEDEGLKGGKIS 180
 Db 504 TNDKGRSLKKEIERMVOEAEKYKAEDVQRRVSAKNALSAVEDEGLKGGKIN 563

Qy 181 EADKKKVLDCQEVISWLDANTLAEKDFEHRKLEBOVCNPIISGLYQAGG-PG--PG 237
 Db 564 DEDKQKLDKCNELIISWLDKNQTAKEBEFHOQKELEKVCNPIITKLYQSAGGMPGMPG 623

Qy 238 GF--GAQGPKGSGSGPTIEVD 258
 Db 624 GFPGGAPPSGSGSGPTIEVD 646

RESULT 25
 ID_HSC RAT STANDARD; PRT; 646 AA.
 AC P63018; P08109; P12225; Q62373; Q62374; Q62375;
 DT 01-AUG-1988 (Rel. 08, Created)
 DT 01-AUG-1988 (Rel. 08, Last sequence update)
 DT 25-OCT-2004 (Rel. 45, Last annotation update)
 DE Heat shock cognate 71 kDa protein.
 GN Name=Hsp8; Synonyms=Hsc70, Hsc73;
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=87246537; PubMed=35955567;
 RA Sorger P.K., Pelham H.R.B.;
 RT "Cloning and expression of a gene encoding hsc73, the major hsp70-like
 RT protein in unstressed rat cells.";
 RL EMBO J. 6:993-998(1987).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=86310827; PubMed=3939319;
 RA O'Walley K., Mauron A., Barchas J.D., Keddes L.;
 RT "Constitutively expressed rat mRNA encoding a 70-kilodalton heat-
 RT shock-like protein.";
 RL Mol. Cell. Biol. 5:3476-3483(1985).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Pituitary;
 RG NIH - Mammalian Gene Collection (MGC) project;
 RL Submitted (NOV-2003) to the EMBL/GenBank/DBJ databases.
 RN [4]
 RP STRUCTURE BY NMR OF 385-543.
 RX MEDLINE=99303702; PubMed=10373374; DOI=10.1006/jmbi.1999.2776;
 RA Morshauser R.C., Hu W., Wang H., Pang Y., Flynn G.C.,
 RA Zunderweg E.R.P.;
 RT "High-resolution solution structure of the 18 kDa substrate-binding
 RT domain of the mammalian chaperone protein Hsc70.";
 RL J. Mol. Biol. 289:1387-1403(1999).
 CC - FUNCTION: Chaperone
 CC - SUBCELLULAR LOCATION: Translocates rapidly from the cytoplasm to
 CC the nuclei, and especially to the nucleoli, upon heat shock (By
 CC similarity).

CC -!- INDUCTION: Constitutively synthesized.
 CC -!- SIMILARITY: Belongs to the heat shock protein 70 family.
 CC
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 CC
 CC EMBL; Y00054; CAA68265.1; -;
 CC EMBL; M11942; AAA41354.1; -;
 CC EMBL; BC061547; AAH61547.1; -;
 CC PIR; S07197; S07197
 CC PDB; 1CKR; NMR; A=385-543.
 CC PDB; 7HSC; NMR; A=385-543.
 CC RGD; 621725; Hspa8.
 CC InterPro; IPR001023; Hsp70.
 CC Pfam; PF00012; HSP70; 1.
 CC PRINTS; PR00301; HEATSHOCK70.
 CC TIGRPFAMs; TIGR01991; Hsca; 1.
 CC PROSITE; PS00297; HSP70_1; 1.
 CC PROSITE; PS00329; HSP70_2; 1.
 CC PROSITE; PS01036; HSP70_3; 1.
 CC 3D-structure; ATP-binding; Chaperone; Heat shock; Multigene family;
 KW Nuclear protein.
 FT STRAND 396 397
 FT STRAND 401 405
 FT TURN 406 408
 FT STRAND 409 411
 FT TURN 416 417
 FT STRAND 418 419
 FT STRAND 422 429
 FT STRAND 438 444
 FT STRAND 454 461
 FT TURN 469 470
 FT STRAND 473 481
 FT TURN 482 484
 FT STRAND 485 492
 FT TURN 493 496
 FT STRAND 497 503
 FT TURN 505 506
 FT HELIX 511 518
 FT TURN 519 521
 FT HELIX 522 527
 FT TURN 528 530
 FT TURN 532 534
 FT STRAND 541 541
 SQ SEQUENCE 646 AA; 70871 MW; 03A27B30B6C076ED CRC64;

Query Match 83.8%; Score 1100.5; DB 1; Length 646;
 Best Local Similarity 81.7%; Pred. No. 6.3e-60;
 Matches 215; Conservative 23; Mismatches 20; Indels 5; Gaps 3;

Qy 1 KSENVQDLLLLLDVAPLSGLGTAGVMTALIKRNTSTPTKQTQTFYSDNQPGVLIQVY 60
 Db 384 KSENVQDLLLLLDVAPLSGLGTAGVMTALIKRNTSTPTKQTQTFYSDNQPGVLIQVY 443

Qy 61 EGERAMTKDNNLLGRFELSGIPPPAPRGVPOLEVTFDIDANGILNVATDKSTGKANKITI 120
 Db 444 EGERAMTKDNNLLGKFELTGIPPPAPRGVPOLEVTFDIDANGILNVATDKSTGKANKITI 503

Qy 121 TNDKGRSLKKEIERMVOEAEKYKAEDVQRRVSAKNALSAVEDEGLKGGKIS 180
 Db 504 TNDKGRSLKKEIERMVOEAEKYKAEDVQRRVSAKNALSAVEDEGLKGGKIN 563

Qy 181 EADKKKVLDCQEVISWLDANTLAEKDFEHRKLEBOVCNPIISGLYQAGG-PG--PG 237
 Db 564 DEDKQKLDKCNELIISWLDKNQTAKEBEFHOQKELEKVCNPIITKLYQSAGGMPGMPG 623

Qy 238 GF--GAQGPKGSGSGPTIEVD 258
 Db 624 GFPGGAPPSGSGSGPTIEVD 646

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Db 624 GPPGGAPPSCGASSGPTIEVD 646
RESULT 26
Q75PJ4 ID Q75PJ4 PRELIMINARY; PRT; 646 AA.
AC Q75PJ4
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DN Heat shock protein.
GN Name=hsp98;
OS Numida meleagris (Helmeted guineafowl).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Numididae; Numida.
OX NCBI_TaxID=8996;
RN 1
RP SEQUENCE FROM N.A.
RA Imamoto S., Hara H., Yoshida Y., Hanzawa K., Watanabe S.;
RL Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: Belongs to the heat shock protein 70 family.
DR EMBL; AB167744; BAD12572.1; -.
DR HSSP; P19120; IATR.
DR GO; GO:0005524; P:ATP binding; IEA.
DR GO; GO:0006457; P:protein folding; IEA.
DR GO; GO:0006986; P:response to unfolded protein; IEA.
DR InterPro; IPR001023; Hsp70.
DR Pfam; PF00012; Hsp70; 1.
DR PRODOM; PD000089; Hsp70; 1.
DR PROSITE; PS00297; Hsp70; 1.
DR PROSITE; PS00329; Hsp70_2; 1.
DR PROSITE; PS01036; Hsp70_3; 1.
KW ATP-binding; Heat shock.
SQ SEQUENCE 646 AA; 70870 MW; EDD8CB1E52A6EFC CRC64;
Query Match 83.8%; Score 1100.5; DB 2; Length 646;
Best Local Similarity 81.7%; Pred. No. 6.3e-60;
Matches 215; Conservative 23; Mismatches 20; Indels 5; Gaps 3;
Qy 1 KSENVQDLLLDVAPLSIGLETAGVMTALIKRNTIPTKTQTFTTYSNQPGLVQVY 60
Db 384 KSENVQDLLLDVTPLSIGLETAGVMTLVTKRNTIPTKTQTFTTYSNQPGLVQVY 443
Qy 61 EGERAMTKNNLLGRFELSGIPPPAPRGVPQIEVTFDANGILNVATDKSTGKANKITI 120
Db 444 EGERAMTKNNLLGKFKELTGIPPPAPRGVPQIEVTFDANGILNVATDKSTGKANKITI 503
Qy 121 TNDKGRLSKEIEIRMVQEAKEYKAEDVQREVRSAKNALESYAFNMKSAVEDEGLKGKIS 180
Db 504 TNDKGRLSKEDIERMVQEAKEYKAEDKQRDKVSKNSLESYAFNMKATVDEKLGKIS 563
Qy 181 EADKKVLDKQCVISWLDANTLAEDKDFEHRKLEQVNCNPIISGLYQAGG-PG-PG 237
Db 564 DEDKQKILDKCNEVINWLDKNQTAERDSYEHQKELEKVCNPIITKLQYQSGMPPGMPG 623
Qy 238 GF--GAQGPKGSGSGPTIEVD 258
Db 624 GPPGGAPPSCGASSGPTIEVD 646
RESULT 27
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AC Q6TDUO
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DN Name=hsp70;
GN Dicertrarchus labrax (European sea bass).
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes; Percoidae;
OC Moronidae; Dicertrarchus.
OX NCBI_TaxID=13489;
RN 1
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RA Gornati R., Vigetti D., Saroglia M., Bernardini G.;
RL Submitted (DEC-2003) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: Belongs to the heat shock protein 70 family.
DR EMBL; AY423555; AAR01102.2; -.
DR HSSP; P19120; IATR.
DR GO; GO:0005524; P:ATP binding; IEA.
DR InterPro; IPR001023; Hsp70.
DR Pfam; PF00012; Hsp70; 1.
DR PRODOM; PD000089; Hsp70; 1.
DR PROSITE; PS00297; Hsp70; 1.
DR PROSITE; PS00329; Hsp70_2; 1.
DR PROSITE; PS01036; Hsp70_3; 1.
KW ATP-binding.
SQ SEQUENCE 653 AA; 71367 MW; 8E14197F9189E1D8 CRC64;
Query Match 83.6%; Score 1098; DB 2; Length 653;
Best Local Similarity 80.2%; Pred. No. 9.2e-60;
Matches 215; Conservative 21; Mismatches 22; Indels 10; Gaps 3;
Qy 1 KSENVQDLLLDVAPLSIGLETAGVMTALIKRNTIPTKTQTFTTYSNQPGLVQVY 60
Db 386 KSENVQDLLLDVTPLSIGLETAGVMTLVTKRNTIPTKTQTFTTYSNQPGLVQVY 445
Qy 61 EGERAMTKNNLLGRFELSGIPPPAPRGVPQIEVTFDANGILNVATDKSTGKANKITI 120
Db 446 EGERAMTRDNNLLGKFKELTGIPPPAPRGVPQIEVTFDANGILNVATDKSTGKANKITI 505
Qy 121 TNDKGRLSKEIEIRMVQEAKEYKAEDVQREVRSAKNALESYAFNMKSAVEDEGLKGKIS 180
Db 506 TNDKGRLSKEDIERMVQEAKEYKAEDDVQKDDVQKDDVQKDDVQKDDVQKDDVQKDDV 565
Qy 181 EADKKVLDKQCVISWLDANTLAEDKDFEHRKLEQVNCNPIISGLYQAGG-PG-PG 235
Db 566 DDDKQKILDKCNEVINWLDKNQTAERDSYEHQKELEKVCNPIITKLQYQSGMPPGMPG 625
Qy 236 --PGGP---GAQGPKGSGSGPTIEVD 258
Db 626 GPPGGAPPSCGASSGSGPTIEVD 653
RESULT 28
Q96BEO ID Q96BEO PRELIMINARY; PRT; 269 AA.
AC Q96BEO;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Hypothetical protein (fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN 1
RP SEQUENCE FROM N.A.
RC TISSUE=Uterus;
RA Strausberg R.;
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: Belongs to the heat shock protein 70 family.
DR EMBL; BC015699; AAH15699.1; -.
DR HSSP; P04475; 1Q5L.
DR GO; GO:0005524; P:ATP binding; IEA.
DR InterPro; IPR001023; Hsp70.
DR Pfam; PF00012; Hsp70; 1.
DR PRINTS; PR00301; HEATSHOCK70.
KW ATP-binding; Hypothetical protein.
FT NON_TER 1
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RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Schetz T.B.,
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Lequellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Sanchez A.,
 RA Fahney J., Helton E., Kettelman M., Madan A., Rodrigues S.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalish D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.,
 RA "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences.";
 RL [5].
 RN Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
 RP SEQUENCE OF 50-55; 103-107 AND 580-596.
 RX MEDLINE=93162043; PubMed=1286667;
 RA Rasmussen H.H., van Damme J., Puype M., Gesser B., Celis J.E.,
 RA Vandekerckhove J.;
 RT "Microsequences of 145 proteins recorded in the two-dimensional gel
 RT protein database of normal human epidermal keratinocytes.";
 RL Electrophoresis 13:960-969 (1992).
 RN [6].
 RP SEQUENCE OF 77-86; 221-236 AND 302-311.
 RX MEDLINE=96311348; PubMed=8713105; DOI=10.1006/bbr.1996.1082;
 RA Egerton M., Moritz R.L., Drucker B., Kelsa A., Simpson R.J.;
 RT "Identification of the 70kd heat shock cognate protein (Hsc70) and
 RT alpha-actinin-1 as novel phosphotyrosine-containing proteins in T
 RT lymphocytes.";
 RL Biochem. Biophys. Res. Commun. 224:666-674 (1996).
 RN [7].
 RP SUBCELLULAR LOCATION.
 RX PubMed=1586970;
 RA Hattori H., Liu Y.-C., Tohnai I., Ueda M., Kaneda T., Kobayashi T.,
 RA Tanabe K., Ohtsuka K.;
 RT "Intracellular localization and partial amino acid sequence of a
 RT stress-inducible 40-kDa protein in HeLa cells.";
 RL Cell Struct. Funct. 17:77-86 (1992).
 CC -!- FUNCTION: Chaperone. Isoform 2 may function as an endogenous
 CC inhibitory regulator of HSC70 by competing the cochaperones.
 CC -!- SUBCELLULAR LOCATION: Translocates rapidly from the cytoplasm to
 CC the nuclei, and especially to the nucleoli, upon heat shock.
 CC -!- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=2;
 CC Name=1;
 CC IsoId=P11142-1; Sequence=Displayed;
 CC Name=2; Synonyms=HSC54;
 CC IsoId=P11142-2; Sequence=VSP_002427;
 CC -!- TISSUE SPECIFICITY: Ubiquitous.
 CC -!- INDUCTION: Constitutively synthesized.
 CC -!- SIMILARITY: Belongs to the heat shock protein 70 family.
 CC
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 CC
 CC EMBL; Y00371; CAA68445.1; --
 CC EMBL; AB034951; BAB18615.1; --
 CC EMBL; AF352832; AAK17898.1; --
 CC EMBL; BC016179; AAI16179.1; --
 CC EMBL; BC016660; AAI16660.1; --
 CC EMBL; BC019816; AAI19816.1; --
 CC PIR; A27077; A27077.
 CC HSP; P19120; IATR.
 CC SWISS-2DPAGE; P11142; HUMAN.
 CC Aarhus/Ghent-2DPAGE; 6504; IEF.
 CC HSC-2DPAGE; P11142; HUMAN.

DR OGP; P11142; --
 DR PHCI-2DPAGE; P11142; --
 DR Genew; HGNC:5241; HSPA8.
 DR H-InVDB; HIX0010213; --
 DR MIM; 600816; --
 DR GO; GO:0005622; C:intracellular; NAS.
 DR GO; GO:0042823; P:ATPase activity; coupled; NAS.
 DR GO; GO:0006457; P:protein folding; NAS.
 DR InterPro; IPR001023; Hsp70.
 DR Pfam; PF00012; HSP70; 1.
 DR PRINTS; PR00301; HEATSHOCK70.
 DR ProDom; PD000089; Hsp70; 1.
 DR TIGRFAMs; TIGR01991; HscA; 1.
 DR PROSITE; PS00297; HSP70_1; 1.
 DR PROSITE; PS00329; HSP70_2; 1.
 DR PROSITE; PS01036; HSP70_3; 1.
 KW Alternative splicing; ATP-binding; Chaperone;
 KW Direct protein sequencing; Heat shock; Multigene family;
 KW Nuclear protein.
 FT VAKSPDIC 464 616 Missing (in isoform 2).
 FT SQ SEQUENCE 646 AA; 70898 MW; 9AA27B210730670C CRC64;
 Query Match 83.5%; Score 1097.5; DB 1; Length 646;
 Best Local Similarity 81.4%; Pred. No. 9.7e-60;
 Matches 214; Conservative 24; Mismatches 20; Indels 5; Gaps 3;
 QY 1 KSENVQDLLLLLDVAPLSGLTAGGVMTALIKRNTPTKTQTQITFTTYSNQPGVLIQVY 60
 DB 384 KSENVQDLLLLLDVTPLSGLTAGGVMTALIKRNTPTKTQTQITFTTYSNQPGVLIQVY 443
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 DB 504 TNDKGRUSKEDIERMVQAEKYKAEDEKQDKVSSKNSLSYAFNMKATVDEKLQGGKIN 563
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 DB 564 DEDQKILDKCNELIINWLDKNQTAKEEFHQKELEKVCNPIITKLYQSAGMGMPG 623
 QY 238 GF--GAQPGKGGSGPTIEVD 258
 DB 624 GFPGGAPPSSGSGSGPTIEVD 646
 RESULT 31
 HS7C SAGOE
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 AC Q71UJ34;
 DT 25-OCT-2004 (Rel. 45, Created)
 DT 25-OCT-2004 (Rel. 45, Last sequence update)
 DT 25-OCT-2004 (Rel. 45, Last annotation update)
 DE Heat shock cognate 71 kDa protein (intracellular vitamin D binding
 DE protein 1).
 GN Name=HSPA8; Synonyms=IDBP1;
 OS *Saguinus oedipus* (Cotton-top tamarin).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Platyrrhini; Callitrichidae; Saguinus.
 OX NCBI_TaxID=9490;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Wu S., Ren S., Chen H., Chien R., Gacad M.A., Adams J.S.;
 RT "Cloning and expression of two novel cDNAs for hsp-70-related
 RT intracellular vitamin D binding proteins.";
 RL Submitted (APR-1999) to the EMBL/GenBank/DBJ databases.
 CC -!- FUNCTION: Chaperone. Isoform 2 may function as an endogenous
 CC inhibitory regulator of HSC70 by competing the cochaperones (By
 CC similarity).
 CC -!- SUBCELLULAR LOCATION: Translocates rapidly from the cytoplasm to
 CC the nuclei, and especially to the nucleoli, upon heat shock (By

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CC similarity).
CC -I- INDUCTION: Constitutively synthesized.
CC -I- SIMILARITY: Belongs to the heat shock protein 70 family.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC use by non-profit institutions as long as its content is in no way
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CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; AF142571; AAF66593.1; -
CC InterPro; IPR001023; Hsp70.
CC Pfam; PF00012; HSP70; 1.
CC PRINTS; PR00301; HEATSHOCK70.
CC PRODOM; PD000089; Hsp70; 1.
CC PROSITE; PS00297; HSP70_1; 1.
CC PROSITE; PS00329; HSP70_2; 1.
CC PROSITE; PS01036; HSP70_3; 1.
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CC Query Match 83.5%; Score 1097.5; DB 1; Length 646;
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CC 61 EGERAMTKNNLLGRFELSGIPAPRGVPOIEVTFDIDANGILNVTATDKSTGKANKITI 120
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CC -----
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CC -----
CC 181 EADKKKVLDCQEVISWLDANTLAEKDFEHKRELFQVCNPIISGLYQAGG-PG--PG 237
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CC 624 GFPGGAPPSSGASGSGPTIEVD 646
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CC RESULT 32
CC Q7ZVJ1 PRELIMINARY; PRT; 649 AA.
CC AC Q7ZVJ1
CC DT 01-JUN-2003 (TrEMBLrel. 24, Created)
CC DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
CC DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
CC DE Hsp88 protein.
CC GN Name=hsp88;
CC OS Brachydanio rerio (Zebrafish) (Danio rerio).
CC OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
CC OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
CC OC Cyprinidae; Danio.
CC OX NCBI_TaxID=7955;
CC RN [1]
CC RP SEQUENCE FROM N.A.
CC RC STRAIN=AB; TISSUE=Whole body;
CC RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
CC RA Klausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
CC RA Klausner R.D., Collins P.S., Wagner L., Shenmen C.M., Schuler G.D.,
CC RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
CC RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
CC RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
CC RA Scapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
CC RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

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RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McSwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Sanchez A.,
RA Fahney J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blackley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RA "Generation and initial analysis of more than 15,000 full-length human
RA and mouse cDNA sequences."
RA Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RA [2]
RA SEQUENCE FROM N.A.
RA STRAIN=AB; TISSUE=Whole body;
RA Strausberg R.;
RA Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.
CC -I- SIMILARITY: Belongs to the heat shock protein 70 family.
CC EMBL; BC045841; AAH45841.1; -
CC DR HSP; P19120; IATR.
CC DR ZFIN; ZDB-GENE-990415-92; hsp88.
CC GO; GO:0005524; F:ATP binding; IEA.
CC InterPro; IPR001023; Hsp70.
CC Pfam; PF00012; HSP70; 1.
CC PRINTS; PR00301; HEATSHOCK70.
CC PRODOM; PD000089; Hsp70; 1.
CC PROSITE; PS00297; HSP70_1; 1.
CC PROSITE; PS00329; HSP70_2; 1.
CC PROSITE; PS01036; HSP70_3; 1.
CC ATP-binding.
CC SEQUENCE 649 AA; 71198 MW; 9C006B747724919B CRC64;
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CC Query Match 83.5%; Score 1097; DB 2; Length 649;
CC Best Local Similarity 81.2%; Pred. No. 1e-59;
CC Matches 216; Conservative 19; Mismatches 23; Indels 8; Gaps 3;
CC -----
CC 1 KSENVQDLLLLLDVAPLSLGLETAGVMTALIKRNTTPTKTQTFTTYSNQPGLVQVY 60
CC 384 KSENVQDLLLLLDVTPLSLGLETAGVMTLVTKRNTTPTKTQTFTTYSNQPGLVQVY 443
CC -----
CC 61 EGERAMTKNNLLGRFELSGIPAPRGVPOIEVTFDIDANGILNVTATDKSTGKANKITI 120
CC 444 EGERAMTKNNLLGKLFELTGIPTAPRGVPOIEVTFDIDANGIMNVSADVSTGKANKITI 503
CC -----
CC 121 TNDKGRLSKEEIERMVQEAKEYKAEDVQERVSAKNALSYAFNMKSASVEDEGLKGKIS 180
CC 504 TNDKGRLSKEDIERMVQEAKEYKAEDDQKRVSAKNGLSYAFNMKSTVEDEKLKGKIS 563
CC -----
CC 181 EADKKKVLDCQEVISWLDANTLAEKDFEHKRELFQVCNPIISGLYQAGG-PG---- 235
CC 564 DEDQKILDKCNEVIGWLDKNTAEREFEFHQKELEKVCNPIITKLYQAGGMPGMPG 623
CC -----
CC 236 --PGGP-GAQPCKGGSGSGPTIEVD 258
CC 624 GMPGGPAGAAPGGSGSGPTIEVD 649
CC -----
CC RESULT 33
CC Q6NZD0 PRELIMINARY; PRT; 646 AA.
CC AC Q6NZD0
CC DT 05-JUL-2004 (TrEMBLrel. 27, Created)
CC DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
CC DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
CC DE Heat shock protein 8.
CC GN Name=hsp88;
CC OS Mus musculus (Mouse).
CC OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
CC OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
CC OX NCBI_TaxID=10090;
CC RN [1]
CC RP SEQUENCE FROM N.A.

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RC STRAIN=CS7BL/6J; TISSUE=Embryonic Germ Cell;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.2426038999;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
 RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
 RA Krzywinski M.I., Skalska U., Smallus D.E., Schnerch A., Schein J.E.,
 RA Jones S.J., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CS7BL/6J; TISSUE=Embryonic Germ Cell;
 RA Strausberg R.;
 RL Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: Belongs to the heat shock protein 70 family.
 DR EMBL; BC066191; AAH66191.1; -.
 DR HSP; P19120; IATR.
 DR GO; GO:0042623; F:ATPase activity, coupled; IDA.
 DR GO; GO:0003754; F:chaperone activity; IDA.
 DR GO; GO:0005155; F:protein binding; IPI.
 DR GO; GO:0051085; P:chaperone cofactor dependent protein folding; IGI.
 DR GO; GO:0006457; P:protein folding; IDA.
 DR GO; GO:0000074; P:regulation of cell cycle; IDA.
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 DR Pfam; PF00012; Hsp70; 1.
 DR PRINTS; PR00301; HEATSHOCK70.
 DR PRODOM; PD000089; Hsp70; 1.
 DR PROSITE; PS00297; Hsp70_1; 1.
 DR PROSITE; PS00329; Hsp70_2; 1.
 DR PROSITE; PS01036; Hsp70_3; 1.
 DR ATP-binding; Heat shock.
 KW SEQUENCE 646 AA; 70871 MW; 03AC7530B8CE76ED CRC64;
 QY
 Db 1 KSENVQDLLLDVAPLSGLGTAGVMTALIKRNSTIPTKTQTFTTYSNQPGLVQVY 60
 384 KSENVQDLLLDVTPLSGLGTAGVMTLVTKRNTIPTKTQTFTTYSNQPGLVQVY 443
 QY 61 EGERAMTKDNNLLGRFELSGIPAPRGVQPIEVTFDIDANGILNVTATDSTGKANKITI 120
 444 EGERAMTKDNNLLGKFLGTIPAPRGVQPIEVTFDIDANGILNVSADKSTGKANKITI 503
 QY 121 TNDKGRLSKEIERMVOAEKYEKAEDEQVQERVSQKNALESYAFNMKSAVEDGLKGGKIS 180
 504 TNDKGRLSKEDIERNVOAEKYEKAEDEKQDRQKRSKNSLESYAFNMKATVEDEKLQSKIN 563
 QY 181 EADKKVKLDKQCEVISWLDANTLAEKDFEHRKELEQVNCNPIISGLYQAGG-PG--PG 237
 564 DEDKQILDKCNELISWLDKNOTAEFEHQQEKELEKVCNPIITKLQYQAGGPGGMPG 623
 QY 238 GF--GAQGPKGSGSGPTIEVD 258
 624 GFPGGGAPPSSGGASGSGPTIEVD 646
 Db
 RESULT 34
 Q8AVE2

ID Q8AVE2 PRELIMINARY; PRT; 650 AA.
 AC Q8AVE2;
 DT 01-MAR-2003 (TrEMBLrel. 23, Created)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE Hsc70-prov protein.
 OS Xenopus laevis (African clawed frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;
 OC Xenopodinae; Xenopus.
 OX NCBI_TaxID=8355;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Embryo;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.2426038999;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
 RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
 RA Krzywinski M.I., Skalska U., Smallus D.E., Schnerch A., Schein J.E.,
 RA Jones S.J., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Embryo;
 RX MEDLINE=22341132; PubMed=12454917; DOI=10.1002/dvdy.10174;
 RA Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,
 RA Richardson P.;
 RT "Genetic and genomic tools for Xenopus research: The NIH Xenopus
 RT initiative.";
 RL Dev. Dyn. 225:384-391(2002).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Embryo;
 RA Klein S., Strausberg R.;
 RL Submitted (DEC-2002) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: Belongs to the heat shock protein 70 family.
 DR EMBL; BC041201; AAH41201.1; -.
 DR HSP; P19120; IATR.
 DR GO; GO:0005524; F:ATP binding; IDA.
 DR InterPro; IPR001023; Hsp70.
 DR Pfam; PF00012; Hsp70; 1.
 DR PRINTS; PR00301; HEATSHOCK70.
 DR PRODOM; PD000089; Hsp70; 1.
 DR PROSITE; PS00297; Hsp70_1; 1.
 DR PROSITE; PS00329; Hsp70_2; 1.
 DR PROSITE; PS01036; Hsp70_3; 1.
 DR ATP-binding.
 KW SEQUENCE 650 AA; 71188 MW; CAE53D1D3275E6B5 CRC64;
 QY
 Db 1 KSENVQDLLLDVAPLSGLGTAGVMTALIKRNSTIPTKTQTFTTYSNQPGLVQVY 60
 384 KSENVQDLLLDVTPLSGLGTAGVMTLVTKRNTIPTKTQTFTTYSNQPGLVQVY 443
 QY 61 EGERAMTKDNNLLGRFELSGIPAPRGVQPIEVTFDIDANGILNVTATDSTGKANKITI 120
 444 EGERAMTKDNNLLGKFLGTIPAPRGVQPIEVTFDIDANGILNVSADKSTGKANKITI 503
 QY 121 TNDKGRLSKEIERMVOAEKYEKAEDEQVQERVSQKNALESYAFNMKSAVEDGLKGGKIS 180
 504 TNDKGRLSKEDIERNVOAEKYEKAEDEKQDRQKRSKNSLESYAFNMKATVEDEKLQSKIN 563
 QY 181 EADKKVKLDKQCEVISWLDANTLAEKDFEHRKELEQVNCNPIISGLYQAGG-PG--PG 237
 564 DEDKQILDKCNELISWLDKNOTAEFEHQQEKELEKVCNPIITKLQYQAGGPGGMPG 623
 QY 238 GF--GAQGPKGSGSGPTIEVD 258
 624 GFPGGGAPPSSGGASGSGPTIEVD 646
 Db
 RESULT 34
 Q8AVE2

Query Match 83.4%; Score 1096.5; DB 2; Length 650;
 Best Local Similarity 81.3%; Pred. No. 1.le-59;
 Matches 217; Conservative 23; Mismatches 18; Indels 9; Gaps 4;
 Qy 1 KSENVQDLLLDVAPLSGLGTAGVMTALIKRNSTIPTKTQTFTTYSNQPGLVQVY 60
 Db 384 KSENVQDLLLDVTPLSGLGTAGVMTLVTKRNTIPTKTQTFTTYSNQPGLVQVY 443
 Qy 61 EGERAMTKDNNLLGRFELSGIPAPRGVQPIEVTFDIDANGILNVTATDSTGKANKITI 120

Db 444 EGERAMTKDNNLLGKFLTGTPAPRGVPOIEVTFDIDANGILNVSADVSTGKKNKITI 503
Qy 121 TNDKGRLSKEEIERMVOEAEKYKAEDVQERVSAAKNALESYAFNMKSASVEDEGLGKGIS 180
Db 504 TNDKGRLSKEEIERMVOEAEKYKAEDVQERVSAAKNALESYAFNMKSATVDEKLGKGIS 563
Qy 181 EADKKVLDKCOEIVSWLDANTLAEDKDFEHRKELEQVNCNPIISGLYQAGG---PG 235
Db 564 DEDQKLEKNEVIAWLDKQNTAKDFEHRKELEQVNCNPIITKLYQSAGGMPGMPG 623
Qy 236 --PGGP-GAOG-PKGGSGSGPTIEVD 258
Db 624 GMPGGFGAGPTGGASSGPTIEVD 650

RESULT 35

Q8NE72 ID Q8NE72 PRELIMINARY; PRT; 641 AA.
AC Q8NE72
DT 01-OCT-2002 (TREMBLrel. 22, Created)
DT 01-OCT-2002 (TREMBLrel. 22, Last sequence update)
DE 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
GN Heat shock 70kDa protein i-like.
CN Name=HSPALL;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Testis;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Rana S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaney S.J.,
RA Bosak S.A., McWan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Wozley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bonfield G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickinson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences".
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Testis;
RX Strausberg R.;
RA Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: Belongs to the heat shock protein 70 family.
DR EMBL; BC034483; AAH34483.1; -.
DR HSP; P08107; IH30.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0006457; P:protein folding; IEA.
DR GO; GO:0006986; P:response to unfolded protein; IEA.
DR InterPro; IPR001023; Hsp70.
DR Pfam; PF00012; HSP70; 1.
DR PRINTS; PR00301; HEATSHOCK70.
DR PRODOM; PD000089; Hsp70; 1.
DR PROSITE; PS00297; HSP70; 1.
DR PROSITE; PS00329; HSP70; 2; 1.
DR PROSITE; PS01036; HSP70; 3; 1.
KW ATP-binding; Heat shock.
SQ SEQUENCE 641 AA; 70393 MW; E4417F62C6D86ACA CRC64;

Query Match 83.3%; Score 1095; DB 2; Length 641;
Best Local Similarity 81.5%; Pred. No. 1.4e-59;
Matches 216; Conservative 19; Mismatches 16; Indels 16; Gaps 2;
Qy 1 KSENVQDLLLLDVAPLSGLTAGGVMTALIKENSTIPTKTQTQITFTTYSNQPGVLIQVY 60
Db 386 KSENVQDLLLLDVAPLSGLTAGGVMTALMKRNSTIPTKTQTQITFTTYSNQPGVLIQVY 445
Qy 61 EGERAMTKDNNLLGRFELSGIPAPRGVPOIEVTFDIDANGILNVTATDKSTGKANKITI 120
Db 446 EGERAMTKDNNLLGRFELSGIPAPRGVPOIEVTFDIDANGILNVTATDKSTGKANKITI 505
Qy 121 TNDKGRLSKEEIERMVOEAEKYKAEDVQERVSAAKNALESYAFNMKSASVEDEGLGKGIS 180
Db 506 ANDKGRLSKEEIERMVOEAEKYKAEDVQERVSAAKNALESYAFNMKSASVEDEGLGKGIS 565
Qy 181 EADKKVLDKCOEIVSWLDANTLAEDKDFEHRKELEQVNCNPIISGLYQAGGPGGFG 240
Db 566 ESDKNKILDKCNELLWLVNQLAEDKDFEHRKELEQVNCNPIITKLYQG-----G 616
Qy 241 AQGPKGGSG-----SGPTIEVD 258
Db 617 CTGPACGTGYVGRPATGPTIEVD 641

RESULT 36

Q801X8 ID Q801X8 PRELIMINARY; PRT; 631 AA.
AC Q801X8
DT 01-JUN-2003 (TREMBLrel. 24, Created)
DT 01-JUN-2003 (TREMBLrel. 24, Last sequence update)
DE 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
DE Heat shock cognate 70 kDa (Fragment).
GN Name=HSC70;
OS Carassius auratus (Goldfish).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Carassius.
OX NCBI_TaxID=7957;
RN [1]
RP SEQUENCE FROM N.A.
RC Watabe S., Kondo H., Hashimoto S.;
RA Submitted (OCT-2002) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: Belongs to the heat shock protein 70 family.
DR EMBL; AB092840; BAC67185.1; -.
DR HSP; P19120; 3HSC.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0006457; P:protein folding; IEA.
DR GO; GO:0006986; P:response to unfolded protein; IEA.
DR InterPro; IPR001023; Hsp70.
DR Pfam; PF00012; HSP70; 1.
DR PRINTS; PR00301; HEATSHOCK70.
DR PRODOM; PD000089; Hsp70; 1.
DR PROSITE; PS00329; HSP70; 2; 1.
DR PROSITE; PS01036; HSP70; 3; 1.
KW ATP-binding; Heat shock.
FT NON TER 1
SQ SEQUENCE 631 AA; 69436 MW; 6CA60C9B66DDDBIA CRC64;

Query Match 83.3%; Score 1094; DB 2; Length 631;
Best Local Similarity 81.2%; Pred. No. 1.6e-59;
Matches 216; Conservative 19; Mismatches 23; Indels 8; Gaps 3;
Qy 1 KSENVQDLLLLDVAPLSGLTAGGVMTALIKENSTIPTKTQTQITFTTYSNQPGVLIQVY 60
Db 366 KSENVQDLLLLDVAPLSGLTAGGVMTALIKENSTIPTKTQTQITFTTYSNQPGVLIQVY 425
Qy 61 EGERAMTKDNNLLGRFELSGIPAPRGVPOIEVTFDIDANGILNVTATDKSTGKANKITI 120
Db 426 EGERAMTKDNNLLGKFLTGTPAPRGVPOIEVTFDIDANGILNVSAASTGKANKITI 485
Qy 121 TNDKGRLSKEEIERMVOEAEKYKAEDVQERVSAAKNALESYAFNMKSASVEDEGLGKGIS 180

DR	GO; GO:006986; P:response to unfolded protein; IEA.
DR	Pfam; PF00012; HSP70; 1.
DR	PRINTS; PR00301; HEATSHOCK70.
DR	ATP-binding; Heat shock.
FT	NON TER
FT	1
SQ	SEQUENCE 282 AA; 30884 MW; D8177623CF106307 CRC64;
	Query Match 83.1%; Score 1092; DB 2; Length 282;
	Best Local Similarity 84.5%; Pred. No. 7.9e-60;
	Matches 218; Conservative 17; Mismatches 21; Indels 2; Gaps 2;
Qy	1 KSENVQDLLLLDVAPLSIGLETAGGVMTALIKRNSTTPKTQTQITFTTYSNQPGLIQVY 60
Dd	27 KSEKVQDLLLLDVAPLSIGLETAGGVMTVLIKRNSTTPKTQTQITFTTYSNQPGLIQVY 86
Qy	61 EGERAMTKNNLGRPELSGIPPAPRGVPOLEVTFDIDANGILNVATDKSTGKANKITI 120
Dd	87 EGERAMTRDNNLGRFOLDTGIPPAPRGVPOLEVTFDIDANGILNVATMDKSTGKANKITI 146
Qy	121 TNDKGRLSKEEIERMVQEAERYKAEDVEQRVERVSAAKNALSYAFNMKSASVEDGLKGKIS 180
Dd	147 TNDKGRLSKEEIERMVQEAERYKAEDSGREKIAAKNALSYAFNMKSASVDEGLKDKIS 206
Qy	181 EADKKVKLDKCQEVISWLDANTLAEKDFEPHKRKLQVNCPIISGLYQGAGGPGPGFG 240
Dd	207 ESDKKKILDKCNELSWLEANQLAEKDEFHKKRLELENWCNPITIKLYQ-SGCTGPTCTP 265
Qy	241 AQGPKGSGSGPTIEVD 258
Dd	266 GYTP-GRAATGPTIEVD 282
RESULT 38	
Q91ZU4	PRELIMINARY; PRT; 461 AA.
ID	Q91ZU4
AC	Q91ZU4;
DT	01-DEC-2001 (TREMBLrel. 19, Created)
DT	01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT	01-MAR-2004 (TREMBLrel. 26, Last annotation update)
DE	Heat shock protein Hsc70t (Fragment).
GN	Name=Hsc70t;
OS	Mus musculus (Mouse).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus.
OX	NCBI_TaxID=10090;
RN	[1]
RP	SEQUENCE FROM N.A.
RC	STRAIN=B10.A;
RC	MEDLINE=92216447; PubMed=10199925; DOI=10.1007/s002510050522;
RX	Noek M., van Vugt H.;
RT	"The sequence and organization of the mouse valyl-tRNA synthetase gene
RT	G7a/Bat6 located in the MHC class III region.";
RL	Immunogenetics 49:468-470(1999).
RN	[2]
RP	SEQUENCE FROM N.A.
RC	STRAIN=B10.A;
RC	MEDLINE=97124840; PubMed=8954773; DOI=10.1006/geno.1996.0585;
RX	Noek M., van Dinten L., van Vugt H.;
RT	"A novel gene, G7e, resembling a viral envelope gene, is located at
RT	the recombinational hot spot in the class III region of the mouse
RL	MHC.";
RN	Genomics 38:5-12(1996).
RN	[3]
RP	SEQUENCE FROM N.A.
RC	STRAIN=B10.A;
RX	MEDLINE=94239288; PubMed=8026864;
RA	Noek M., Olafsen M.G., van Vugt H., Milner C.M., Teuscher C.,
RA	Campbell R.D.;
RT	"Coding sequences and levels of expression of Hsc70t are identical in
RT	mice with different Orch-1 alleles.";
RL	Immunogenetics 40:159-162(1994).
RN	[4]
RP	SEQUENCE FROM N.A.

RC STRAIN=B10.A;
RX MEDLINE=98211706; PubMed=9551980;
RA Snoek M., Teuscher C., van Vugt H.;
RT "Molecular analysis of the major MHC recombinational hot spot located
RT within the G7c gene of the murine class III region that is involved in
RT disease susceptibility.";
RL J. Immunol. 160:266-272(1998).
RN [5]
RP SEQUENCE FROM N.A.
RC STRAIN=B10.A;
RX MEDLINE=21655112; PubMed=11797099; DOI=10.1007/s00251-001-0381-0;
RA van Kooij M., de Groot K., van Vugt H., Aten J., Snoek M.;
RT "Genotype versus phenotype: conflicting results in mapping a lung
RT tumor susceptibility locus to the G7c recombination interval in the
RT mouse MHC class III region.";
RL Immunogenetics 53:656-661(2001).
CC -1- SIMILARITY: Belongs to the heat shock protein 70 family.
DR EMBL; AF397036; AAL14456.1; -.
DR HSP; P08107; I53X.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0006457; P:protein folding; IEA.
DR GO; GO:0006986; P:response to unfolded protein; IEA.
DR Pfam; PF00012; HSP70; 1.
DR PRINTS; PR00301; HEATSHOCK70.
DR PROSITE; PS00329; HSP70_2; 1.
DR PROSITE; PS01036; HSP70_3; 1.
KW ATP-binding; Heat shock.
FT NON TER 1
SQ SEQUENCE 461 AA; 50982 MW; C08082B37DB90C75 CRC64;

Query Match 83.1%; Score 1092; DB 2; Length 461;
Best Local Similarity 84.5%; Pred. No. 1.4e-59;
Matches 218; Conservative 17; Mismatches 21; Indels 2; Gaps 2;

Qy 1 KSENVQDLLLDVAPLSGLTAGVMTALIKRNTIPTKTQTFTTYSNQPGLVLIQVY 60
Db 206 KSEKVDLLLDVAPLSGLTAGVMTALIKRNTIPTKTQTFTTYSNQPGLVLIQVY 265

Qy 61 EGERAMTKNNLLGRFELSGIPAPRGVPOIEVTFDIDANGILNVTATDKSTGKANKITI 120
Db 266 EGERAMTKNNLLGRFELSGIPAPRGVPOIEVTFDIDANGILNVTATDKSTGKANKITI 325

Qy 121 TNDKGRLSKEEIERMVOEAEYKAEDVQERVSAAKNALESYAFNMKSAVEDEGLKDKIS 180
Db 326 TNDKGRLSKEEIERMVOEAEYKAEDVQERVSAAKNALESYAFNMKSAVGEGLKDKIS 385

Qy 181 EADKKKVLDCQEVISWLDANTLAEDKDFHKKRKELEOVNCPPIISGLYQAGGPGGFG 240
Db 386 ESDKKKILDKCNELVSLWLANQLAEKDFHKKRKELENCNPIITKLYQ-SGCTGPTCTP 444

Qy 241 AQGPKGGSGGPTIEVD 258
Db 445 GYTP-GRAATGPTIEVD 461

RESULT 39
Q9QWU1 PRELIMINARY; PRT; 552 AA.
ID Q9QWU1
AC Q9QWU1
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Hsc70t (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OC NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=129;
RX PubMed=14656967; DOI=10.1101/gr.1736803;
RA Xie T., Rowen L., Aguado B., Ahearn M.E., Madan A., Qin S.,
RA Campbell R.D., Hood L.;

RT "Analysis of the gene-dense major histocompatibility complex class III
RT region and its comparison to mouse.";
RL Genome Res. 13:2621-2636(2003).
CC -1- SIMILARITY: Belongs to the heat shock protein 70 family.
DR EMBL; AF109905; AAC84149.1; -.
DR HSP; P08107; I53X.
DR GO; GO:0005524; F:ATP binding; IEA.
DR InterPro; IPR001023; Hsp70.
DR Pfam; PF00012; HSP70; 1.
DR PRINTS; PR00301; HEATSHOCK70.
DR PRODOM; PD000089; Hsp70; 1.
DR PROSITE; PS00329; HSP70_2; 1.
DR PROSITE; PS01036; HSP70_3; 1.
KW ATP-binding.
FT NON TER 1
SQ SEQUENCE 552 AA; 61020 MW; AB81C1BA1F55DCAC CRC64;

Query Match 83.1%; Score 1092; DB 2; Length 552;
Best Local Similarity 84.5%; Pred. No. 1.8e-59;
Matches 218; Conservative 17; Mismatches 21; Indels 2; Gaps 2;

Qy 1 KSENVQDLLLDVAPLSGLTAGVMTALIKRNTIPTKTQTFTTYSNQPGLVLIQVY 60
Db 297 KSEKVDLLLDVAPLSGLTAGVMTALIKRNTIPTKTQTFTTYSNQPGLVLIQVY 356

Qy 61 EGERAMTKNNLLGRFELSGIPAPRGVPOIEVTFDIDANGILNVTATDKSTGKANKITI 120
Db 357 EGERAMTKNNLLGRFELSGIPAPRGVPOIEVTFDIDANGILNVTATDKSTGKANKITI 416

Qy 121 TNDKGRLSKEEIERMVOEAEYKAEDVQERVSAAKNALESYAFNMKSAVEDEGLKDKIS 180
Db 417 TNDKGRLSKEEIERMVOEAEYKAEDVQERVSAAKNALESYAFNMKSAVGEGLKDKIS 476

Qy 181 EADKKKVLDCQEVISWLDANTLAEDKDFHKKRKELEOVNCPPIISGLYQAGGPGGFG 240
Db 477 ESDKKKILDKCNELVSLWLANQLAEKDFHKKRKELENCNPIITKLYQ-SGCTGPTCTP 535

Qy 241 AQGPKGGSGGPTIEVD 258
Db 536 GYTP-GRAATGPTIEVD 552

RESULT 40
HS7C BOVIN
ID HS7C BOVIN STANDARD; PRT; 650 AA.
AC P19120;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Heat shock cognate 71 kDa protein.
GN Name=HSPA8; Synonyms=HSC70;
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovinae; Bos.
OC NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain cortex;
RX MEDLINE=91016866; PubMed=2216746;
RA Deluca-Flaherty C., McKay D.B.;
RT "Nucleotide sequence of the cDNA of a bovine 70 kilodalton heat shock
RT cognate protein.";
RL Nucleic Acids Res. 18:5569-5569(1990).
RN [2]
RP X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS) OF 1-385.
RX MEDLINE=90348961; PubMed=2143562; DOI=10.1038/346623a0;
RA Flaherty K.M., de Luca-Flaherty C., McKay D.B.;
RT "Three-dimensional structure of the ATPase fragment of a 70K heat-
RT shock cognate protein.";
RL Nature 346:623-628(1990).
RN [3]
RP X-RAY CRYSTALLOGRAPHY (2.4 ANGSTROMS) OF 1-385.

RX MEDLINE=94230372; PubMed=8175707;
 RA Flaherty K.M., Wilbanks S.M., Deluca-Flaherty C., McKay D.B.;
 RT "Structural basis of the 70-kilodalton heat shock cognate protein ATP
 RT hydrolytic activity. II. Structure of the active site with ADP or ATP
 RT bound to wild type and mutant ATPase fragment.";
 RL J. Biol. Chem. 269:12899-12907(1994).
 RN [4]
 RP X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS) OF 1-385.
 RX MEDLINE=98254532; PubMed=9585559; DOI=10.1021/bi973046m;
 RA Wilbanks S.M., McKay D.B.;
 RT "Structural replacement of active site monovalent cations by the
 RT epsilon-amino group of lysine in the ATPase fragment of bovine
 RT Hsc70.";
 RL Biochemistry 37:7456-7462(1998).
 RN [5]
 RP X-RAY CRYSTALLOGRAPHY (1.7 ANGSTROMS) OF 1-381.
 RX MEDLINE=99017893; PubMed=9799500; DOI=10.1021/bi981510x;
 RA Sousa M.C., McKay D.B.;
 RT "The hydroxyl of threonine 13 of the bovine 70-kDa heat shock cognate
 RT protein is essential for transducing the ATP-induced conformational
 RT change.";
 RL Biochemistry 37:15392-15399(1998).
 RN [6]
 RP X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS) OF 1-381 OF MUTANTS.
 RX MEDLINE=99379828; PubMed=10451379; DOI=10.1021/bi990816g;
 RA Johnson E.R., McKay D.B.;
 RT "Mapping the role of active site residues for transducing an ATP-
 RT induced conformational change in the bovine 70-kDa heat shock cognate
 RT protein.";
 RL Biochemistry 38:10823-10830(1999).
 CC -1- FUNCTION: Chaperone.
 CC -1- SUBCELLULAR LOCATION: Translocates rapidly from the cytoplasm to
 CC the nuclei, and especially to the nucleoli, upon heat shock (By
 CC similarity).
 CC -1- TISSUE SPECIFICITY: Ubiquitous.
 CC -1- INDUCTION: Constitutively synthesized.
 CC -1- SIMILARITY: Belongs to the heat shock protein 70 family.
 CC -----
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 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL; X53827; CAA37823.1; -;
 DR EMBL; X53335; CAA37422.1; -;
 DR PIR; S11456; S11456.
 DR PDB; 1ATR; X-ray; @=1-386.
 DR PDB; 1ATS; X-ray; @=1-386.
 DR PDB; 1BA0; X-ray; @=1-386.
 DR PDB; 1BA1; X-ray; @=1-386.
 DR PDB; 1BUP; X-ray; @=1-386.
 DR PDB; 1HPM; X-ray; @=1-386.
 DR PDB; 1HX1; X-ray; @=1-381.
 DR PDB; 1KAX; X-ray; @=1-381.
 DR PDB; 1KAY; X-ray; @=1-381.
 DR PDB; 1KAZ; X-ray; @=1-381.
 DR PDB; 1NGA; X-ray; @=1-386.
 DR PDB; 1NGB; X-ray; @=1-386.
 DR PDB; 1NGC; X-ray; @=1-386.
 DR PDB; 1NGD; X-ray; @=1-386.
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 DR PDB; 1NGF; X-ray; @=1-386.
 DR PDB; 1NGH; X-ray; @=1-386.
 DR PDB; 1NGI; X-ray; @=1-386.
 DR PDB; 1NGJ; X-ray; @=1-386.
 DR PDB; 1QOM; X-ray; A=4-381.
 DR PDB; 1QON; X-ray; A=4-381.
 DR PDB; 1QOO; X-ray; A=4-381.
 DR PDB; 2BUP; X-ray; A=1-381.

DR PDB; 3HSC; X-ray; @=1-386.
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 DR Pfam; PF00012; HSP70; 1.
 DR PRINTS; PR00301; HEATSHOCK70.
 DR ProDom; PD000089; Hsp70; 1.
 DR TIGRFAMs; TIGR01991; HscA; 1.
 DR PROSITE; PS00297; HSP70_1; 1.
 DR PROSITE; PS00329; HSP70_2; 1.
 DR PROSITE; PS01036; HSP70_3; 1.
 DR 3D-structure; ATP-binding; Chaperone; Heat shock; Multigene family;
 KW Nuclear protein.
 FT STRAND 7 10
 FT STRAND 15 22
 FT TURN 23 24
 FT STRAND 25 28
 FT TURN 32 33
 FT STRAND 38 39
 FT STRAND 42 44
 FT STRAND 49 51
 FT TURN 52 52
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 FT HELIX 63 65
 FT STRAND 66 67
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 FT STRAND 110 114
 FT HELIX 116 135
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 SQ SEQUENCE 650 AA; 71239 MW; 5BEBA36C2AF3D493 CRC64;

Query Match 83.1%; Score 1091.5; DB 1; Length 650;
 Best Local Similarity 79.8%; Pred. No. 2.3e-59;
 Matches 213; Conservative 25; Mismatches 20; Indels 9; Gaps 3;

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Qy 1 KSENVQDILLDVLAPLSGLTAGVMTALIKRNSTIPTKTQIETFTYSDNQPGVLIQVY 60
Db 384 KSENVQDILLDVLAPLSGLTAGVMTALIKRNTIPTKTQIETFTYSDNQPGVLIQVY 443
Qy 61 EGERAMTKDNNLLGRFELSGIPPPAPRGVPQIEVTFDIDANGILNVTATDKSTGKANKITI 120
Db 444 EGERAMTKDNNLLGKFELTGIPPPAPRGVPQIEVTFDIDANGILNVSADVSTGKANKITI 503
Qy 121 TNDKGRLSKEIERMVOEAEKYKAEDVQERVRSAKNALESYAFNMKSAVEDEGLKGKIS 180
Db 504 TNDKGRLSKEDIERMVOEAEKYKAEDVQERVRSAKNALESYAFNMKSTVEDEKLKGKIS 563
Qy 181 EADKKKVLDCQOEVI SWLDANTLAEKDFEHRKLEQVNCNPIISGLYQAGG-----PG 235
Db 564 DEDQKQILDKCNEVIGWLDKXNQTAEREFHQKLEKVCNPIITKLYQSAGGPGGMPG 623
Qy 236 --PGGF--GAQPKGGSGSGPTIEVD 258
Db 624 GMPGGFGGAGAPGGSGSGPTIEVD 650

RESULT 41
Q6TEQ5 PRELIMINARY; PRT; 649 AA.
AC Q6TEQ5;
DT 05-JUL-2004 (TREMBlrel. 27, Created)
DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)
DE Heat shock 70kDa protein 8.
GN Name=hsp8; Synonyms=hsp8;
OS Brachydanio rerio (Zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Kidney marrow;
RA Song H.D., Wu X.Y., Sun X.J., Zhou Y., Liu T.X., Deng M., Zhang G.W.,
RA Sheng Y., Chen Y., Ruan Z., Jiang C.L., Fan H.Y., Zou L.I.,
RA Kanki J.P., Look A.T., Chen Z.;
RL Submitted (SEP-2003) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: Belongs to the heat shock protein 70 family.
DR EMBL; AY422994; AAQ97970.1; -.
DR HSP; P19120; IATR.
DR ZFIN; ZDB-GENE-990415-92; hsp8.
DR GO; GO:0005524; P:ATP binding; IEA.
DR GO; GO:0006457; P:protein folding; IEA.
DR GO; GO:0006986; P:response to unfolded protein; IEA.
DR InterPro; IPR01023; Hsp70.
DR Pfam; PF00012; Hsp70; 1.
DR PRINTS; PR00301; HEATSHOCK70.
DR PRODOM; PD000089; Hsp70; 1.
DR PROSITE; PS00297; Hsp70_1; 1.
DR PROSITE; PS00329; Hsp70_2; 1.
DR PROSITE; PS01036; Hsp70_3; 1.
DR ATP-binding; Heat shock.
KW SEQUENCE 649 AA; 71228 MW; AB7AB34156B817EE CRC64;

Query Match 83.0%; Score 1091; DB 2; Length 649;
Best Local Similarity 80.8%; Pred. No. 2.5e-59;
Matches 215; Conservative 19; Mismatches 24; Indels 8; Gaps 3;

Qy 1 KSENVQDILLDVLAPLSGLTAGVMTALIKRNSTIPTKTQIETFTYSDNQPGVLIQVY 60
Db 384 KSENVQDILLDVLAPLSGLTAGVMTALIKRNTIPTKTQIETFTYSDNQPGVLIQVY 443
Qy 61 EGERAMTKDNNLLGRFELSGIPPPAPRGVPQIEVTFDIDANGILNVTATDKSTGKANKITI 120
Db 444 EGERAMTKDNNLLGKFELTGIPPPAPRGVPQIEVTFDIDANGILNVSADVSTGKANKITI 503
Qy 121 TNDKGRLSKEIERMVOEAEKYKAEDVQERVRSAKNALESYAFNMKSAVEDEGLKGKIS 180
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Db 504 TNDKGRLSKEDIERMVOEAEKYKAEDVQERVRSAKNALESYAFNMKSTVEDEKLKGKIS 563
Qy 181 EADKKKVLDCQOEVI SWLDANTLAEKDFEHRKLEQVNCNPIISGLYQAGG-PG----- 235
Db 564 DEDQKQILDKCNEVIGWLDKXNQTAEREFHQKLEKVCNPIITKLYQSAGGPGGMPG 623
Qy 236 --PGGF--GAQPKGGSGSGPTIEVD 258
Db 624 GMPGGFGGAGAPGGSGSGPTIEVD 649

RESULT 42
Q6XVG4 PRELIMINARY; PRT; 655 AA.
AC Q6XVG4;
DT 05-JUL-2004 (TREMBlrel. 27, Created)
DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)
DE Heat shock protein 70.
GN Name=hsp70;
OS Chlamys farreri.
OC Eukaryota; Metazoa; Mollusca; Bivalvia; Pteriomorpha; Pectinoida;
OC Pectinoidea; Pectinidae; Chlamys.
OX NCBI_TaxID=202578;
RN [1]
RP SEQUENCE FROM N.A.
RC Wu L., Song L., Xu W., Li H., Guo X., Xiang J.;
RA "Identification and Cloning of Heat Shock Protein 70 Gene from Scallop
RA Chlamys farreri.";
RL GaoJishu Tongxun 13:75-79(2003).
CC -1- SIMILARITY: Belongs to the heat shock protein 70 family.
DR EMBL; AY206871; AA038780.1; -.
DR HSP; P19120; IATR.
DR GO; GO:0005524; P:ATP binding; IEA.
DR GO; GO:0006457; P:protein folding; IEA.
DR GO; GO:0006986; P:response to unfolded protein; IEA.
DR InterPro; IPR01023; Hsp70.
DR Pfam; PF00012; HSP70; 1.
DR PRINTS; PR00301; HEATSHOCK70.
DR PRODOM; PD000089; Hsp70; 1.
DR PROSITE; PS00297; HSP70_1; 1.
DR PROSITE; PS00329; HSP70_2; 1.
DR PROSITE; PS01036; HSP70_3; 1.
DR ATP-binding; Heat shock.
KW SEQUENCE 655 AA; 71261 MW; PP8A456694F7E078 CRC64;

Query Match 83.0%; Score 1090.5; DB 2; Length 655;
Best Local Similarity 79.7%; Pred. No. 2.7e-59;
Matches 216; Conservative 16; Mismatches 26; Indels 13; Gaps 3;

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Db 385 KSENVQDILLDVLAPLSGLTAGVMTALIKRNTIPTKTQIETFTYSDNQPGVLIQVY 444
Qy 61 EGERAMTKDNNLLGRFELSGIPPPAPRGVPQIEVTFDIDANGILNVTATDKSTGKANKITI 120
Db 445 EGERAMTKDNNLLGKFELTGIPPPAPRGVPQIEVTFDIDANGILNVSADVSTGKANKITI 504
Qy 121 TNDKGRLSKEIERMVOEAEKYKAEDVQERVRSAKNALESYAFNMKSAVEDEGLKGKIS 180
Db 505 TNDKGRLSKEIERMVDNAEYKAEDVQERVRSAKNALESYAFNMKSTAEDEDLKDKKIS 564
Qy 181 EADKKKVLDCQOEVI SWLDANTLAEKDFEHRKLEQVNCNPIISGLYQAGG----- 233
Db 565 EEDKKTITDKCEVIGWLDANQLAKEEFHQKLEAVCNPIITKLYQAGGAGGMPG 624
Qy 234 --PGGF--GAQPKGGSGSGPTIEVD 258
Db 625 GMPGMPGMPGGAGGAGGSGSGPTIEVD 655

RESULT 43
Q76N60
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ID Q76N60 PRELIMINARY; PRT; 650 AA.
AC Q76N60;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hsc71
GN Name=HSC71;
OS Paralichthys olivaceus (Japanese flounder).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Pleuronectiformes;
OC Pleuronectoidei; Paralichthyidae; Paralichthys.
OX NCBI_TaxID=8255;
RN [1]
RP SEQUENCE FROM N.A.
RA Yokoyama Y., Hashimoto H., Kubota S., Kinoshita M., Toyohara H.,
RA Sakaguchi M., Kanamori M.;
RT "Complementary DNA cloning of HSC71, a 71 kDa heat shock cognate
protein, in Japanese flounder Paralichthys olivaceus,"
RL Fisheries Sci. 64:388-392(1998).
CC -I- SIMILARITY: Belongs to the heat shock protein 70 family.
DR EMBL; AB006814; BAD05136.1; --
DR HSP; P19120; IATR.
DR GO; GO:0005524; F:ATP binding; IEA.
DR InterPro; IPR001023; Hsp70.
DR PRINTS; PR00301; HEATSHOCK70.
DR Pfam; PF00012; HSP70; 1.
DR PROSITE; PS00297; HSP70_1; 1.
DR ProDom; PD000089; Hsp70; 1.
DR PROSITE; PS00297; Hsp70; 1.
DR PROSITE; PS00329; HSP70_2; 1.
DR PROSITE; PS01036; HSP70_3; 1.
KW ATP-binding.
SQ SEQUENCE 650 AA; 71158 MW; 9F6A4A573342EBA5 CRC64;
Query Match 82.9%; Score 1089.5; DB 2; Length 650;
Best Local Similarity 80.1%; Pred. No. 3.1e-59;
Matches 214; Conservative 20; Mismatches 24; Indels 9; Gaps 3;
QY 1 KSENVQDLLLDVAPLSGLTETAGVMTALIKRNTTPTKTQITFTTYSNQPGLVQVY 60
DB 384 KSENVQDLLLDVTPSLGTTETAGVMTLVIKRNTTPTKTQITFTTYSNQPGLVQV 443
QY 61 EGERAMTKNNLGRFELSGIPAPRGVPOEVTFDIDANGILNVTATDSTGKANKITI 120
DB 444 EGERAMTRDNNLGRFELSGIPAPRGVPOEVTFDIDANGIMNVAADSTGKANKITI 503
QY 121 TNDKGRLSKEIEIEMVQAEKYKAEDVQRRVSAKNALESYAFNMSKSAVEDEGLGKIS 180
DB 504 TNDKGRLSKEDIEMVQAEKYKTEDDQVRDKVSAKNGVSEYAFNMSKTVEDEKLAKGIS 563
QY 181 EADKKKVLDCQEVISWLDANTLAEKDFEHRKLEQVNCNPIISGLYQAGG-PG--- 235
DB 564 DEDKQKLLDKCNVVISWLDNKNQTAKEDEYHQKELEKVCNPIITKLYQSAGGPMGMPGE 623
QY 236 --PGGFGAQQ--PRKGGSGGPTIEVD 258
DB 624 GMPGFGGAGGAGPAGSGSGPTIEVD 650
RESULT 44
Q6MG67
ID Q6MG67 PRELIMINARY; PRT; 641 AA.
AC Q6MG67;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Heat shock 70kD protein 1L.
GN Name=Hspall;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]

RP SEQUENCE FROM N.A.
RC STRAIN=Brown Norway;
RX PubMed=15060004; DOI=10.1101/gr.1987704;
RA Hurt P., Walter L., Sudbrak R., Klages S., Mueller I., Shiina T.,
RA Inoko H., Lehrach H., Guenther E., Reinhardt R., Himmelbauer H.,
RT "The genomic sequence and comparative analysis of the rat major
histocompatibility complex,";
RL Genome Res. 14:631-639(2004).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=Brown Norway;
RA Boehm S., Borzym K., Gelling S., Gimmel V., Heitmann K., Kosiura A.,
RA Lang N., Lehrach S., Thiel J., Sontag M., Hurt P., Himmelbauer H.,
RA Sudbrak R., Reinhardt R.;
RL Submitted (DEC-2003) to the EMBL/GenBank/DBJ databases.
CC -I- SIMILARITY: Belongs to the heat shock protein 70 family.
DR EMBL; BX883045; CAE83979.1; --
DR HSP; P19120; IBA1.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0006457; P:protein folding; IEA.
DR GO; GO:0006986; P:response to unfolded protein; IEA.
DR InterPro; IPR001023; Hsp70.
DR Pfam; PF00012; HSP70; 1.
DR PRINTS; PR00301; HEATSHOCK70.
DR ProDom; PD000089; Hsp70; 1.
DR PROSITE; PS00297; HSP70_1; 1.
DR PROSITE; PS00329; HSP70_2; 1.
DR PROSITE; PS01036; HSP70_3; 1.
KW ATP-binding; Heat shock.
SQ SEQUENCE 641 AA; 70549 MW; C9FAE59B4685DD51 CRC64;
Query Match 82.9%; Score 1089; DB 2; Length 641;
Best Local Similarity 83.5%; Pred. No. 3.2e-59;
Matches 218; Conservative 17; Mismatches 18; Indels 8; Gaps 3;
QY 1 KSENVQDLLLDVAPLSGLTETAGVMTALIKRNTTPTKTQITFTTYSNQPGLVQVY 60
DB 386 KSENVQDLLLDVAPLSGLTETAGVMTLVIKRNTTPTKTQITFTTYSNQPGLVQV 445
QY 61 EGERAMTKNNLGRFELSGIPAPRGVPOEVTFDIDANGILNVTATDSTGKANKITI 120
DB 446 EGERAMTRDNNLGRFELSGIPAPRGVPOEVTFDIDANGILNVTATDSTGKANKITI 505
QY 121 TNDKGRLSKEIEIEMVQAEKYKAEDVQRRVSAKNALESYAFNMSKSAVEDEGLGKIS 180
DB 506 TNDKGRLSKEIEIEMVQAEKYKAEDGQREKIAAKNALESYAFNMSKSAVDEGLDKIS 565
QY 181 EADKKKVLDCQEVISWLDANTLAEKDFEHRKLEQVNCNPIISGLYQ-GAGGP--GP 237
DB 566 ESDKKKLLDKCNVLSWLEANQLAEKEFDHKKRKELENMNCNPIITKLYQSGCTGTCAPG 625
QY 238 GFGAGQPGKGGSGGPTIEVD 258
DB 626 -----YTPGRAATGPTIEVD 641
RESULT 45
HS7C ICTPU
ID HS7C ICTPU STANDARD; PRT; 649 AA.
AC P47773;
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Heat shock cognate 71 kDa protein.
GN Name=HSC70;
OS Ictalurus punctatus (Channel catfish).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Osteiophysi; Siluriformes;
OC Ictaluridae; Ictalurus.
OX NCBI_TaxID=7998;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97090143; PubMed=8936051; DOI=10.1016/0305-0491(95)02022-5;

RA Luft J.C., Wilson M.R., Bly J.E., Miller N.W., Clem L.W.;
RT "Identification and characterization of a heat shock protein 70 family
RT member in channel catfish (Ictalurus punctatus).";
RL Comp. Biochem. Physiol. 113B:169-174 (1996).
CC -!- SIMILARITY: Belongs to the heat shock protein 70 family.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; U22460; AAA64872.1; -;
DR HSSP; P08109; 1CKR.
DR InterPro; IPR001023; HSP70.
DR Pfam; PF00012; HSP70; 1.
DR PRINTS; PR00301; HEATSHOCK70.
DR ProDom; PD000089; Hsp70; 1.
DR TIGRFAMs; TIGR01991; Hsca; 1.
DR PROSITE; PS00297; HSP70_1; 1.
DR PROSITE; PS00329; HSP70_2; 1.
DR PROSITE; PS01036; HSP70_3; 1.
KW ATP-binding; Heat shock; Multigene family.
SQ SEQUENCE 649 AA; 71340 MW; D31B8D348D7583CB CRC64;

Query Match 82.8%; Score 1088; DB 1; Length 649;
Best Local Similarity 80.8%; Pred. No. 3.8e-59;
Matches 215; Conservative 19; Mismatches 24; Indels 8; Gaps 3;

QY 1 KSENVQDLLLDVAPLSGLGTAGGVTALIKRNTIPTKTQTQFTTYSNQPGLVQVY 60
DB 384 KSENVQDLLLDVTPLSGLGTAGGVTALIKRNTIPTKTQTQFTTYSNQPGLVQVY 443

QY 61 EGERAMTKNNLLGRFELSGIPPPAPRGVPOIEVTFDIDANGILNVATDSTGKANKITI 120
DB 444 EGERAMTKNNLLGKLFELTGIPPPAPRGVPOIEVTFDIDANGILNVSAVDKSTGKANKITI 503

QY 121 TNDKGRLSKEEIERMVQAEKYEKAEDEVQRRVSAKNALSYAFNMKSAVEDEGLKGIS 180
DB 504 TNDKGRLSKEDIERMVQAEKYEKAEDEVQRRVSAKNALSYAFNMKSAVEDEGLKGIS 563

QY 181 EADKKVLDKQEVISWLDANTLAEKDFEKKELQVNCNPIISGLYQAGG-PG---- 235
DB 564 DEDKHKLKCNVEISWLDKNTAKQAEYEHQKLEKVCNPIITKLYQSDGGMGMPD 623

QY 236 --PGGFGAQQ-PKGSGSGPTIEVD 258
DB 624 GMPGGFQELGAAPGGSGSGPTIEVD 649

RESULT 46
Q8UV14 PRELIMINARY; PRT; 651 AA.
ID Q8UV14
AC Q8UV14
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Heat shock protein 70.
DE Name=HSP70;
OS Ambystoma mexicanum (Axolotl).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Caudata; Salamandroidea; Ambystomatidae;
OC Ambystoma.
OX NCBI_TaxID=8296;
RN [1]
RP SEQUENCE FROM N.A.
RA Ordenez M.R., Pichon L.L., Laurens V.;
RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: Belongs to the heat shock protein 70 family.
DR EMBL; AY029210; AAK31583.1; -;
DR HSSP; P19120; 1ATR.

DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0006457; P:protein folding; IEA.
DR GO; GO:0006986; P:response to unfolded protein; IEA.
DR Pfam; PF00012; HSP70; 1.
DR PRINTS; PR00301; HEATSHOCK70.
DR ProDom; PD000089; Hsp70; 1.
DR PROSITE; PS00297; HSP70_1; 1.
DR PROSITE; PS00329; HSP70_2; 1.
DR PROSITE; PS01036; HSP70_3; 1.
KW ATP-binding; Heat shock.
SQ SEQUENCE 651 AA; 71055 MW; 86C75FA0DCEFCB9D CRC64;

Query Match 82.8%; Score 1088; DB 2; Length 651;
Best Local Similarity 80.6%; Pred. No. 3.8e-59;
Matches 216; Conservative 22; Mismatches 20; Indels 10; Gaps 4;

QY 1 KSENVQDLLLDVAPLSGLGTAGGVTALIKRNTIPTKTQTQFTTYSNQPGLVQVY 60
DB 384 KSENVQDLLLDVTPLSGLGTAGGVTALIKRNTIPTKTQTQFTTYSNQPGLVQVY 443

QY 61 EGERAMTKNNLLGRFELSGIPPPAPRGVPOIEVTFDIDANGILNVATDSTGKANKITI 120
DB 444 EGERAMTKNNLLGKLFELTGIPPPAPRGVPOIEVTFDIDANGILNVSAVDKSTGKANKITI 503

QY 121 TNDKGRLSKEEIERMVQAEKYEKAEDEVQRRVSAKNALSYAFNMKSAVEDEGLKGIS 180
DB 504 TNDKGRLSKEDIERMVQAEKYEKAEDEVQRRVSAKNALSYAFNMKSAVEDEGLKGIS 563

QY 181 EADKKVLDKQEVISWLDANTLAEKDFEKKELQVNCNPIISGLYQAGG----PG 235
DB 564 DDDTKTLEKCNRIIAWLDKNTAKQAEYEHQKLEKVCNPIITKLYQAGGMPGMPG 623

QY 236 --PGGP-GAQGPKGSGG--SGPTIEVD 258
DB 624 GMPGGFQELGAAPGGSGSGPTIEVD 651

RESULT 47
HS1A_RAT STANDARD; PRT; 641 AA.
ID HS1A_RAT
AC P55063; 1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Heat shock protein 1A (Heat shock 70 kDa protein 3) (HSP70.3).
DE Name=Hsp1A; Synonyms=Hsp70-3;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=LEW.1W/GUN;
RX MEDLINE=95012453; PubMed=7927536;
RA Walter L., Rauh F., Guenther E.;
RT "Comparative analysis of the three major histocompatibility complex-
RT linked heat shock protein 70 (Hsp70) genes of the rat."
RL Immunogenetics 40:325-330 (1994).
CC -!- FUNCTION: In cooperation with other chaperones, Hsp70s stabilize
CC of newly translated polypeptides in the cytosol as well as within
CC organelles. These chaperones participate in all these processes
CC through their ability to recognize nonnative conformations of
CC other proteins. They bind extended peptide segments with a net
CC hydrophobic character exposed by polypeptides during translation
CC and membrane translocation, or following stress-induced damage.
CC -!- INDUCTION: By heat shock.
CC -!- SIMILARITY: Belongs to the heat shock protein 70 family.
CC -----
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way

KW ATP-binding; Heat shock.
 FT NON TER 1 1
 SQ SEQUENCE 644 AA; 70594 MW; CD8E8269BA7776F4 CRC64;
 Query Match 82.6%; Score 1086; DB 2; Length 644;
 Best Local Similarity 80.5%; Pred. No. 5e-59;
 Matches 214; Conservative 21; Mismatches 23; Indels 8; Gaps 3;
 Qy 1 KSENVQDILLDLVAPLSGLTAGVMTALIKRNSTIPTKTQTFTTYSNQPGVLIQVY 60
 Db KSENVQDILLDLVAPLSGLTAGVMTALIKRNSTIPTKTQTFTTYSNQPGVLIQVY 438
 Qy 61 EGERAMTKDNNLLGRFELSGIPPRGVPQIEVTFDIDANGILNVATDSTGKANKITI 120
 Db EGDVPLTKDNNLLGKFLTGIPPRGVPQIEVTFDIDANGILNVATDSTGKANKITI 498
 Qy 121 TNDKGRLSKEEIERMVOEAKYKAEDVQRRVSNAKNALESYAFNMKSAVEDEGLKGKIS 180
 Db TNDKGRLSKEDIEMRWQAEAKYKVEDDVQRRKVSNAKNALESYAFNMKSTVEDEKLKGKIS 558
 Qy 181 EADKKVKLDKQCVISWLDANTLAEDKDFEHHKKELEQVNCNPISGLYQAGGPG-- 235
 Db DEDKKTIVDKCSEVITWLDANQAEKDEYEHKQKELEGVNCNPITTKLYQAGGAGMPGG 618
 Qy 236 --PGGF-GAOGPKGGSGGPTIEVD 258
 Db GMPGGFFGAGSAGSGGPTIEVD 644
 RESULT 50
 Q6RYT8 PRELIMINARY; PRT; 659 AA.
 AC Q6RYT8
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 DE Heat shock protein 70.
 GN Name=hsp70;
 OS Aequipecten irradians (Bay scallop).
 OC Eukaryota; Metazoa; Mollusca; Bivalvia; Pteriomorpha; Pectinoida;
 OC Pectinoidea; Pectinidae; Argopecten.
 OX NCBI_TaxID=31199;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Wu L., Song L., Xu W., Guo X., Xiang J.;
 RL Submitted (NOV-2003) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: Belongs to the heat shock protein 70 family.
 DR EMBL; AY485261; AAS17723.1; -
 DR HSP; P19120; 1BA1.
 DR GO; GO:0005524; F:ATP binding; IEA.
 DR GO; GO:0006457; P:protein folding; IEA.
 DR GO; GO:0006986; P:response to unfolded protein; IEA.
 DR InterPro; IPR001023; Hsp70.
 DR Pfam; PF00012; Hsp70; 1.
 DR PRINTS; PR00301; HEATSHOCK70.
 DR ProDom; PD000089; Hsp70; 1.
 DR PROSITE; PS00297; HSP70_1; 1.
 DR PROSITE; PS00329; HSP70_2; 1.
 DR PROSITE; PS01036; HSP70_3; 1.
 KW ATP-binding; Heat shock.
 SQ SEQUENCE 659 AA; 71801 MW; 43C3E8EA71B51AB3 CRC64;
 Query Match 82.6%; Score 1086; DB 2; Length 659;
 Best Local Similarity 78.1%; Pred. No. 5.1e-59;
 Matches 214; Conservative 18; Mismatches 26; Indels 16; Gaps 2;
 Qy 1 KSENVQDILLDLVAPLSGLTAGVMTALIKRNSTIPTKTQTFTTYSNQPGVLIQVY 60
 Db KSENVQDILLDLVAPLSGLTAGVMTALIKRNSTIPTKTQTFTTYSNQPGVLIQVY 445
 Qy 61 EGERAMTKDNNLLGRFELSGIPPRGVPQIEVTFDIDANGILNVATDSTGKANKITI 120
 Db EGERAMTKDNNLLGKFLTGIPPRGVPQIEVTFDIDANGILNVATDSTGKANKITI 505

Qy 121 TNDKGRLSKEEIERMVOEAKYKAEDVQRRVSNAKNALESYAFNMKSAVEDEGLKGKIS 180
 Db TNDKGRLSKEDIEMRWQAEAKYKAEDDVQRRKVSNAKNALESYAFNMKSTVEDEKLKGKIS 565
 Qy 181 EADKKVKLDKQCVISWLDANTLAEDKDFEHHKKELEQVNCNPISGLYQAGGPG-- 235
 Db EDDKKTIVDKCSEVITWLDANQAEKDEYEHKQKELEGVNCNPITTKLYQAGGAGMPGG 625
 Qy 236 -----PGGF-GAOGPKGGSGGPTIEVD 258
 Db MPGGMPGMPGMPGGGADSGSGGPTIEVD 659
 RESULT 51
 HS7T MOUSE
 ID HS7T MOUSE STANDARD; PRT; 641 AA.
 AC P16627; Q61693;
 DT 01-AUG-1990 (Rel. 15, Created)
 DT 01-FEB-1996 (Rel. 33, Last sequence update)
 DT 25-OCT-2004 (Rel. 45, Last annotation update)
 DE Heat shock 70 kDa-like protein 1.
 GN Name=Hspall; Synonyms=Hsc70t;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA MEDLINE=90147735; PubMed=2302214;
 RX Matsumoto M., Fujimoto H.;
 RT "Cloning of a hsp70-related gene expressed in mouse spermatids.";
 RL Biochem. Biophys. Res. Commun. 166:43-49(1990).
 RN [2]
 RP REVISIONS.
 RA Fujimoto H.;
 RL Submitted (AUG-1995) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Testis;
 RX MEDLINE=94299288; PubMed=8026864;
 RA Snoek M., Olavesen M.G., van Vugt H., Milner C.M., Teuscher C.,
 RA Campbell R.D.;
 RT "Coding sequences and levels of expression of Hsc70t are identical in
 mice with different Orch-1 alleles.";
 RL Immunogenetics 40:159-162(1994).
 CC -1- TISSUE SPECIFICITY: Expressed in spermatids.
 CC -1- DEVELOPMENTAL STAGE: Specifically expressed in postmeiotic phases
 of spermatogenesis.
 CC -1- SIMILARITY: Belongs to the heat shock protein 70 family.
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 or send an email to license@isb-sib.ch).
 DR EMBL; M32218; AAA74906.1; -
 DR EMBL; L27086; AAA59362.1; -
 DR PIR; A34041; A34041.
 DR PIR; I49761; I49761.
 DR HSP; P08107; 1HJO.
 DR MGD; MGI:96231; Hspall.
 DR InterPro; IPR001023; Hsp70.
 DR Pfam; PF00012; HSP70; 1.
 DR PRINTS; PR00301; HEATSHOCK70.
 DR ProDom; PD000089; Hsp70; 1.
 DR TIGRFAMs; TIGR01991; HscA; 1.
 DR PROSITE; PS00297; HSP70_1; 1.
 DR PROSITE; PS00329; HSP70_2; 1.
 DR PROSITE; PS01036; HSP70_3; 1.

KW ATP-binding; Heat shock; Multigene family; Spermatogenesis.
 FT CONFLICT 634 D -> G (in Ref. 3).
 SQ SEQUENCE 641 AA; 70695 MW; 3BCA15217B03BC2A CRC64;

Query Match 82.6%; Score 1085; DB 1; Length 641;
 Best Local Similarity 84.1%; Pred. No. 5.7e-59;
 Matches 217; Conservative 17; Mismatches 22; Indels 2; Gaps 2;

Qy 1 KSENVQDLLLLDVAPLSIGLETAGGVMTALIKRNSTIPTKTQTFTTYSNDQPGVLIQVY 60
 |||||
 Db 386 KSEKVDLLLLDVAPLSIGLETAGGVMTLVIKRNSTIPTKTQTFTTYSNDQPGVLIQVY 445

Qy 61 EGERAMTKNNLLGRFELSGIPPPAPRGVQIEVTFDIDANGILNVTATDKSTGKANKITI 120
 |||||
 Db 446 EGERAMTKNNLLGRFELSGIPPPAPRGVQIEVTFDIDANGILNVTATDKSTGKANKITI 505

Qy 121 TNDKGRLSKEIEIRMVQEAERYKAEDVQERVSAAKNALESYAFNMKSAVDEGLKGGKIS 180
 |||||
 Db 506 TNDKGRLSKEIEIRMVQEAERYKAEDVQERVSAAKNALESYAFNMKSAVDEGLKGGKIS 565

Qy 181 EADKKKVLDDKCOEIVSWLDANTLAEDKDFEHKREKEQVNCNPIISGLYQAGGPGGFG 240
 |||||
 Db 566 ESDKKKILDKCNVLSWLEAQLAEKDFDHRKELENCNPIITKLYQ-SGCTGPTCTP 624

Qy 241 AQGPKGSGSGPTIEEVD 258
 |||||
 Db 625 GYTP-GRAATDPTIEEVD 641

RESULT 52
 HS70 ONCMY STANDARD; PRT; 651 AA.
 AC P08108;
 DT 01-AUG-1988 (Rel. 08, Created)
 DT 01-AUG-1988 (Rel. 08, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Heat shock cognate 70 kDa protein (HSP70).
 GN Name=HSC71;
 OS Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
 OC Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
 OX NCBI_TaxID=8022;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=92174952; PubMed=1371753;
 RA Zafarullah M., Wisniewski J., Shworak N.W., Schieman S., Misra S.;
 RA Gedamu L.;
 RT "Molecular cloning and characterization of a constitutively expressed
 RT heat-shock-cognate hsc71 gene from rainbow trout.";
 RL Eur. J. Biochem. 204:893-900(1992).
 RN [2]
 RP SEQUENCE OF 1-213 FROM N.A.
 RX MEDLINE=85036330; PubMed=6092938;
 RA Kothary R.K., Jones D., Candido E.P.M.;
 RT "70-Kilodalton heat shock polypeptides from rainbow trout:
 RT characterization of cDNA sequences.";
 RL Mol. Cell. Biol. 4:1785-1791(1984).
 CC -1- SIMILARITY: Belongs to the heat shock protein 70 family.
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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 CC or send an email to license@sb-sib.ch).
 CC -----
 CC EMBL; S85730; AAB21658.1; -;
 CC EMBL; K02550; AAA49563.1; -;
 CC PIR; S21175; S21175.
 CC HSP70; P08109; 1CKR.
 DR InterPro; IPR001023; Hsp70.

DR Pfam; PF00012; HSP70; 1.
 DR PRINTS; PR00301; HEATSHOCK70.
 DR PRODOM; PD000089; Hsp70; 1.
 DR TIGRFAMs; TIGR01991; HscA; 1.
 DR PROSITE; PS00297; HSP70_1; 1.
 DR PROSITE; PS00329; HSP70_2; 1.
 DR PROSITE; PS01036; HSP70_3; 1.
 KW ATP-binding; Heat shock.
 FT CONFLICT 182 183
 SQ SEQUENCE 651 AA; 71283 MW; 8701630A0CBC4BEO CRC64;

Query Match 82.5%; Score 1084; DB 1; Length 651;
 Best Local Similarity 79.5%; Pred. No. 6.7e-59;
 Matches 213; Conservative 21; Mismatches 24; Indels 10; Gaps 3;

Qy 1 KSENVQDLLLLDVAPLSIGLETAGGVMTALIKRNSTIPTKTQTFTTYSNDQPGVLIQVY 60
 |||||
 Db 384 KSENVQDLLLLDVAPLSIGLETAGGVMTLVIKRNSTIPTKTQTFTTYSNDQPGVLIQVY 443

Qy 61 EGERAMTKNNLLGRFELSGIPPPAPRGVQIEVTFDIDANGILNVTATDKSTGKANKITI 120
 |||||
 Db 444 EGERAMTKNNLLGRFELSGIPPPAPRGVQIEVTFDIDANGILNVTATDKSTGKANKITI 503

Qy 121 TNDKGRLSKEIEIRMVQEAERYKAEDVQERVSAAKNALESYAFNMKSAVDEGLKGGKIS 180
 |||||
 Db 504 TNDKGRLSKEIEIRMVQEAERYKAEDVQERVSAAKNALESYAFNMKSAVDEGLKGGKIS 563

Qy 181 EADKKKVLDDKCOEIVSWLDANTLAEDKDFEHKREKEQVNCNPIISGLYQAGG-PG----- 235
 |||||
 Db 564 DEDTKILEKCNVIGWLDKKNQTAKEEYHHQLEKVCNPIITKLYQAGGPGGMPGE 623

Qy 236 --PGGP---GAQPKGSGSGPTIEEVD 258
 |||||
 Db 624 GMAGGPPGAGGAAPGGSGSGPTIEEVD 651

RESULT 53
 O73885
 ID O73885 PRELIMINARY; PRT; 646 AA.
 AC O73885;
 DT 01-AUG-1998 (TRENBLrel. 07, Created)
 DT 01-AUG-1998 (TRENBLrel. 07, Last sequence update)
 DT 01-MAR-2004 (TRENBLrel. 26, Last annotation update)
 DE Heat shock cognate 70.
 GN Name=hsc70;
 OS Gallus gallus (Chicken).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
 OC Gallus.
 OX NCBI_TaxID=9031;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=White Leghorn; TISSUE=Whole embryo;
 RX MEDLINE=98374286; PubMed=9707581; DOI=10.1073/pnas.95.17.9950;
 RA de la Rosa E.J., Vega-Nunez E., Morales A.V., Serna J., Rubio E.,
 RA de Pablo F.;
 RT "Modulation of the chaperone heat shock cognate 70 by embryonic
 RT (pro)insulin correlates with prevention of apoptosis.";
 RL Proc. Natl. Acad. Sci. U.S.A. 95:9950-9955(1998).
 CC -1- SIMILARITY: Belongs to the heat shock protein 70 family.
 CC EMBL; AJ004940; CAA06233.1; -;
 CC HSP70; P19120; IATR.
 DR GO; GO:0005524; F:ATP binding; IEA.
 DR GO; GO:0006457; P:protein folding; IEA.
 DR GO; GO:0006986; P:response to unfolded protein; IEA.
 DR InterPro; IPR001023; Hsp70.
 DR Pfam; PF00012; HSP70; 1.
 DR PRINTS; PR00301; HEATSHOCK70.
 DR PRODOM; PD000089; Hsp70; 1.
 DR PROSITE; PS00297; HSP70_1; 1.
 DR PROSITE; PS00329; HSP70_2; 1.
 DR PROSITE; PS01036; HSP70_3; 1.
 KW ATP-binding; Heat shock.

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SQ SEQUENCE 646 AA; 70826 MW; 2151332ED42C5B9B CRC64;
Query Match 82.1%; Score 1078.5; DB 2; Length 646;
Best Local Similarity 80.2%; Pred. No. 1.5e-58;
Matches 211; Conservative 23; Mismatches 24; Indels 5; Gaps 3;

Qy 1 KSENVQDILLDVLAPLSGLGTAGGVTALIKRNSITPTKQTQFTTYSNQPGLVLIQVY 60
Db 384 KSENVQDILLDVLAPLSGLGTAGGVTALIKRNTTPTKQTQFTTYSNQPGLVLIQVY 443

Qy 61 EGERAMTKDNNLLGRFELSGIPAPRGVPOIEVTFDIDANGILNVATDSTGKANKITI 120
Db 444 EGERAMTKDNNLLGKFLGTGIPAPRGVPOIEVTFDIDANGILNVATDSTGKANKITI 503

Qy 121 TNDKGRLSKEEIERMWQEAKEYKAEDVQERVSAAKNALSYAFNMKSASVEDGLKGKIS 180
Db 504 TNDKGRLSKEDIERMWQEAKEYKAEDQKQDEKQRTAAKNGLSYAFNMKSTVDDEKLKDKIS 563

Qy 181 EADKKVKLDKQCEVISWLDANTLAEDKDFEHRKELEQVNCNPIISGLYQAGG-PG--PG 237
Db 564 DEDHQNLIDKCNELIINWLDKNTAEKEFEHRKELEQVNCNPIITKLYQSAGGMPGMPG 623

Qy 238 GF--GAQPGKGGSGGPTIEVD 258
Db 624 GFPGGAPPSSGGSGGPTIEVD 646

RESULT 54
Q9XZJ2 PRELIMINARY; PRT; 659 AA.
AC Q9XZJ2;
DT 01-NOV-1999 (TrEMBLrel. 12, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Heat shock protein 70 (71kDa heat shock connate protein).
GN Name=hsp70; Synonyms=HSC71;
OS Crassostrea gigas (Pacific oyster).
OC Eukaryota; Metazoa; Mollusca; Bivalvia; Pteriomorpha; Ostreoida;
OC Ostreoida; Ostreidae; Crassostrea.
OX NCBI_TaxID=29159;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=20541285; PubMed=11092738;
RX Gourdine I., Gricourt L., Kellner K., Roch P., Escoubas J.-M.;
RT "Characterization of a cDNA encoding a 72 kDa heat shock cognate
RT protein (Hsc72) from the Pacific oyster, Crassostrea gigas.";
RL DNA Seq. 11:265-270(2000).
RN [2]
RP SEQUENCE FROM N.A.
RA Yokoyama Y.;
RL Submitted (OCT-2003) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: Belongs to the heat shock protein 70 family.
DR EMBL; AF144646; AAD31042.1; -.
DR EMBL; AB122084; BADI5287.1; -.
DR HSP; P19120; 3HSC.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0006457; P:protein folding; IEA.
DR GO; GO:0006986; P:response to unfolded protein; IEA.
DR InterPro; IPR001023; Hsp70.
DR Pfam; PF00012; HSP70; 1.
DR PRINTS; PR00301; HEATSHOCK70.
DR PROSITE; PS00297; HSP70_1; 1.
DR PROSITE; PS00329; HSP70_2; 1.
DR PROSITE; PS01036; HSP70_3; 1.
DR ATP-binding; Heat shock.
KW ATP-binding; Heat shock.
SQ SEQUENCE 659 AA; 72042 MW; 907C52AB780AD3F8 CRC64;
Query Match 82.0%; Score 1077; DB 2; Length 659;
Best Local Similarity 79.3%; Pred. No. 1.8e-58;
Matches 214; Conservative 19; Mismatches 25; Indels 12; Gaps 4;

Qy 1 KSENVQDILLDVLAPLSGLGTAGGVTALIKRNSITPTKQTQFTTYSNQPGLVLIQVY 60
Db 384 KSENVQDILLDVLAPLSGLGTAGGVTALIKRNTTPTKQTQFTTYSNQPGLVLIQVY 443

Qy 61 EGERAMTKDNNLLGRFELSGIPAPRGVPOIEVTFDIDANGILNVATDSTGKANKITI 120
Db 444 EGERAMTKDNNLLGKFLGTGIPAPRGVPOIEVTFDIDANGILNVATDSTGKANKITI 503

Qy 121 TNDKGRLSKEEIERMWQEAKEYKAEDVQERVSAAKNALSYAFNMKSASVEDGLKGKIS 180
Db 504 TNDKGRLSKEDIERMWQEAKEYKAEDQKQDEKQRTAAKNGLSYAFNMKSTVDDEKLKDKIS 563

Qy 181 EADKKVKLDKQCEVISWLDANTLAEDKDFEHRKELEQVNCNPIISGLYQAGG-PG--PG 237
Db 564 DEDHQNLIDKCNELIINWLDKNTAEKEFEHRKELEQVNCNPIITKLYQSAGGMPGMPG 623

Qy 238 GF--GAQPGKGGSGGPTIEVD 258
Db 624 GFPGGAPPSSGGSGGPTIEVD 646

RESULT 54
Q9XZJ2 PRELIMINARY; PRT; 659 AA.
AC Q9XZJ2;
DT 01-NOV-1999 (TrEMBLrel. 12, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Heat shock protein 70 (71kDa heat shock connate protein).
GN Name=hsp70; Synonyms=HSC71;
OS Crassostrea gigas (Pacific oyster).
OC Eukaryota; Metazoa; Mollusca; Bivalvia; Pteriomorpha; Ostreoida;
OC Ostreoida; Ostreidae; Crassostrea.
OX NCBI_TaxID=29159;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=20541285; PubMed=11092738;
RX Gourdine I., Gricourt L., Kellner K., Roch P., Escoubas J.-M.;
RT "Characterization of a cDNA encoding a 72 kDa heat shock cognate
RT protein (Hsc72) from the Pacific oyster, Crassostrea gigas.";
RL DNA Seq. 11:265-270(2000).
RN [2]
RP SEQUENCE FROM N.A.
RA Yokoyama Y.;
RL Submitted (OCT-2003) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: Belongs to the heat shock protein 70 family.
DR EMBL; AF144646; AAD31042.1; -.
DR EMBL; AB122084; BADI5287.1; -.
DR HSP; P19120; 3HSC.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0006457; P:protein folding; IEA.
DR GO; GO:0006986; P:response to unfolded protein; IEA.
DR InterPro; IPR001023; Hsp70.
DR Pfam; PF00012; HSP70; 1.
DR PRINTS; PR00301; HEATSHOCK70.
DR PROSITE; PS00297; HSP70_1; 1.
DR PROSITE; PS00329; HSP70_2; 1.
DR PROSITE; PS01036; HSP70_3; 1.
DR ATP-binding; Heat shock.
KW ATP-binding; Heat shock.
SQ SEQUENCE 659 AA; 72042 MW; 907C52AB780AD3F8 CRC64;
Query Match 82.0%; Score 1077; DB 2; Length 659;
Best Local Similarity 79.3%; Pred. No. 1.8e-58;
Matches 214; Conservative 19; Mismatches 25; Indels 12; Gaps 4;

Qy 1 KSENVQDILLDVLAPLSGLGTAGGVTALIKRNSITPTKQTQFTTYSNQPGLVLIQVY 60
Db 384 KSENVQDILLDVLAPLSGLGTAGGVTALIKRNTTPTKQTQFTTYSNQPGLVLIQVY 443

Qy 61 EGERAMTKDNNLLGRFELSGIPAPRGVPOIEVTFDIDANGILNVATDSTGKANKITI 120
Db 444 EGERAMTKDNNLLGKFLGTGIPAPRGVPOIEVTFDIDANGILNVATDSTGKANKITI 503

Qy 121 TNDKGRLSKEEIERMWQEAKEYKAEDVQERVSAAKNALSYAFNMKSASVEDGLKGKIS 180
Db 504 TNDKGRLSKEDIERMWQEAKEYKAEDQKQDEKQRTAAKNGLSYAFNMKSTVDDEKLKDKIS 563

Qy 181 EADKKVKLDKQCEVISWLDANTLAEDKDFEHRKELEQVNCNPIISGLYQAGG-PG--PG 237
Db 564 DEDHQNLIDKCNELIINWLDKNTAEKEFEHRKELEQVNCNPIITKLYQSAGGMPGMPG 623

Qy 238 GF--GAQPGKGGSGGPTIEVD 258
Db 624 GFPGGAPPSSGGSGGPTIEVD 646

RESULT 54
Q9XZJ2 PRELIMINARY; PRT; 345 AA.
AC Q9XZJ2;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Heat shock protein 70 (Fragment).
OS Dirofilaria immitis (Canine heartworm).
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Spirurida; Filarioidea;
OC Onchocercidae; Dirofilaria.
OX NCBI_TaxID=6287;
RN [1]
RP SEQUENCE FROM N.A.
RA Culpepper J.A., Friedman L., Dale B.;
RL Submitted (AUG-1992) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: Belongs to the heat shock protein 70 family.
DR EMBL; M95648; AAA28298.1; -.
DR HSP; P19120; 3HSC.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0006457; P:protein folding; IEA.
DR GO; GO:0006986; P:response to unfolded protein; IEA.
DR InterPro; IPR001023; Hsp70.
DR Pfam; PF00012; HSP70; 1.
DR PRINTS; PR00301; HEATSHOCK70.
DR PROSITE; PS01036; HSP70_3; 1.
DR ATP-binding; Heat shock.
KW ATP-binding; Heat shock.
FT NON TER 345
SQ SEQUENCE 345 AA; 37497 MW; 42963D21A7585F09 CRC64;
Query Match 81.7%; Score 1074; DB 2; Length 345;
Best Local Similarity 80.9%; Pred. No. 1.3e-58;
Matches 212; Conservative 18; Mismatches 28; Indels 4; Gaps 3;

Qy 1 KSENVQDILLDVLAPLSGLGTAGGVTALIKRNSITPTKQTQFTTYSNQPGLVLIQVY 60
Db 84 KSENVQDILLDVLAPLSGLGTAGGVTALIKRNTTPTKQTQFTTYSNQPGLVLIQVY 143

Qy 61 EGERAMTKDNNLLGRFELSGIPAPRGVPOIEVTFDIDANGILNVATDSTGKANKITI 120
Db 144 EGERAMTKDNNLLGKFLGTGIPAPRGVPOIEVTFDIDANGILNVATDSTGKANKITI 203

Qy 121 TNDKGRLSKEEIERMWQEAKEYKAEDVQERVSAAKNALSYAFNMKSASVEDGLKGKIS 180
Db 204 TNDKGRLSKEDIERMWQEAKEYKAEDQKQDEKQRTAAKNGLSYAFNMKSTVDDEKLKDKIS 263

Qy 181 EADKKVKLDKQCEVISWLDANTLAEDKDFEHRKELEQVNCNPIISGLYQAGG-PG--PG 237
Db 264 EDDKKKIQEKDETVRWLDGNQTAEDKDFEHRKELEQVNCNPIITKLYQSAGGMPGMPG 323

Qy 238 GF--GAQPGKGGSGGPTIEVD 258
Db 324 GFPGGAPPSSGGSGGPTIEVD 345
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RESULT 56
ID 073788
AC 073788; PRELIMINARY; PRT; 650 AA.
DT 01-AUG-1998 (TrEMBLrel. 07, Created)
DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Heat shock protein 70.
GN Name=HSP70;
OS Paralicthys olivaceus (Japanese flounder).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percormorpha; Pleuronectiformes;
OC Pleuronectoidae; Paralicthysidae; Paralicthys.
OX NCBI_TaxID=8255;
RN [1]
RP SEQUENCE FROM N.A.
RA Kim W.J., Lee J.H., Kim K.K., Lee S.J., Kang H.S., Kim H.D.;
RT "Molecular cloning and characterization of a heat shock protein 70-
RL related cDNA from olive flounder (Paralicthys olivaceus).";
CC Han-gug yangig Hag-hoeji 12:91-100(1999).
CC -1- SIMILARITY: Belongs to the heat shock protein 70 family.
DR EMBL; AF053059; AAC33859.1; --
DR HSP; P19120; IATR.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0006457; P:protein folding; IEA.
DR GO; GO:0006986; P:response to unfolded protein; IEA.
DR InterPro; IPR001023; Hsp70.
DR Pfam; PF00012; Hsp70; 1.
DR PRINTS; PR00301; HEATSHOCK70.
DR PRODOM; PD000089; Hsp70; 1.
DR PROSITE; PS00297; HSP70_1; 1.
DR PROSITE; PS00329; HSP70_2; 1.
DR PROSITE; PS01036; HSP70_3; 1.
KW ATP-binding; Heat shock.
SQ SEQUENCE 650 AA; 71115 MW; 6B24E7D409FC76EA CRC64;

Query Match 81.7%; Score 1073.5; DB 2; Length 650;
Best Local Similarity 79.0%; Pred. No. 3e-58;
Matches 211; Conservative 22; Mismatches 25; Indels 9; Gaps 3;

Qy 1 KSENVQDLLLLDVAPLSGLGTAGVMTALIKRNTIPTKTQTFTTYSNDNQPVLIQVY 60
Db 384 KSENVQDLLLLDVTPLSGLGTAGVMTALIKRNTIPTKTQTFTTYSNDNQPVLIQV 443

Qy 61 EGERAMTKDNNLLGRFELSGIPAPRGVPQIEVTFDIDANGILNVTATDKSTGKANKITI 120
Db 444 EGERAMTRDNNLLGKFLTGIPAPRGVPQIEVTFDIDANGIMNVSADKSTGKANKITI 503

Qy 121 TNDKGRLSKKEIERMVQAEKYKAEDVQERVSQAKNALESYAFNMKSAVEDEGLKGKIS 180
Db 504 TNDKGRLSKDEIERMVQAEADRYKTEDEAQRDKISAKNSLESIAFNMKSTVDEDEKLKOKIS 563

Qy 181 EADKKKVLDCQEVISWLDANTLAEKDFEHRKELSOVCNPIISGLYQAGGPG- 235
Db 564 QEDKQKILDKCNVISWLDNRQMAEKSEYEHQKELQNLCLNPIITKLYQAGGAGMPGGM 623

Query Match 81.7%; Score 1073.5; DB 2; Length 652;
Best Local Similarity 77.3%; Pred. No. 3e-58;
Matches 208; Conservative 25; Mismatches 25; Indels 11; Gaps 2;

Qy 1 KSENVQDLLLLDVAPLSGLGTAGVMTALIKRNTIPTKTQTFTTYSNDNQPVLIQVY 60
Db 384 KSENVQDLLLLDVTPLSGLGTAGVMTALIKRNTIPTKTQTFTTYSNDNQPVLIQV 443

Qy 61 EGERAMTKDNNLLGRFELSGIPAPRGVPQIEVTFDIDANGILNVTATDKSTGKANKITI 120
Db 444 EGERAMTKDNNLLGKFLTGIPAPRGVPQIEVTFDIDANGIMNVSADKSTGKANKITI 503

Qy 121 TNDKGRLSKKEIERMVQAEKYKAEDVQERVSQAKNALESYAFNMKSAVEDEGLKGKIS 180
Db 504 TNDKGRLSKDEIERMVQAEADRYKTEDEAQRDKISAKNSLESIAFNMKSTVDEDEKLKOKIS 563

Qy 181 EADKKKVLDCQEVISWLDANTLAEKDFEHRKELSOVCNPIISGLYQAGGPG- 235
Db 564 QEDKQKILDKCNVISWLDNRQMAEKSEYEHQKELQNLCLNPIITKLYQAGGAGMPGGM 623

RESULT 57
ID 06AZH8
AC 06AZH8; PRELIMINARY; PRT; 652 AA.
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Hypothetical protein.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

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Qy 236 ----PGGF--GAQPKGSGSGPTIEVD 258
Db 624 PGMPGGPGAGAGGGSGSGPTIEVD 652

RESULT 58
Q86QW8
ID Q86QW8 PRELIMINARY; PRT; 654 AA.
AC Q86QW8;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Hsp70 family member (Fragment).
OS Locusta migratoria (Migratory locust).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Orthopteroidea; Orthoptera; Caelifera; Acridomorpha;
OC Acridoidea; Acrididae; Oedipodinae; Locusta.
OX NCBI_TaxID=7004;
RN [1]
RP SEQUENCE FROM N.A.
RA Qin W., Tyshenko M.G., Wu B.S., Walker V.K., Robertson M.R.;
RL Submitted (NOV-2002) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: Belongs to the heat shock protein 70 family.
DR EMBL; AY178988; AA021473.1; -.
DR HSSP; P19120; 3HSC.
DR GO; GO:0005524; F:ATP binding; IEA.
DR InterPro; IPR001023; Hsp70.
DR Pfam; PF00012; HSP70; 1.
DR PRINTS; PR00301; HEATSHOCK70.
DR PRODOM; PD00089; Hsp70; 1.
DR PROSITE; PS00297; HSP70_1; 1.
DR PROSITE; PS00329; HSP70_2; 1.
DR PROSITE; PS01036; HSP70_3; 1.
KW ATP-binding.
FT NON TER 654
SQ SEQUENCE 654 AA; 71408 MW; 3389F746D03B2F4B CRC64;

Query Match 81.4%; Score 1070; DB 2; Length 654;
Best Local Similarity 78.5%; Pred. No. 5e-58;
Matches 212; Conservative 19; Mismatches 27; Indels 12; Gaps 3;

Qy 1 KSENVQDLLLDVAPLSLGLETAGVMTALIKRNSTIPTKTQITFTTYSNDQPGVLIQVY 60
Db 385 KSEEVQDLLLDVPLSLGIETAGVMTLLIKRNTTPTKTQITFTTYSNDQPGVLIQVY 444

Qy 61 EGERAMTKDNNLGRFELSGIPAPRGVPQIEVTFDIDANGILNVTATDKSTGKANKITI 120
Db 445 EGERAMTKDNNLGRFELSGIPAPRGVPQIEVTFDIDANGILNVTATDKSTGKANKITI 504

Qy 121 TNDKGRLSKEIERMVOEAERYKAEDVQERVSANAKLESYAFNMKSAVEDGLKKGKIS 180.
Db 505 TNDKGRLSKEIERMVOEAERYKAEDVQERVSANAKLESYCFNMKSTVEDEKLKOKIS 564

Qy 181 EADKKVLDKCOEIVSWLDANTLAEKDFEHRKELEQVNCNPIISGLYQAGG-----PG 235
Db 565 DSDKQTILDKCNVIRWLDANQLAEKFEKQKELEQICNPITIKLYQAGGAPGGMPG 624

Qy 236 --PGGF--GAQPKGSGSGPTIEVD 258
Db 625 GFPGGPGAGGAGGAGGAGPTIEVD 654

RESULT 59
Q6AWA3
ID Q6AWA3 PRELIMINARY; PRT; 655 AA.
AC Q6AWA3;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Heat shock protein 70.
OS Locusta migratoria (Migratory locust).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Orthopteroidea; Orthoptera; Caelifera; Acridomorpha;
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OC Acridoidea; Acrididae; Oedipodinae; Locusta.
OX NCBI_TaxID=7004;
RN [1]
RP SEQUENCE FROM N.A.
RA Wang X.H., Chen B., Kang L.;
RL Submitted (OCT-2003) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: Belongs to the heat shock protein 70 family.
DR EMBL; AY299637; AAP57537.3; -.
DR HSSP; P19120; 1ATR.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0006457; P:protein folding; IEA.
DR GO; GO:0006986; P:response to unfolded protein; IEA.
DR InterPro; IPR001023; Hsp70.
DR Pfam; PF00012; HSP70; 1.
DR PRINTS; PR00301; HEATSHOCK70.
DR PRODOM; PD00089; Hsp70; 1.
DR PROSITE; PS00297; HSP70_1; 1.
DR PROSITE; PS00329; HSP70_2; 1.
DR PROSITE; PS01036; HSP70_3; 1.
KW ATP-binding; Heat shock.
SQ SEQUENCE 655 AA; 71481 MW; 42B2D2812F239651 CRC64;

Query Match 81.4%; Score 1070; DB 2; Length 655;
Best Local Similarity 78.5%; Pred. No. 5e-58;
Matches 212; Conservative 19; Mismatches 27; Indels 12; Gaps 3;

Qy 1 KSENVQDLLLDVAPLSLGLETAGVMTALIKRNSTIPTKTQITFTTYSNDQPGVLIQVY 60
Db 386 KSEEVQDLLLDVPLSLGIETAGVMTLLIKRNTTPTKTQITFTTYSNDQPGVLIQVY 445

Qy 61 EGERAMTKDNNLGRFELSGIPAPRGVPQIEVTFDIDANGILNVTATDKSTGKANKITI 120
Db 446 EGERAMTKDNNLGRFELSGIPAPRGVPQIEVTFDIDANGILNVTATDKSTGKANKITI 505

Qy 121 TNDKGRLSKEIERMVOEAERYKAEDVQERVSANAKLESYAFNMKSAVEDGLKKGKIS 180
Db 506 TNDKGRLSKEIERMVOEAERYKAEDVQERVSANAKLESYCFNMKSTVEDEKLKOKIS 565

Qy 181 EADKKVLDKCOEIVSWLDANTLAEKDFEHRKELEQVNCNPIISGLYQAGG-----PG 235
Db 566 DSDKQTILDKCNVIRWLDANQLAEKFEKQKELEQICNPITIKLYQAGGAPGGMPG 625

Qy 236 --PGGF--GAQPKGSGSGPTIEVD 258
Db 626 GFPGGPGAGGAGGAGGAGPTIEVD 655

RESULT 60
Q6PH56
ID Q6PH56 PRELIMINARY; PRT; 643 AA.
AC Q6PH56;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hsp70 protein.
GN Name=hsp70;
OS Brachydanio rerio (Zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Embryo;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altshul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
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RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Rulyk S.W.,
RA Villalon D.K., Muzny D.C., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettner M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smallus J., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Embryo;
RA Strausberg R.;
RL Submitted (AUG-2003) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: Belongs to the heat shock protein 70 family.
DR EMBL; BC056709; AAH56709.1; -.
DR HSP; F19120; IATR.
DR ZFIN; ZDB-GENE-990415-91; hsp70.
DR GO; GO:0005524; F:ATP binding; IEA.
DR InterPro; IPR001023; Hsp70.
DR Pfam; PF00012; HSP70; 1.
DR PRINTS; PR00301; HEATSHOCK70.
DR ProDom; PD000089; Hsp70; 1.
DR PROSITE; PS00297; HSP70_1; 1.
DR PROSITE; PS00329; HSP70_2; 1.
DR PROSITE; PS01036; HSP70_3; 1.
KW ATP-binding.
SQ SEQUENCE 643 AA; 70469 MW; EBC67C8CAD366161 CRC64;

Query Match 81.4%; Score 1069; DB 2; Length 643;
Best Local Similarity 80.3%; Pred. No. 5.6e-58;
Matches 208; Conservative 26; Mismatches 21; Indels 4; Gaps 2;

QY 2 SENVQDLLLDVAPLSLGLTAGGVTALIKRNTIPTKQTQFTTYSNDQPGVLIQVY 61
DB 387 SGNVQDLLLDVAPLSLGLTAGGVTALIKRNTIPTKQTQFTTYSNDQPGVLIQVY 446

QY 62 GERAMTKNNLLGRFELSGIPAPRGVQIEVTFDIDANGILNVATDKSTGKANKITI 121
DB 447 GERAMTKNNLLGKLFELTGIPAPRGVQIEVTFDIDANGILNVSAADKSTGKANKITI 506

QY 122 NDKGRLSKEIERMVQEAQKAEDEVQRRVSAKNALESYAFNMKSAVEDSLGKIS 181
DB 507 NDKGRLSKEIERMVQEAQKAEEDLQREKISAKNSLESYAFNMKNSVEDDNLGKISE 566

QY 182 ADKKKVLDCQEVISWLDANTLAEKDFEHRKELEQVNCNPIISGLYQAGGPGGFGA 241
DB 567 EDKRVIEKCNKAVSWLENQNLADKEEYHQLKELEKVCNPIISKLYQ--GGMPAGGCGA 624

QY 242 Q--GPKGGSGSGPTIEVD 258
DB 625 QARGASGASAGPTIEVD 643

RESULT 61
Q7Z1W9 PRELIMINARY; PRT; 658 AA.
AC Q7Z1W9;
DT 01-OCT-2003 (TRENBLrel. 25, Created)
DT 01-OCT-2003 (TRENBLrel. 25, Last sequence update)
DT 01-MAR-2004 (TRENBLrel. 26, Last annotation update)
DE Heat shock protein 70.
OS Crassostrea ariakensis.
OC Eukaryota; Metazoa; Mollusca; Bivalvia; Pteriomorpha; Ostreoida;
OC Ostreoidae; Ostreidae; Crassostrea.
OX NCBI_TaxID=94323;
RN [1]
RP SEQUENCE FROM N.A.
RA Zhang Q.-Z., Wu X.-Z., Pan J.-P., Gao J.-S., Zhang G.;
RL Submitted (OCT-2002) to the EMBL/GenBank/DBJ databases.

CC -1- SIMILARITY: Belongs to the heat shock protein 70 family.
DR EMBL; AY172024; AAO41703.1; -.
DR HSP; P19120; IATR.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0006457; P:protein folding; IEA.
DR GO; GO:0006986; P:response to unfolded protein; IEA.
DR InterPro; IPR001023; Hsp70.
DR Pfam; PF00012; HSP70; 1.
DR ProDom; PD000089; Hsp70; 1.
DR PROSITE; PS00297; HSP70_1; 1.
DR PROSITE; PS00329; HSP70_2; 1.
DR PROSITE; PS01036; HSP70_3; 1.
KW ATP-binding; Heat shock.
SQ SEQUENCE 658 AA; 71933 MW; 39C1DEF29A71F0E1 CRC64;

Query Match 81.2%; Score 1067; DB 2; Length 658;
Best Local Similarity 78.5%; Pred. No. 7.7e-58;
Matches 212; Conservative 20; Mismatches 26; Indels 12; Gaps 4;

QY 1 KSENVQDLLLDVAPLSLGLTAGGVTALIKRNTIPTKQTQFTTYSNDQPGVLIQVY 60
DB 389 KSEEVQDLLLDVAPLSLGLTAGGVTALIKRNTIPTKQTQFTTYSNDQPGVLIQVY 448

QY 61 EGERAMTKNNLLGRFELSGIPAPRGVQIEVTFDIDANGILNVATDKSTGKANKITI 120
DB 449 EGERAMTKNNLLGKLFELTGIPAPRGVQIEVTFDIDANGILNVSAVDKSTGKANKITI 508

QY 121 TNDKGRLSKEIERMVQEAQKAEDEVQRRVSAKNALESYAFNMKSAVEDSLGKIS 180
DB 509 TNDKGRLSKEIDRMVNEAEKQDEKQREIAAKSGLESYAFNMKSTVDEKLKDKIS 568

QY 181 EADKKVLDKQEVISWLDANTLAEKDFEHRKELEQVNCNPIISGLYQAGG--PG---P 236
DB 569 EGDKTKTLDKCEIIKWMDQNLADKEEYHQLKELEKVCNPIITKLYQASGGAPGGMP 628

QY 237 GGP-----GAG-----PKGGSGSGPTIEVD 258
DB 629 GGMPNFGGAPGGAPGGSGGSGPTIEVD 658

RESULT 62
Q6QAN5 PRELIMINARY; PRT; 490 AA.
ID Q6QAN5
AC Q6QAN5;
DT 05-JUL-2004 (TRENBLrel. 27, Created)
DT 05-JUL-2004 (TRENBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TRENBLrel. 27, Last annotation update)
DE 70 kDa heat shock protein (Fragment).
GN Name=HSP70;
OS Megachile rotundata (alfalfa leafcutting bee).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata; Apoidea;
OC Megachilidae; Megachilinae; Megachile.
OX NCBI_TaxID=143995;
RN [1]
RP SEQUENCE FROM N.A.
RA Yocum G.D., Kemp W.P.;
RL Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: Belongs to the heat shock protein 70 family.
DR EMBL; AY550115; AAS57864.1; -.
DR HSP; P19120; IATR.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0006457; P:protein folding; IEA.
DR GO; GO:0006986; P:response to unfolded protein; IEA.
DR InterPro; IPR001023; Hsp70.
DR Pfam; PF00012; HSP70; 1.
DR PRINTS; PR00301; HEATSHOCK70.
DR ProDom; PD000089; Hsp70; 1.
DR PROSITE; PS00329; HSP70_2; 1.
DR PROSITE; PS01036; HSP70_3; 1.
KW ATP-binding; Heat shock.
FN NON-TER 1
SQ SEQUENCE 490 AA; 53882 MW; 09D2D6F0F038CEDBD CRC64;

Query Match 81.1%; Score 1066; DB 2; Length 490;
Best Local Similarity 79.5%; Pred. No. 6.2e-58;
Matches 205; Conservative 21; Mismatches 32; Indels 0; Gaps 0;

QY 1 KSENVQDLLLLDVAPLSGLTAGVMTALIKRSTIPTKTQTFTTYSNDQPGVLIQVY 60
DB 233 KSENVQDLLLLDVAPLSGLTAGVMTALIKRSTIPTKTQTFTTYSNDQPGVLIQVY 292

QY 61 EGERAMTKDNNILGRFELSGIPPPAPRGVQPIEVTFDIDANGILNVATDKSTGKANKITI 120
DB 293 EGERAMTKDNNILGRFELSGIPPPAPRGVQPIEVTFDIDANGILNVATDKSTGKANKITI 352

QY 121 TNDKGRLSKEIERMVQAEYKAEDEVRERVSANNALESYAFNMKSAVDEGLKGIKIS 180
DB 353 TNDKGRLSKEIERMVQAEYKAEDEVRERVSANNALESYAFNMKSAVDEGLKGIKID 412

QY 181 EADKKVLDKCOEIVSWLDANTLAEKDFEHRKELEOVNPIISGLYQAGGPGGFG 240
DB 413 PSDKDKVLNKCNEVSWLDNRQLAEKEEFVDKQKELESVCNPIVTKLYQAGGAGPGGFP 472

QY 241 AQGPKGSGSGPTIEVD 258
DB 473 GSAPGGGAGGPTIEVD 490

RESULT 63

Q6PGX4 PRELIMINARY; PRT; 647 AA.

ID Q6PGX4
AC Q6PGX4
DT 05-JUL-2004 (TReMBLrel. 27, Created)
DT 05-JUL-2004 (TReMBLrel. 27, Last sequence update)
DE Hypothetical protein zgc:63663.
GN ORFNames=zgc:63663;
OS Brachydanio rerio (Zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Whole body;
RX MEDLINE=22389257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heide F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J.J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grinwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smallos D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)."
RL [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Whole body;
RX Strausberg R.;
RL Submitted (AUG-2003) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: Belongs to the heat shock protein 70 family.
DR EMBL; BC056797; AAH56797.1; -.
DR HSPF; P19120; IATR.
DR ZFIN; ZDB-GENE-040426-1221; zgc:63663.

DR GO; GO:0005524; F:ATP binding; IEA.
DR InterPro; IPR001023; Hsp70.
DR Pfam; PF00012; HSP70; 1.
DR PRINTS; PR00301; HEATSHOCK70.
DR PRODOM; PD000089; Hsp70; 1.
DR PROSITE; PS00297; HSP70_1; 1.
DR PROSITE; PS00329; HSP70_2; 1.
DR PROSITE; PS01036; HSP70_3; 1.
KW ATP-binding; Hypothetical protein.
SQ SEQUENCE 647 AA; 70946 MW; 2D956FB5F0FC6D65 CRC64;

Query Match 81.1%; Score 1066; DB 2; Length 647;
Best Local Similarity 80.8%; Pred. No. 8.6e-58;
Matches 212; Conservative 21; Mismatches 22; Indels 10; Gaps 4;

QY 2 SENVQDLLLLDVAPLSGLTAGVMTALIKRSTIPTKTQTFTTYSNDQPGVLIQVYE 61
DB 385 SENVQDLLLLDVAPLSGLTAGVMTALIKRSTIPTKTQTFTTYSNDQPGVLIQVYE 444

QY 62 GERAMTKDNNILGRFELSGIPPPAPRGVQPIEVTFDIDANGILNVATDKSTGKANKITI 121
DB 445 GERAMTKDNNILGRFELSGIPPPAPRGVQPIEVTFDIDANGILNVATDKSTGKANKITI 504

QY 122 NDKGRLSKEIERMVQAEYKAEDEVRERVSANNALESYAFNMKSAVDEGLKGIKISE 181
DB 505 NDKGRLSKEIERMVQAEYKAEDEVRERVSANNALESYAFNMKSAVDEGLKGIKISE 564

QY 182 ADKKVLDKCOEIVSWLDANTLAEKDFEHRKELEOVNPIISGLYQAGG-----PG- 235
DB 565 EDKTIYDKCNEVSWLDNRQLAEKEEFVDKQKELESVCNPIVTKLYQAGGAGGPGG 624

QY 236 -PGGF-GAQPCKGSGSGPTIEVD 258
DB 625 MPGGYFGQG--SGSSSGPTIEVD 647

RESULT 64

Q8IS62 PRELIMINARY; PRT; 656 AA.

ID Q8IS62
AC Q8IS62
DT 01-MAR-2003 (TReMBLrel. 23, Created)
DT 01-MAR-2003 (TReMBLrel. 23, Last sequence update)
DT 01-MAR-2004 (TReMBLrel. 26, Last annotation update)
DE Heat-shock protein 70.
OS Cotesia rubecula.
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Hymenoptera; Apocrita; Ichneumonidea;
OC Braconidae; Microgasterinae; Cotesia.
OX NCBI_TaxID=32392;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22578532; PubMed=12692281; DOI=10.1099/vir.0.19026-0;
RA Agari S., Zhang G., Schmidt O.;
RT "Polydnavirus particle proteins with similarities to molecular
chaperones, heat-shock protein 70 and calreticulin.";
J. Gen. Virol. 84:1165-1171(2003).
CC -1- SIMILARITY: Belongs to the heat shock protein 70 family.
DR EMBL; AY150371; AA73310.1; -.
DR HSPF; P19120; IATR.
DR GO; GO:0005524; F:ATP binding; IEA.
DR InterPro; IPR001023; Hsp70.
DR InterPro; IPR00169; Pept_cys_acsite.
DR Pfam; PF00012; HSP70; 1.
DR PRINTS; PR00301; HEATSHOCK70.
DR PROSITE; PS00297; HSP70_1; 1.
DR PROSITE; PS01036; HSP70_3; 1.
DR PROSITE; PS00639; THIOL_PROTEASE_HIS; UNKNOWN_1.
KW ATP-binding.
SQ SEQUENCE 656 AA; 71486 MW; 49D46612B84AB020 CRC64;

Query Match 81.0%; Score 1064.5; DB 2; Length 656;
Best Local Similarity 76.9%; Pred. No. 1.1e-57;
Matches 210; Conservative 20; Mismatches 28; Indels 15; Gaps 2;

[illegible]

Qy 241 A QGPKGGSGPTIEVD 258
 Db 627 -----GPTIEVD 634
 RESULT 66
 Q9NGK9 PRELIMINARY; PRT; 645 AA.
 ID Q9NGK9
 AC Q9NGK9
 DT 01-OCT-2000 (TrEMBLrel. 15, Created)
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE Heat shock protein 70.
 OS Wuchereria bancrofti.
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Spirurida; Filarioidea;
 OC Enchocercidae; Wuchereria.
 OX NCBI_TaxID=6293;
 RN [1]
 RN SEQUENCE FROM N.A.
 RX PubMed=15013783; DOI=10.1016/j.exppara.2004.01.001;
 RA Ravi V., Kubofcik J., Bandopadhyaya S., Geetha M., Narayanan R.B.,
 RA Numan T.B., Kaliraj P.;
 RT "Wuchereria bancrofti: cloning and characterization of heat shock
 RT protein 70 from the human lymphatic filarial parasite.";
 RL Exp. Parasitol. 106:1-10(2004).
 RN [2]
 RN SEQUENCE FROM N.A.
 RP Varatharajulu V., Kubofcik J., Vijayalakshmi P., Narayanan R.,
 RA Kaliraj P., Kunthala J., Numan T.;
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: Belongs to the heat shock protein 70 family.
 DR EMBL; AF250996; AAF66987.1; -.
 DR HSP; P19120; 3HSC.
 DR GO; GO:0005524; F:ATP binding; IEA.
 DR GO; GO:0006457; P:protein folding; IEA.
 DR GO; GO:0006986; P:response to unfolded protein; IEA.
 DR InterPro; IPR001023; Hsp70.
 DR Pfam; PF00012; HSP70; 1.
 DR PRINTS; PR00301; HEATSHOCK70.
 DR PROSITE; PS00297; HSP70_1; 1.
 DR PROSITE; PS00329; HSP70_2; 1.
 DR PROSITE; PS01036; HSP70_3; 1.
 KW ATP-binding; Heat shock.
 SQ SEQUENCE 645 AA; 70415 MW; BDE9F3A6D8EAC5D9 CRC64;
 Query Match 81.0%; Score 1064; DB 2; Length 645;
 Best Local Similarity 79.8%; Pred. No. 11e-57;
 Matches 209; Conservative 21; Mismatches 28; Indels 4; Gaps 3;
 Qy 1 KSNVQDLLLVDVAPISLGLETAGGVMTALIKRNSIPTTKQTQFTTYSNQGVLIQVY 60

Db 384 KSEAVQDLLLLDVAPLSLGIEGTAGGVTALIKRNTTPTKTSQTTTYSNQPGLVQVY 443
 Qy 61 EGERAMTKDNNLLGRFELSGIPPPAPRGVPOIEVTFDIDANGILNVATDSTGKANKITI 120
 Db 444 EGERALTNDNNLLGRFELSGIPPPAPRGVPOIEVTFDIDANGILNVASQDKSTGKANKITI 503
 Qy 121 TNDKGRLSKEIERMWQAEKYKAEDVQERVSANNALESYAFNMKSAVEDGLKGGKIS 180
 Db 504 TNDKGRLSKEIERMWQAEKYKAEDVQERVSANNALESYAFNMKQTIIEDEKFKKIS 563
 Qy 181 EADKKVKLDKQEVISWLDANTLAEKDFEHRKELEQVNCNPIISGLYQAGG--PG--PG 237
 Db 564 EEDKKIKPEKCDTEVTWLDGNTQAEKDFEHRKELEQVNCNPIITKLQYQAGGMEGMPG 623
 Qy 238 GFAGQPKGGS--GSQPTTIEVD 258
 Db 624 GMPGAPGAGSGTGGPTTIEVD 645

RESULT 67

P79984 PRELIMINARY; PRT; 649 AA.
 AC P79984;
 DT 01-MAY-1997 (TReMBLrel. 03, Created)
 DT 01-MAY-1997 (TReMBLrel. 03, Last sequence update)
 DT 01-MAR-2004 (TReMBLrel. 26, Last annotation update)
 DE HSC70 protein.
 GN Name=hsp8; Synonyms=hsc70;
 OS Brachydanio rerio (zebrafish)
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
 OC Cyprinidae; Danio.
 OX NCBI_TaxID=7955;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=98059927; PubMed=9397538;
 RX DOI=10.1002/(SICI)1520-6408(1997)21:3<223::AID-DVGS>3.3.CO;2-5;
 RA Santacruz H., Vriz S., Angelier N.;
 RT "Molecular characterization of a heat shock cognate cDNA of zebrafish,
 RT hsc70, and developmental expression of the corresponding
 RT transcripts.";
 RL Dev. Genet. 21:223-233(1997).
 CC -I- SIMILARITY: Belongs to the heat shock protein 70 family.
 DR EMBL; Y11413; CAA72216.1; -;
 DR HSP; P19120; 3HSC.
 DR ZFIN; ZDB-GENE-990415-92; hsp8.
 DR GO; GO:0005524; F:ATP binding; IEA.
 DR InterPro; IPR001023; Hsp70.
 DR Pfam; PF00012; HSP70; 1.
 DR PRINTS; PR00301; HEATSHOCK70.
 DR ProDom; PD000089; Hsp70; 1.
 DR PROSITE; PS00297; HSP70_1; 1.
 DR PROSITE; PS00329; HSP70_2; 1.
 DR PROSITE; PS01036; HSP70_3; 1.
 KW ATP-binding.
 SQ SEQUENCE 649 AA; 71175 MW; 775FPA285B3DF444 CRC64;

Query Match 81.0%; Score 1064; DB 2; Length 649;
 Best Local Similarity 79.8%; Pred. No. 1.2e-57;
 Matches 213; Conservative 20; Mismatches 24; Indels 10; Gaps 4;

Qy 1 KSENVQDLLLLDVAPLSLGIEGTAGGVTALIKRNTTPTKTSQTTTYSNQPGLVQVY 60
 Db 384 KSENVQDLLLLDVAPLSLGIEGTAGGVTALIKRNTTPTKTSQTTTYSNQPGLVQVY 443
 Qy 61 EGERAMTKDNNLLGRFELSGIPPPAPRGVPOIEVTFDIDANGILNVATDSTGKANKITI 120
 Db 444 EGERAMTKDNNLLGRFELSGIPPPAPRGVPOIEVTFDIDANGILNVASVDSKSTGKANKITI 503
 Qy 121 TNDKGRLSKEIERMWQAEKYKAEDVQERVSANNALESYAFNMKSAVEDGLKGGKIS 180
 Db 504 TNDKGRLSKEIERMWQAEKYKAEDVQERVSANNALESYAFNMKSTVEDEKFKKIS 563

Qy 181 EADKKVKLDKQEVISWLDANTLAEKDFEHRKELEQVNCNPIISGLYQAGG-----PG 235
 Db 564 DEDKKILDKCNKENVIGWLDKNQTAERBEFHOQR--LEKVCNPIITKLQYQAGACLVECPN 622
 Qy 236 -PGGF--GAQPKGSGSGPTTIEVD 258
 Db 623 VPGGPPGAGAAPAGGSSSGPTTIEVD 649

RESULT 68

Q6GUAB PRELIMINARY; PRT; 652 AA.
 AC Q6GUAB;
 DT 05-JUL-2004 (TReMBLrel. 27, Created)
 DT 05-JUL-2004 (TReMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TReMBLrel. 27, Last annotation update)
 DE Heat shock protein 70.
 OS Penaeus vannamei (Penaeid shrimp) (European white shrimp).
 OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
 OC Eumalacostraca; Eucarida; Decapoda; Dendrobranchiata; Penaeoidea;
 OC Penaeidae; Litopenaeus.
 OX NCBI_TaxID=6689;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Xie S.T.;
 RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
 CC -I- SIMILARITY: Belongs to the heat shock protein 70 family.
 DR EMBL; AY645906; AAT46566.1; -;
 DR GO; GO:0005524; F:ATP binding; IEA.
 DR GO; GO:0006986; P:response to unfolded protein; IEA.
 DR InterPro; IPR001023; Hsp70.
 DR Pfam; PF00012; HSP70; 1.
 DR PRINTS; PR00301; HEATSHOCK70.
 DR ProDom; PD000089; Hsp70; 1.
 DR PROSITE; PS00297; HSP70_1; 1.
 DR PROSITE; PS00329; HSP70_2; 1.
 DR PROSITE; PS01036; HSP70_3; 1.
 KW ATP-binding; Heat shock.
 SQ SEQUENCE 652 AA; 71522 MW; 956F88CD06C0AB4 CRC64;

Query Match 80.9%; Score 1063.5; DB 2; Length 652;
 Best Local Similarity 78.1%; Pred. No. 1.2e-57;
 Matches 210; Conservative 18; Mismatches 30; Indels 11; Gaps 3;

Qy 1 KSENVQDLLLLDVAPLSLGIEGTAGGVTALIKRNTTPTKTSQTTTYSNQPGLVQVY 60
 Db 384 KSENVQDLLLLDVAPLSLGIEGTAGGVTALIKRNTTPTKTSQTTTYSNQPGLVQVY 443
 Qy 61 EGERAMTKDNNLLGRFELSGIPPPAPRGVPOIEVTFDIDANGILNVATDSTGKANKITI 120
 Db 444 EGERAMTKDNNLLGRFELSGIPPPAPRGVPOIEVTFDIDANGILNVASVDSKSTGKANKITI 503
 Qy 121 TNDKGRLSKEIERMWQAEKYKAEDVQERVSANNALESYAFNMKSAVEDGLKGGKIS 180
 Db 504 TNDKGRLSKEIERMWQAEKYKAEDVQERVSANNALESYAFNMKSTVEDEKFKKIS 563
 Qy 181 EADKKVKLDKQEVISWLDANTLAEKDFEHRKELEQVNCNPIISGLYQAGG--PG--P 236
 Db 564 EEDRNKILETCNETIKWLDNQLGEKEEYEHKQIEBQVCNPIITKMYAAGGAPPGMP 623
 Qy 237 GGF-----GAQPKGSGSGPTTIEVD 258
 Db 624 GGPFGAPGAGAAPAGGSSSGPTTIEVD 652

RESULT 69

Q71KW5 PRELIMINARY; PRT; 652 AA.
 AC Q71KW5;
 DT 05-JUL-2004 (TReMBLrel. 27, Created)
 DT 05-JUL-2004 (TReMBLrel. 27, Last sequence update)

DT 05-JUL-2004 (Tremblrel. 27, Last annotation update)
DE Heat shock protein 70.
OS Penaeus monodon (Penaeid shrimp).
OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
OC Eumalacostraca; Eucarida; Decapoda; Dendrobranchiata; Penaeoidea;
OC Penaeidae; Penaeus.
OX NCBI_TaxID=6687;
RN [1]
RP SEQUENCE FROM N.A.
RA Lo W.-Y., Song Y.-L.;
RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: Belongs to the heat shock protein 70 family.
DR EMBL; AF474375; AAQ05768.1; -.
DR HSSP; P19120; 3HSC.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0006457; P:protein folding; IEA.
DR GO; GO:0006986; P:response to unfolded protein; IEA.
DR InterPro; IPR001023; Hsp70.
DR Pfam; PF00012; Hsp70; 1.
DR PRINTS; PR00301; HEATSHOCK70.
DR PRODOM; PD000089; Hsp70; 1.
DR PROSITE; PS00297; Hsp70_1; 1.
DR PROSITE; PS00329; Hsp70_2; 1.
DR PROSITE; PS01036; Hsp70_3; 1.
DR ATP-binding; Heat shock.
KW ATP-binding; Heat shock.
SQ SEQUENCE 652 AA; 71481 MW; FDFADA929ECF6413 CRC64;

Query Match 80.9%; Score 1063.5; DB 2; Length 652;
Best Local Similarity 78.1%; Pred. No. 1.2e-57;
Matches 210; Conservative 18; Mismatches 30; Indels 11; Gaps 3;

QY 1 KSENVQDLLLLDVAPLSLGLTAGVMTALIKRNSTIPTKQTQIFTTYSNDQPGVLIQVY 60
Db 384 KSEAVQDLLLLDVAPLSLGLTAGVMTALIKRNSTIPTKQTQIFTTYSNDQPGVLIQVY 443

QY 61 EGERAMTKONLLGRFELSGIPPPARGVPQIEVTFDIDANGILNVTATDKSTGKANKITI 120
Db 444 EGERAMTKONLLGRFELSGIPPPARGVPQIEVTFDIDANGILNVTATDKSTGKANKITI 503

QY 121 TNDKGRLSKEELRMVQAEKYKAEDVQRRVRSNAKNALESYAFNMKSAVEDGLKGIS 180
Db 504 TNDKGRLSKEELRMVQAEKYKAEDVQRRVRSNAKNALESYAFNMKSTVEDEKPEKIS 563

QY 181 EADKKKVLDCQEVISWLDANTLAEKDFEHRKELEQVNCNPIISGLYQGAGG--PG--P 236
Db 564 EEDRNKILETCNETIKWLDNMQLGEKEEYEHQKEIEQVNCNPIITKMYAAGGAPPGGMP 623

QY 237 GGF-----GAGPKGSGSGPTIEVD 258
Db 624 GGFPGGAPGAGGAPGAGSGSGPTIEVD 652

RESULT 70
Q17267 PRELIMINARY; PRT; 335 AA.
AC Q17267;
DT 01-NOV-1996 (Tremblrel. 01, Created)
DT 01-NOV-1996 (Tremblrel. 01, Last sequence update)
DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)
DE Heat shock protein 70, hsp70A2 (Fragment).
GN Name=hsc70;
OS Brugia pahangi (Filarial nematode worm).
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Spirurida; Filarioidea;
OC Onchocercidae; Brugia.
OX NCBI_TaxID=6280;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=89278663; PubMed=2659668;
RA Selkirk M.E., Denham D.A., Partono F., Maizels R.M.;
RT "Heat shock cognate 70 is a prominent immunogen in Brugian filariasis."
RL J. Immunol. 143:299-308 (1989).
CC -!- SIMILARITY: Belongs to the heat shock protein 70 family.

DR EMBL; M27191; AAA27857.1; -.
DR PIR; A45805; A45805.
DR HSSP; P19120; 3HSC.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0006457; P:protein folding; IEA.
DR GO; GO:0006986; P:response to unfolded protein; IEA.
DR InterPro; IPR001023; Hsp70.
DR Pfam; PF00012; Hsp70; 1.
DR PRINTS; PR00301; HEATSHOCK70.
DR PROSITE; PS01036; Hsp70_3; 1.
KW ATP-binding; Heat shock.
FT NON_TER 1
SQ SEQUENCE 335 AA; 36241 MW; B4717A8B99D80C0B CRC64;

Query Match 80.9%; Score 1063; DB 2; Length 335;
Best Local Similarity 79.8%; Pred. No. 6.1e-58;
Matches 209; Conservative 20; Mismatches 29; Indels 4; Gaps 3;

QY 1 KSENVQDLLLLDVAPLSLGLTAGVMTALIKRNSTIPTKQTQIFTTYSNDQPGVLIQVY 60
Db 74 KSEAVQDLLLLDVAPLSLGLTAGVMTALIKRNSTIPTKQTQIFTTYSNDQPGVLIQVY 133

QY 61 EGERAMTKONLLGRFELSGIPPPARGVPQIEVTFDIDANGILNVTATDKSTGKANKITI 120
Db 134 EGERAMTKONLLGRFELSGIPPPARGVPQIEVTFDIDANGILNVTATDKSTGKANKITI 193

QY 121 TNDKGRLSKEELRMVQAEKYKAEDVQRRVRSNAKNALESYAFNMKSAVEDGLKGIS 180
Db 194 TNDKGRLSKEELRMVQAEKYKAEDVQRRVRSNAKNALESYAFNMKSTVEDEKPEKIS 253

QY 181 EADKKKVLDCQEVISWLDANTLAEKDFEHRKELEQVNCNPIISGLYQGAGG--PG--P 237
Db 254 EEDKKIKQEKDCTVRLWDGNTAEKDFEHRKELEQVNCNPIITKLYQSAGGMPGGMPG 313

QY 238 GFGAGPKGSG--GSGPTIEVD 258
Db 314 GMPGAPGAGSGSGPTIEVD 335

RESULT 71
HS70_BRUWA
ID HS70_BRUWA STANDARD; PRT; 644 AA.
AC P27541;
DT 01-AUG-1992 (Rel. 23, Created)
DT 01-AUG-1992 (Rel. 23, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Heat shock 70 kDa protein.
GN Name=Hsp70;
OS Brugia malayi (Filarial nematode worm).
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Spirurida; Filarioidea;
OC Onchocercidae; Brugia.
OX NCBI_TaxID=6279;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=92131059; PubMed=1775166; DOI=10.1016/0166-6851(91)90066-F;
RA Rothstein N., Rajan T.V.;
RT "Characterization of an hsp70 gene from the human filarial parasite, Brugia malayi (Nematoda)."
RL Mol. Biochem. Parasitol. 49:229-238 (1991).
CC -!- SIMILARITY: Belongs to the heat shock protein 70 family.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See [http://www.isb-sib.ch/](http://www.isb-sib.ch/announce/) or send an email to license@isb-sib.ch)
CC -----
DR EMBL; M68933; AAC17926.1; -.
DR PIR; A45635; A45635.
DR HSSP; P19120; 3HSC.
DR InterPro; IPR001023; Hsp70.

```
DR Pfam; PF00012; HSP70; 1.
DR PRINTS; PR00301; HEATSHOCK70.
DR PRODOM; PD000089; Hsp70; 1.
DR TIGRFAMs; TIGR01991; HscA; 1.
DR PROSITE; PS00297; HSP70_1; 1.
DR PROSITE; PS00329; HSP70_2; 1.
DR PROSITE; PS01036; HSP70_3; 1.
DR ATP-binding; Heat shock.
KW SEQUENCE 644 AA; 70220 MW; DE07774C9CAB2925 CRC64;

Query Match 80.9%; Score 1063; DB 1; Length 644;
Best Local Similarity 79.8%; Pred. No. 1.3e-57;
Matches 209; Conservative 20; Mismatches 29; Indels 4; Gaps 3;

Qy 1 KSENVQDLLLLDVAPLSGLTAGGVTALIKRNTIPTKTQTQITFTTYSNQPGVLIQVY 60
Db |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
383 KSEAVQDLLLLDVAPLSGLTAGGVTALIKRNTIPTKTSETFTTYSNQPGVLIQVY 442
Qy |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

Qy 61 EGERAMTKDNLLGRFELSGIPAPRGVPQIEVTFDIDANGILNVATDKSTGKANKITI 120
Db |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
443 EGERALTKDNLLGRFELSGIPAPRGVPQIEVTFDIDANGILNVSAQDKSTGKANKITI 502
Qy |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

Qy 121 TNDKGRLSKEIERMVQEAERYKAEDVQERVSNAKNALESYAFNMKSAVEDEGLKGKIS 180
Db |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
503 TNDKGRLSKEIERMVQEAERYKADDEAQKRIAANKNALESYAFNMKQTIKDEKLKDKIS 562
Qy |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

Qy 181 EADKKVLDKQCEVISWLDANTLAEKDFEHRKELEQVNCPIISGLYQAGG-PG- 237
Db |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
563 BEDKKIKQCEQDETWRWDGNTAQKDFEHRKELESCVNCPIITKLYQSAAGMPGMPG 622
Qy |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

Qy 238 GFAGAGKPGGS-GSPPTIEVD 258
Db |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
623 GMPGAPGAGTGSGPTIEVD 644

RESULT 72
Q6QAN4 PRELIMINARY; PRT; 583 AA.
ID Q6QAN4
AC Q6QAN4;
DT 05-JUL-2004 (TRENBLrel. 27, Created)
DT 05-JUL-2004 (TRENBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TRENBLrel. 27, Last annotation update)
DE 70 kDa heat shock cognate protein (Fragment).
CN Name=HSC70;
OS Megachile rotundata (alfalfa leafcutting bee).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata; Apoidea;
OC Megachilidae; Megachilinae; Megachile.
OX NCBI_TaxID=143995;
RN [1]
RP SEQUENCE FROM N.A.
RA Yocum G.D., Kemp W.P.;
RL Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: Belongs to the heat shock protein 70 family.
DR EMBL; AY550116; AAS57865.1; -.
DR HSP; P19120; 1ATF.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0006457; P:protein folding; IEA.
DR GO; GO:0006986; P:response to unfolded protein; IEA.
DR InterPro; IPR001023; HSP70.
DR Pfam; PF00012; HSP70; 1.
DR PRINTS; PR00301; HEATSHOCK70.
DR PRODOM; PD000089; HSP70_1.
DR PROSITE; PS00329; HSP70_2; 1.
DR PROSITE; PS01036; HSP70_3; 1.
DR ATP-binding; Heat shock.
KW NON TER
FT
SQ SEQUENCE 583 AA; 64023 MW; 3EDB8051BEC5F88 CRC64;

Query Match 80.7%; Score 1060; DB 2; Length 583;
Best Local Similarity 77.6%; Pred. No. 1.8e-57;
Matches 208; Conservative 23; Mismatches 27; Indels 10; Gaps 3;

Qy 1 KSENVQDLLLLDVAPLSGLTAGGVTALIKRNTIPTKTQTQITFTTYSNQPGVLIQVY 60
Db |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
316 KSEVQDLLLLDVTPLSGLTAGGVTALIKNTIPTKTQTFTTYADNQPGVLIQVY 375
Qy |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
61 EGERAMTKDNLLGRFELSGIPAPRGVPQIEVTFDIDANGILNVATDKSTGKANKITI 120
Db |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
376 EGERAMTKDNLLGKLFELSGIPAPRGVPQIEVTFDIDANGILNVSAVDKSTGKANKITI 435
Qy |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
121 TNDKGRLSKEIERMVQEAERYKAEDVQERVSNAKNALESYAFNMKSAVEDEGLKGKIS 180
Db |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
436 TNDKGRLSKEDIERMVNEAEKYSDEKQETTAANKLSYCFNMKSTVEDEKLKDKIS 495
Qy |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
181 EADKKVLDKQCEVISWLDANTLAEKDFEHRKELEQVNCPIISGLYQAGG-PG- 235
Db |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
496 ASDKQVLDKNDIILKWDANQLADKEEYEHKQELKESICNPIVTKLYQGTGGMPGMPG 555
Qy |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
236 --PGFQAQ---GPKGGSGSPPTIEVD 258
Db |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
556 GFGAGGAAPGGGAPGGSGSPPTIEVD 583

RESULT 73
HS72 HUMAN
ID HS72 HUMAN STANDARD; PRT; 639 AA.
AC PS4652; Q15508; Q9UE78;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Heat shock-related 70 kDa protein 2 (Heat shock 70 kDa protein 2).
CN Name=HSPA2;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Goralski T.J., Krensky A.M.;
RL Submitted (APR-1996) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RA Klauster R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins S.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.B.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.H.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny K.C., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smallos D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [4]
RP SEQUENCE OF 1-126 FROM N.A.
RX MEDLINE=95152505; PubMed=7849706;
```

RA Roux A.-F., Nguyen V.T.T., Squire J.A., Cox D.W.;
 RL "A heat shock gene at 14q22: mapping and expression";
 Hum. Mol. Genet. 3:1819-1822(1994).
 CC -!- FUNCTION: In cooperation with other chaperones, Hsp70s stabilize
 CC of preexistent proteins against aggregation and mediate the folding
 CC of newly translated polypeptides in the cytosol as well as within
 CC organelles. These chaperones participate in all these processes
 CC through their ability to recognize nonnative conformations of
 CC other proteins. They bind extended peptide segments with a net
 CC hydrophobic character exposed by polypeptides during translation
 CC and membrane translocation, or following stress-induced damage.
 CC -!- SIMILARITY: Belongs to the heat shock protein 70 family.
 CC
 CC This SWISS-PROT entry is copyrighted. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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 CC or send an email to license@isb-sib.ch).
 CC
 CC -----
 CC EMBL; L26336; AAA52698.1; -;
 CC EMBL; U56725; AAD11466.1; -;
 CC EMBL; BC001752; AAH01752.1; -;
 CC EMBL; BC036107; AAH36107.1; -;
 CC EMBL; U10149; AAC50076.1; -;
 CC PIR; A55719; A55719.
 CC HSSP; P19120; 3HSC.
 CC Genew; HGNC:5235; HSPA2.
 CC H-InvDB; HIX0011736; -;
 CC MIM; 140560; -;
 CC GO; GO:0003773; P:heat shock protein activity; TAS.
 CC GO; GO:0007140; P:meiosis; TAS.
 CC GO; GO:0007286; P:spermatid development; TAS.
 CC InterPro; IPR001023; Hsp70.
 CC Pfam; PF00012; HSP70; 1.
 CC PRINTS; PR00301; HEATSHOCK70.
 CC ProDom; PD000089; Hsp70; 1.
 CC TIGRFAMs; TIGR01991; Hsca; 1.
 CC PROSITE; PS00297; HSP70_1; 1.
 CC PROSITE; PS00329; HSP70_2; 1.
 CC PROSITE; PS01036; HSP70_3; 1.
 CC ATP-binding; Chaperone; Heat shock; Multigene family.
 FT CONFLICT 14 14 T -> P (in Ref. 3; AAH36107).
 FT CONFLICT 54 54 Missing (in Ref. 3).
 FT CONFLICT 80 80 E -> G (in Ref. 3; AAH36107).
 FT CONFLICT 266 266 L -> S (in Ref. 2).
 FT CONFLICT 639 639 AA; 70021 MW; 3851755494E7B729 CRC64;
 SQ SEQUENCE 639 AA; 70021 MW; 3851755494E7B729 CRC64;
 Query Match 80.6%; Score 1059.5; DB 1; Length 639;
 Best Local Similarity 79.1%; Pred. No. 2.2e-57;
 Matches 204; Conservative 24; Mismatches 25; Indels 5; Gaps 1;
 Qy 1 KSENVQDLLLLDVAPLSGLTAGVMTALIKRNTIPTKTQTFTTYSNDQPGVLIQVY 60
 Db 387 KSENVQDLLLLDVTPLSGLTAGVMTPLIKRNTIPTKTQTFTTYSNDQSVLVQVY 446
 Qy 61 EGERAMTKNNLLGRFELSGIPAPRGVPQIEVTFDIDANGILNVTATDKSTGKANKITI 120
 Db 447 EGERAMTKNNLLGKFDLTGIPAPRGVPQIEVTFDIDANGILNVTADKSTGKANKITI 506
 Qy 121 TNDKGRSLKSEIERMVOBAEKYKAEDVQRRVSAKNALESYAFNMKSAVEDEGLKGIS 180
 Db 507 TNDKGRSLKSDIDRMVQEAERKSEDEANRVAKNALESYTYNIKQTVDEKLRGIS 566
 Qy 181 EADKKVLDKQEVISWLDANTLAKRDEFEHKKRKELEQVNCPIISGLYQAGGPGGFG 240
 Db 567 EQDKNKILDKQEVINWLDNRQMAEKDEYEHKQKELERVCNPIISKLYQGGPGGGGGG 626
 Qy 241 AQGPKGSGSGGPTIEVD 258
 Db 627 S-----GASGGPTIEVD 639

RESULT 74

Q27121 PRELIMINARY; PRT; 658 AA.
 AC Q27121;
 DT 01-NOV-1996 (TRENBLrel. 01, Created)
 DT 01-NOV-1996 (TRENBLrel. 01, Last sequence update)
 DT 01-MAR-2004 (TRENBLrel. 26, Last annotation update)
 DE Heat shock cognate protein.
 OS Urechis caupo (Innkeeper worm) (Spoonworm).
 OC Eukaryota; Metazoa; Echiura; Xenopneusta; Urechidae; Urechis.
 OC NCBI_TaxID=6431;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=94155469; PubMed=8111976;
 RA Rosenthal E.;
 RT "Sequence analysis of translationally controlled maternal mRNAs from
 RT Urechis caupo";
 RL Dev. Genet. 14:485-491(1993).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Rosenthal E.;
 RL Submitted (JUN-1995) to the EMBL/GenBank/DBJ databases.
 CC -!- SIMILARITY: Belongs to the heat shock protein 70 family.
 DR EMBL; U30456; AAA74394.1; -;
 DR HSSP; P19120; 3HSC.
 DR GO; GO:0005524; P:ATP binding; IEA.
 DR GO; GO:0006457; P:protein folding; IEA.
 DR GO; GO:0006986; P:response to unfolded protein; IEA.
 DR InterPro; IPR001023; Hsp70.
 DR Pfam; PF00012; HSP70; 1.
 DR PRINTS; PR00301; HEATSHOCK70.
 DR ProDom; PD000089; Hsp70; 1.
 DR PROSITE; PS00297; HSP70_1; 1.
 DR PROSITE; PS00329; HSP70_2; 1.
 DR PROSITE; PS01036; HSP70_3; 1.
 DR ATP-binding; Heat shock.
 KW ATP-binding; Heat shock.
 SQ SEQUENCE 658 AA; 71698 MW; DB54FB2425F3357B CRC64;
 Query Match 80.6%; Score 1059.5; DB 2; Length 658;
 Best Local Similarity 75.0%; Pred. No. 2.2e-57;
 Matches 207; Conservative 24; Mismatches 26; Indels 19; Gaps 2;
 Qy 1 KSENVQDLLLLDVAPLSGLTAGVMTALIKRNTIPTKTQTFTTYSNDQPGVLIQVY 60
 Db 384 KSEEVQDLLLLDVAPLSGLTAGVMTSLIKRNTTPTKTQTFTTVDNQPGVLIQVY 443
 Qy 61 EGERAMTKNNLLGRFELSGIPAPRGVPQIEVTFDIDANGILNVTATDKSTGKANKITI 120
 Db 444 EGERAMTKNNLLGKFLSGIPAPRGVPQIEVTFDIDANGILNVSAYDKSTGKANKITI 503
 Qy 121 TNDKGRSLKSEIERMVOBAEKYKAEDVQRRVSAKNALESYAFNMKSAVEDEGLKGIS 180
 Db 504 TNDKGRSLKSEIERMVOBAEKYKGEDEAQRPIITAKNSLESYAFNMKSTVEDEKVKIS 563
 Qy 181 EADKKVLDKQEVISWLDANTLAKRDEFEHKKRKELEQVNCPIISGLYQAGGPGG----- 235
 Db 564 DEDTKIIDKCNVITWLDANQLAKDEFAHQKQKLEGVCFVMTKLYOAGGAPGPGG 623
 Qy 236 -----PGGGAQPGKSGSGGPTIEVD 258
 Db 624 MPGGMPGMPGMPGGAGGAPPGSGSG-GPTIEVD 658
 RESULT 75
 HS70_PLEWA
 ID HS70_PLEWA
 AC Q91291;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Heat shock 70 kDa protein (HSP70).
 GN Name=HSP70;

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OS Pleurodeles wallii (Iberian ribbed newt).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amniibia; Batrachia; Caudata; Salamandroidea; Salamandridae;
OC Pleurodeles.
OX NCBI_TaxID=8319;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=94244484; PubMed=8187647;
RT Bailoud B., Rodriguez-Martin M.L., Berard L., Moreau N., Angelier N.;
RA "Constitutive expression of a somatic heat-inducible hsp70 gene during
RT amphibian oogenesis.";
RC Development 119:921-932(1993).
CC -1- SIMILARITY: Belongs to the heat shock protein 70 family.
-----
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DR ENML; X71951; CAAS0749.1; -.
DR PIR; I51129; I51129.
DR HSP; P08109; 1CKR.
DR InterPro; IPROO1023; Hsp70.
DR Pfam; PF00012; HSP70_1.
DR PRINTS; PR00301; HEATSHOCK70.
DR ProDom; PD000089; Hsp70; 1.
DR TIGRFAMS; TIGR01991; HscA; 1.
DR PROSITE; PS00297; HSP70_1; 1.
DR DR PROSITE; PS00329; HSP70_2; 1.
DR DR PROSITE; PS01036; HSP70_3; 1.
KW ATP-binding; Heat shock; Multigene family.
SQ SEQUENCE 645 AA; 70977 MW; FASIIICDF34I3C CRC64;

Query Match      80.5%; Score 1058; DB 1; Length 645;
Best Local Similarity 79.6%; Pred. No. 2.7e-57;
Matches 207; Conservative 24; Mismatches 27; Indels 2; Gaps 1;

Qy   1 KSENVQLLLLDVAPLSGLGLETAGGVWTLIKNSITPTKQTIFFTYSNQPGVLIOYV 60
Db   386 KSENLODLLLVDAPLSGLGLETAGGVMTLVLIKNSITPTKQTIFFTYSNQPGVLIOYV 445

Qy   61 EGGRAMTKNNLGRLPELSGIIPAPRGVPQIVETFDIDANGILNVTATDKSTCGKANNTI 120
Db   446 EGGRAMTKNNSLGGKLFGELSGIIPAPRGVPQIVETFDIDANGILNVSADKSSGQNKKITI 505

Qy   121 TN DKGRLSKEEIERMWQEAEKYKAEDVRQRERYSAKNALESYA FNMKSAVEDEGLKGKIS 180
Db   506 TNDKGRLSKEEIERMWQEAEARYRADDAEQREKVSAKNLTLESSIAFNKMSTVEGDNLXDKIS 565

Qy   181 EA DKKVKLDKCQEVISM LDANTLA EKDEFPHKRKLEQCVCNP II SGLYOGA --GGP GP GG 238
Db   566 ED DR KKTVDCNK QTI S WENNQA EE KE YEHQQELEKVCNC SI IT KL YQG MP GM PGS GS 625

Qy   239 FG AQGP KGSGSGGTTEEVD 258
Db   626 SGA QR AG QS SS ST GTTIEEVD 645

RESULT *6
Q6RYT7 PRELIMINARY; PRT; 657 AA.
AC Q6RYT7;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DI 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
OT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Heat shock protein 70.
GN Name=hsp70;
OS Patinopecten yessoensis (ezo giant scallop) (Yesso scallop).
OC Eukaryota; Metazoa; Mollusca; Bivalvia; Periomorphia; Pectinoida;
OC Pectinoidea; Pectinidae; Mizuhopecton.
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GO: 0000723; P: telomere maintenance; IMP.	GO: 0000723; P: telomere maintenance; IMP.
DR InterPro: IPR001023; Hsp70.	DR InterPro: IPR001023; Hsp70.
DR Pfam: PF00012; HSP70; 1.	DR Pfam: PF00012; HSP70; 1.
KW ATP-binding; Heat shock.	KW ATP-binding; Heat shock.
FT NON TER	FT NON TER
SEQUENCE 228 AA; 24872 MW; BD7A09314CE0FDC CRC64;	SEQUENCE 228 AA; 24872 MW; BD7A09314CE0FDC CRC64;
Query Match 80.4%; Score 1056; DB 2; Length 228;	Query Match 80.4%; Score 1056; DB 2; Length 228;
Best Local Similarity 91.6%; Pred. No. 1e-57;	Best Local Similarity 91.6%; Pred. No. 1e-57;
Matches 207; Conservative 11; Mismatches 6; Indels 2; Gaps 2;	Matches 207; Conservative 11; Mismatches 6; Indels 2; Gaps 2;
QY 34 NSTPIPTKQTQFTTYSNDQGVLIQYEGERAMTKNNLLGRFELSIPAPRGVPOIEV 93	QY 34 NSTPIPTKQTQFTTYSNDQGVLIQYEGERAMTKNNLLGRFELSIPAPRGVPOIEV 93
DB 4 NSTPIPTKQTQFTTYSNDQGVLIQYEGERAMTKNNLLGRFELSIPAPRGVPOIEV 62	DB 4 NSTPIPTKQTQFTTYSNDQGVLIQYEGERAMTKNNLLGRFELSIPAPRGVPOIEV 62
QY 94 TFDIDANGILNVTATDKSTGKANKITIITNDKRLSKKEIERMVQAEKKADEVDQERV 153	QY 94 TFDIDANGILNVTATDKSTGKANKITIITNDKRLSKKEIERMVQAEKKADEVDQERV 153
DB 63 TFDIDANGILNVTATDKSTGKANKITIITNDKRLSKKEIERMVQAEKKADEVDQERV 122	DB 63 TFDIDANGILNVTATDKSTGKANKITIITNDKRLSKKEIERMVQAEKKADEVDQERV 122
QY 154 SAKNALESYAFNMKMSAVEDGLKGISEADKKKVLDDKQEVISWLDANTLAEKDFEHR 213	QY 154 SAKNALESYAFNMKMSAVEDGLKGISEADKKKVLDDKQEVISWLDANTLAEKDFEHR 213
DB 123 AKNALESYAFNMKMSAVEDGLKGISEADKKKVLDDKQEVISWLDNTLADKEFVHR 182	DB 123 AKNALESYAFNMKMSAVEDGLKGISEADKKKVLDDKQEVISWLDNTLADKEFVHR 182
QY 214 KELEOVNPIISGLYQAGGPGGGAQG-PKGSGSGPTIEVD 258	QY 214 KELEOVNPIISGLYQAGGPGGGAQG-PKGSGSGPTIEVD 258
DB 183 EELERVCSPIISGLYQAGGPGGGAQG-PKGSGSGPTIEVD 228	DB 183 EELERVCSPIISGLYQAGGPGGGAQG-PKGSGSGPTIEVD 228
RESULT 78	RESULT 78
O96541 PRELIMINARY; PRT; 645 AA.	O96541 PRELIMINARY; PRT; 645 AA.
ID O96541	ID O96541
AC O96541	AC O96541
DT 01-MAY-1999 (T-EMBLrel. 10, Created)	DT 01-MAY-1999 (T-EMBLrel. 10, Created)
DT 01-MAY-1999 (T-EMBLrel. 10, Last sequence update)	DT 01-MAY-1999 (T-EMBLrel. 10, Last sequence update)
DT 01-MAR-2004 (T-EMBLrel. 26, Last annotation update)	DT 01-MAR-2004 (T-EMBLrel. 26, Last annotation update)
DE Heat shock protein 70.	DE Heat shock protein 70.
OS Setaria digitata.	OS Setaria digitata.
OC Eukaryota; Metazoa; Chromadorea; Spirurida; Filarioidea;	OC Eukaryota; Metazoa; Chromadorea; Spirurida; Filarioidea;
OC Setariidae; Setaria.	OC Setariidae; Setaria.
OX NCBI_TaxID=48799;	OX NCBI_TaxID=48799;
RN [1]	RN [1]
RP SEQUENCE FROM N.A.	RP SEQUENCE FROM N.A.
RA MEDLINE=99314887; PubMed=10428634; DOI=10.1016/S0020-7519(99)00002-8;	RA MEDLINE=99314887; PubMed=10428634; DOI=10.1016/S0020-7519(99)00002-8;
RA Jayasena S.M., Chandrasekharan N.V., Karunanayake E.H.;	RA Jayasena S.M., Chandrasekharan N.V., Karunanayake E.H.;
RT "Molecular characterisation of a hsp70 gene from the filarial parasite	RT "Molecular characterisation of a hsp70 gene from the filarial parasite
RT Setaria digitata";	RT Setaria digitata";
RL Int. J. Parasitol. 29:581-591(1999).	RL Int. J. Parasitol. 29:581-591(1999).
CC -1- SIMILARITY: Belongs to the heat shock protein 70 family.	CC -1- SIMILARITY: Belongs to the heat shock protein 70 family.
DR EMBL: AF079360; AAD13154.1; -	DR EMBL: AF079360; AAD13154.1; -
DR HSP; P19120; 3HSC.	DR HSP; P19120; 3HSC.
DR GO: 0006524; F:ATP binding; IEA.	DR GO: 0006524; F:ATP binding; IEA.
DR GO: 0006457; P:protein folding; IEA.	DR GO: 0006457; P:protein folding; IEA.
DR GO: 0006986; P:response to unfolded protein; IEA.	DR GO: 0006986; P:response to unfolded protein; IEA.
DR InterPro: IPR001023; Hsp70.	DR InterPro: IPR001023; Hsp70.
DR Pfam: PF00012; HSP70; 1.	DR Pfam: PF00012; HSP70; 1.
DR PRINTS; PR00301; HEATSHOCK70.	DR PRINTS; PR00301; HEATSHOCK70.
DR PROSITE; PS00297; HSP70_1; 1.	DR PROSITE; PS00297; HSP70_1; 1.
DR PROSITE; PS00329; HSP70_2; 1.	DR PROSITE; PS00329; HSP70_2; 1.
DR PROSITE; PS01036; HSP70_3; 1.	DR PROSITE; PS01036; HSP70_3; 1.
KW ATP-binding; Heat shock.	KW ATP-binding; Heat shock.
SEQUENCE 645 AA; 70292 MW; 4D0E39AB64540366 CRC64;	SEQUENCE 645 AA; 70292 MW; 4D0E39AB64540366 CRC64;
Query Match 80.4%; Score 1056; DB 2; Length 645;	Query Match 80.4%; Score 1056; DB 2; Length 645;
Best Local Similarity 79.4%; Pred. No. 3.6e-57;	Best Local Similarity 79.4%; Pred. No. 3.6e-57;
Matches 208; Conservative 21; Mismatches 29; Indels 4; Gaps 3;	Matches 208; Conservative 21; Mismatches 29; Indels 4; Gaps 3;
QY 1 KSENVQDLLLDVAPLSLGLTAGGVTALIKRNSTIPTKQTQFTTYSNDQGVLIQY 60	QY 1 KSENVQDLLLDVAPLSLGLTAGGVTALIKRNSTIPTKQTQFTTYSNDQGVLIQY 60
DB 384 KSEAVQDLLFDVAPLSLGLTAGGVTALIKRNTIPTKTSQTFTTYSNDQGVLIQY 443	DB 384 KSEAVQDLLFDVAPLSLGLTAGGVTALIKRNTIPTKTSQTFTTYSNDQGVLIQY 443
QY 61 EGERAMTKNNLLGRFELSIPAPRGVPOIEVTFIDANGILNVTATDKSTGKANKITI 120	QY 61 EGERAMTKNNLLGRFELSIPAPRGVPOIEVTFIDANGILNVTATDKSTGKANKITI 120
DB 444 EGERAMTKNNLLGRFELSIPAPRGVPOIEVTFIDANGILNVTATDKSTGKANKITI 503	DB 444 EGERAMTKNNLLGRFELSIPAPRGVPOIEVTFIDANGILNVTATDKSTGKANKITI 503

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RESULT 80
HS72 MOUSE
ID HS72 MOUSE STANDARD; PRT; 633 AA.
AC P1V156;
DT 01-AUG-1990 (Rel. 15, Created)
DT 01-AUG-1990 (Rel. 15, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Heat shock-related 70 kDa protein 2 (Heat shock protein 70.2).
GN Name=Hsp2; Synonyms=Hsp70.2, Hsp70-2;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=88302212; PubMed=3405224;
RA Zakari Z.F., Wolgemuth D.J., Hunt C.R.;
RT "Identification and sequence analysis of a new member of the mouse
RT HSP70 gene family and characterization of its unique cellular and
RT developmental pattern of expression in the male germ line.";
RL Mol. Cell. Biol. 8:2925-2932(1988).
CC -!- FUNCTION: In cooperation with other chaperones, Hsp70s stabilize
CC preexistent proteins against aggregation and mediate the folding
CC of newly translated polypeptides in the cytosol as well as within
CC organelles. These chaperones participate in all these processes
CC through their ability to recognize nonnative conformations of
CC other proteins. They bind extended peptide segments with a net
CC hydrophobic character exposed by polypeptides during translation
CC and membrane translocation, or following stress-induced damage.
CC -!- DEVELOPMENTAL STAGE: Specifically expressed in prophage stage of
CC melioidosis.
CC -!- SIMILARITY: Belongs to the heat shock protein 70 family.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (see http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC
CC EMBL; M20567; AAA37859.1; -
CC HSP; P19120; IATV.
CC MGD; MGI:96243; Hsp2.
CC GO; GO:0005515; F:protein binding; IPI.
CC InterPro; IPR001023; Hsp70.
CC Pfam; PF00012; Hsp70; 1.
CC PRINTS; PR00301; HEATSHOCK70.
CC ProDom; PD000089; Hsp70; 1.
CC TIGRFAMs; TIGR01991; HscA; 1.
CC PROSITE; PS00297; HSP70_1; 1.
CC PROSITE; PS00329; HSP70_2; 1.
CC PROSITE; PS01036; HSP70_3; 1.
CC ATP-binding; Chaperone; Heat shock; Multigene family.
CC KW ATP-binding; Chaperone; Heat shock.
CC SEQUENCE 633 AA; 69740 MW; E7F9040F2AB138DD CRC64;

Query Match 80.3%; Score 1054.5; DB 1; Length 633;
Best Local Similarity 79.1%; Pred. No. 4.3e-57;
Matches 204; Conservative 23; Mismatches 20; Indels 11; Gaps 2;

QY 1 KSENVQDLLLLLVAPLSGLGTAGVMTALIKRNSTIPTKTQIFTTYSNDQPGVLIQVY 60
DB 387 KSENVQDLLLLLVAPLSGLGTAGVMTALIKRNSTIPTKTQIFTTYSNDQPGVLIQVY 446
QY 61 EGERAMTKDNLLGLRFLSGIPPAARGVPQIEVTFDIDANGILNVTATDKTGKANKITI 120
DB 447 EGERAMTKDNLLGLRFLSGIPPAARGVPQIEVTFDIDANGILNVTATDKTGKANKITI 506
QY 121 TNDKRLSKETLWVQAEKYKAEVQREVRVSAKNALESYAFNMKSAVDEGLGKGIS 180
DB 507 TNDKRLSKDDIDRWVQAEKYKAEVQREVRVSAKNALESYAFNMKSAVDEGLGKGIS 566
QY 181 EADKKKVLDKCOEIVSWLDANTLAEKDFEHRKELEQVNCNPIISGLYQGAGPGPGGFG 240
```

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Db 567 EQDKNKILDKCOEIVNWLDRNQMAEKDEYEHKQELERVCNFIISKLYQG-----GPGG-- 620
QY 241 AQGPKGSGSGPTIEVD 258
DB 621 -----GGSSGGSGPTIEVD 633

RESULT 81
Q99KD7
ID Q99KD7 PRELIMINARY; PRT; 633 AA.
AC Q99KD7;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Heat shock protein 2.
GN Name=Hsp2;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haie L.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M.J., Udell T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaby S.H.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grinstead J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smallos D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RX STRAIN=FVB/N; TISSUE=Mammary tumor. C3;
RA Strausberg R.;
RA Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RX TISSUE=Testis;
RA Strausberg R.;
RA Submitted (MAY-2003) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: Belongs to the heat shock protein 70 family.
CC EMBL; BC004714; AA04714.1; -
CC EMBL; BC052350; AA052350.1; -
CC HSP; P19120; 3HSC.
CC MGD; MGI:96243; Hsp2.
CC GO; GO:0005739; C:mitochondrion; IDA.
CC GO; GO:0005515; F:protein binding; IPI.
CC InterPro; IPR001023; Hsp70.
CC Pfam; PF00012; Hsp70; 1.
CC PRINTS; PR00301; HEATSHOCK70.
CC ProDom; PD000089; Hsp70; 1.
CC PROSITE; PS00297; HSP70_1; 1.
CC PROSITE; PS00329; HSP70_2; 1.
CC PROSITE; PS01036; HSP70_3; 1.
CC ATP-binding; Heat shock.
CC SEQUENCE 633 AA; 69641 MW; 6F65773C7EFA69F CRC64;

Query Match 80.3%; Score 1054.5; DB 2; Length 633;
```



```
Best Local Similarity 79.1%; Pred. No. 4.3e-57;
Matches 204; Conservative 23; Mismatches 20; Indels 11; Gaps 2;

QY 1 KSENVQDLLLLDVAPLSLGLETAGVMTALIKRNSTIPTKTQIFTTYSNQPGLVQVY 60
DB 387 KSENVQDLLLLDVAPLSLGLETAGVMTPLIKRNTIPTKTQIFTTYSNQPGLVQVY 446
QY 61 EGERAMTKDNNLLGRFELSGIPPPAPRGVPQIEVTFDIDANGILNVATDKSTGKANKITI 120
DB 447 EGERAMTKDNNLLGKFDLTGTPPAPRGVPQIEVTFDIDANGILNVATDKSTGKANKITI 506
QY 121 TNDKRLSKERIERMVQEAERYKAEDVQREVRVSAKNALESYAFNMKSAVDEGLKGGKIS 180
DB 507 TNDKRLSKDDIDRMVQEAERYKSEDEANRDRVAANKAVESYTNIKQTVDEKURGGKIS 566
QY 181 EADKKKVLDKCOEVIWLDANTLAEKDFEHRKKELEQVNCNPIISGLYQGAGGPGPGFG 240
DB 567 EODKKNKILDKCOEVIWLDNRNQMAEKDEYHKQELERVNCNPIISKLQYQ---GPGG-- 620
QY 241 AQGPKGGSGSGPTIEVD 258
DB 621 -----GGSSGGPTIEVD 633

RESULT 82
Q66HL1 PRELIMINARY; PRT; 633 AA.
AC Q66HL1;
DT 25-OCT-2004 (TReMBLrel. 28, Created)
DT 25-OCT-2004 (TReMBLrel. 28, Last sequence update)
DE Testis-specific heat shock protein-related gene hat70.
GN Name=Hsp70;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RX PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Peingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.P., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Rana S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
[2]
RN SEQUENCE FROM N.A.
RP TISSUE=Testis;
RC Director MGC Project;
RL Submitted (SEP-2004) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: Belongs to the heat shock protein 70 family.
DR EMBL; BC081803; AAH81803.1; --
DR InterPro; IPR001023; Hsp70.
DR Pfam; PF00012; Hsp70; 1
DR PRINTS; PR00301; HEATSHOCK70.
DR ProDom; PD000089; Hsp70; 1.
DR PROSITE; PS00297; Hsp70_1; 1.
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DR PROSITE; PS00329; HSP70_2; 1.
DR PROSITE; PS01036; HSP70_3; 1.
KW ATP-binding; Heat shock.
SQ SEQUENCE 633 AA; 69641 MW; 6F65773C7EFA69F CRC64;

Query Match 80.3%; Score 1054.5; DB 2; Length 633;
Best Local Similarity 79.1%; Pred. No. 4.3e-57;
Matches 204; Conservative 23; Mismatches 20; Indels 11; Gaps 2;

QY 1 KSENVQDLLLLDVAPLSLGLETAGVMTALIKRNSTIPTKTQIFTTYSNQPGLVQVY 60
DB 387 KSENVQDLLLLDVAPLSLGLETAGVMTPLIKRNTIPTKTQIFTTYSNQPGLVQVY 446
QY 61 EGERAMTKDNNLLGRFELSGIPPPAPRGVPQIEVTFDIDANGILNVATDKSTGKANKITI 120
DB 447 EGERAMTKDNNLLGKFDLTGTPPAPRGVPQIEVTFDIDANGILNVATDKSTGKANKITI 506
QY 121 TNDKRLSKERIERMVQEAERYKAEDVQREVRVSAKNALESYAFNMKSAVDEGLKGGKIS 180
DB 507 TNDKRLSKDDIDRMVQEAERYKSEDEANRDRVAANKAVESYTNIKQTVDEKURGGKIS 566
QY 181 EADKKKVLDKCOEVIWLDANTLAEKDFEHRKKELEQVNCNPIISGLYQGAGGPGPGFG 240
DB 567 EODKKNKILDKCOEVIWLDNRNQMAEKDEYHKQELERVNCNPIISKLQYQ---GPGG-- 620
QY 241 AQGPKGGSGSGPTIEVD 258
DB 621 -----GGSSGGPTIEVD 633

RESULT 83
Q9NJB7 PRELIMINARY; PRT; 645 AA.
AC Q9NJB7;
DT 01-OCT-2000 (TReMBLrel. 15, Created)
DT 01-OCT-2000 (TReMBLrel. 15, Last sequence update)
DT 01-MAR-2004 (TReMBLrel. 26, Last annotation update)
DE Heat shock protein 70.
OS Eukaryota; Metazoa; Nematoda; Chromadorea; Spirurida; Filarioidea;
OC Onchocercidae; Wuchereria.
OX NCBI_TaxID=6293;
RN [1]
RP SEQUENCE FROM N.A.
RA Wijesundera S.W., Pathiratne B.N., Perera R., Karunanayake E.H.;
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: Belongs to the heat shock protein 70 family.
DR EMBL; AF167352; AAF32254.1; --
DR HSRP; P19120; 3HSC.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0006457; P:protein folding; IEA.
DR GO; GO:0006986; P:response to unfolded protein; IEA.
DR InterPro; IPR001023; Hsp70.
DR Pfam; PF00012; Hsp70; 1.
DR PRINTS; PR00301; HEATSHOCK70.
DR PROSITE; PS00297; HSP70_1; 1.
DR PROSITE; PS00329; HSP70_2; 1.
DR PROSITE; PS01036; HSP70_3; 1.
KW ATP-binding; Heat shock.
SQ SEQUENCE 645 AA; 70304 MW; CBD4BE39E35B69D0 CRC64;

Query Match 80.2%; Score 1054; DB 2; Length 645;
Best Local Similarity 79.4%; Pred. No. 4.8e-57;
Matches 208; Conservative 20; Mismatches 30; Indels 4; Gaps 3;

QY 1 KSENVQDLLLLDVAPLSLGLETAGVMTALIKRNSTIPTKTQIFTTYSNQPGLVQVY 60
DB 384 KSENVQDLLLLDVAPLSLGIVTAGVMTPLIKRNTIPTKTSQTFTTYSNQPGLVQVY 443
QY 61 EGERAMTKDNNLLGRFELSGIPPPAPRGVPQIEVTFDIDANGILNVATDKSTGKANKITI 120
DB 444 EGERAMTKDNNLLGRFELSGIPPPAPRGVPQIEVTFDIDANGILNVATDKSTGKANKITI 503
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[illegible]

RESULT 84	
SEQUENCE 94614	
ID	PRELIMINARY; PRT; 646 AA.
Q94614	
AC	Q94614;
DT	01-FEB-1997 (TrEMBLrel. 02, Created)
DT	01-FEB-1997 (TrEMBLrel. 02, Last sequence update)
DT	01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE	Heat shock 70kDa protein (Fragment).
DE	Name=hsp70;
GN	Mesocestoides corti.
OS	Mesocestoides corti.
OC	Eukaryota; Metazoa; platyhelminthes; Cestoda; Eucestoda;
OC	Cyclophyllidae; Mesocestoididae; Mesocestoides.
OX	NCBI_Taxid=53468;
RP	[1]
RN	SEQUENCE FROM N.A.
RX	MEDLINE=92366447; PubMed=1323828;
RA	Bork P., Sander C., Valencia A.;
RT	"An ATPase domain common to prokaryotic cell cycle proteins, sugar
RT	kinases, actin, and hsp70 heat shock proteins.";
RL	Proc. Natl. Acad. Sci. U.S.A. 89:7290-7294 (1992).
RL	[2]
RN	SEQUENCE FROM N.A.
RP	Teale J.M., Bangs L.A.;
RA	Submitted (SEP-1996) to the EMBL/GenBank/DBJ databases.
CC	1- SIMILARITY: belongs to the heat shock protein 70 family.
DR	EMBL; U70213; AAA18390.1; -.
DR	HSP; P19120; 3HSC.
DR	GO; GO:0005524; F:ATP binding; IEA.
DR	GO; GO:0006457; P:protein folding; IEA.
DR	GO; GO:0006986; P:response to unfolded protein; IEA.
DR	InterPro: IPR001023; Hsp70.
DR	InterPro: IPR000169; Pept_cys_acsite.
DR	Fram: PF00012; HSP70; 1.
DR	PRINTS; PR00301; HEATSHOCK70.
DR	PROSITE; PS00297; HSP70_1; 1.
DR	PROSITE; PS00329; HSP70_2; 1.
DR	PROSITE; PS01036; HSP70_3; 1.
DR	PROSITE; PS00639; THIOL_PROTEASE_HIS; UNKNOWN_1.
DR	ATP-Binding; Heat shock.
FT	NON TER 1
FT	SEQUENCE 646 AA; 70683 MW; FF2014E17FD9F940 CRC64;
SQ	

Query Match	80.1%;	Score 1052.5;	DB 2;	Length 646;
Best Local Similarity	77.7%;	Pred. No. 5.9e-57;		
Matches 209;	Conservative 21;	Mismatches 28;	Indels 11;	Gaps 2;
QY	1	KSENVQDLLLLDVAPLSLGLETAGGVMTALIKRNSTIPTKQTQFTFTYSNQPGVLIQVY	60	
Db	378	KSEAVQDLLLLDVAPLSLGLETAGGVMTALIKRNTTIPTKQTQFTFTYSNQPGVLIQVY	437	
QY	61	EGERAMTKNNLGRPELSGIPAPRGVPQIEVTFDIDANGILNVATATDKSTGKANKITI	120	
Db	438	EGERAMTRDNNLLGKPELSGIPAPRGVPQIEVTFDIDANGILSVSAVDKSTGKANKITI	497	
QY	121	TNDKGRLSKEEIERMVOEAKYKAEDVQRRERSAKNALESYAFNMKSAVEDEGLKKKIS	180	
Db	498	TNDKGRLSKEEIERMVMNDAAKYQEDDKQDRVSAKNALESYAFNMKSTVEDEKVKKIA	557	
QY	181	EADKGGKVLDRKCOEIVISLWDANTLAEKDEFEHKKRKELEQVNCNPIISGLYQAGGPG--	PGG 238	

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558  EGRKKIISKCEETIKWLDAQNQADKGEYHQRKLEISVCNPIITKMTYQEAGGAGCMPOG 617
239  FGAQPGKGGSG-----SGPTIEEVD 258
      |||||
618  MPGMPCGGSGGGMGGDAGSGNRGPTIEVD 646
      |||||

RESULT 85
Q81860
ID Q81860 PRELIMINARY; PRT; 650 AA.
AC Q81860;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Heat shock protein 70 A.
OS Heterodera glycines (Soybean cyst nematode).
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Tylenchida; Tylenchinea;
OC Tylenchoidea; Heteroderidae; Heteroderinae; Heterodera.
OX NCBI_TaxID=51029;
RN [1]
RP SEQUENCE FROM N.A.
RA Kovaleva E.S., Chitwood D.J.;
RL Submitted (OCT-2002) to the EMBL/GenBank/DBJ databases.
RC -1- SIMILARITY: Belongs to the heat shock protein 70 family.
DR EMBL; AY161283; AA078300.1; -.
DR HSP; P19120; IHPM.
DR GO; GO:0005524; P:ATP binding; IEA.
DR GO; GO:0006457; P:protein folding; IEA.
DR GO; GO:0006986; P:response to unfolded protein; IEA.
DR InterPro; IPR001023; Hsp70.
DR Pfam; PF00012; HSP70; 1.
DR PRINTS; PR00301; HEATSHOCK70.
DR ProDom; PD000089; Hsp70; 1.
DR PROSITE; PS00297; HSP70_1; 1.
DR PROSITE; PS00329; HSP70_2; 1.
DR PROSITE; PS01036; HSP70_3; 1.
DR ATP-binding; Heat shock.
KW SEQUENCE 650 AA; 70614 MW; 7CB8123DCBC4BF8D CRC64;

```

Query Match	80.1%	Score 1052.5	DB 2	Length 650
Best Local Similarity	79.4%	Pred. No. 5.9e-57		
Matches 212	Conservative 19	Mismatches 25	Indels 11	Gaps 4

Qy	1	KSENVDDLILLDVAPLSLGLTETAGGVTWALIKENSTIPKOTQFTFTYSNQPGVLQVY	60
Db	386	KSETVQDLLLDVAPLSLGLTETAGGWTSLIKNTTIPKTSQTFTYSNQPGVLQVY	445
Qy	61	EGERAMTKONLLGRFELSGIPAPRGVPOIEVTFDIDANGILNVTATDKSTGKANKITI	121
Db	446	EGERAMTKONLLGKPFELSGIPAPRGVPOIEVTFDIDANGILNVSADKSTGKQNKITI	505
Qy	121	TNDKGRLSKEEIRRMVQEAARKYKAEDVQRERSAKNALESYAFNMKSAVEDEGLKGKIS	180
Db	506	TNDKGRLSKEEIRRMVQEAARKFKSEDEVQRVRSAKNALESYCFNIKQTMEDSNLKDKIS	565
Qy	181	EADKKVLDKCOQVLSWLDANTLAERKDEFEHKKELEQVCNPPIISGLYQAGG-----P	234
Db	566	EDDKKVLEKCGEVLAWLDANQAAKEEFESHQKLEGI CNPIITKLYQAGGAMPGGPMP	625
Qy	235	G- - - PGGFGAQGPKGSGSGPTTIEVD	258
Db	626	GGGMPGGGAAG - AGGAG - GPTTIEVD	650

RESULT 86			
Q9GPKO	PRELIMINARY;	PRT;	650 AA.
ID	Q9GPKO		
AC	Q9GPKO		
DT	01-MAR-2001 (TrEMBLrel. 16, Created)		
DT	01-MAR-2001 (TrEMBLrel. 16, Last sequence update)		
DT	01-MAR-2004 (TrEMBLrel. 26, Last annotation update)		
DE	Heat shock protein 70.		
OS	Heterodera glycines (Soybean cyst nematode).		

DR PRINTS; PRO0301; HEATSHOCK70.
DR ProDom; PD000089; Hsp70_1.
DR PROSITE; PS00297; HSP70_1; 1.
DR PROSITE; PS00329; HSP70_2; 1.
DR PROSITE; PS01036; HSP70_3; 1.
KW ATP-binding; Heat shock.
SQ SEQUENCE 636 AA; 69866 MW; 1844AC35558B7DF6 CRC64;

Query Match 80.0%; Score 1051; DB 2; Length 636;
Best Local Similarity 78.7%; Pred. No. 7.2e-57;
Matches 203; Conservative 24; Mismatches 23; Indels 8; Gaps 2

Qy 1 KSENVQDLLLDVAPLSIGLETAGGVMTALIKRNSTPTKQTQPTTYSNDQPGVLIOVY 60
Db 387 KSENVQDLLLDVTPLSIGLETAGGVMTPLIKRNTTPTKQTQFTTYSNDQSSVLQVY 446

Qy 61 EGERAMTKNNLGRFELSGIPAPRGVQLEVTFDIDANGILNVTADKSTGKANKITI 120
Db 447 EGERAMTKNNLGLKFDLTGIPAPRGVQLEVTFDIDANGILNVTADKSTGKANKITI 506

Qy 121 TNDKGRLSKEIEIRMWQEAERYKAEDVQQRVRSKNALESYAFNMKSAVEDEGLKGKIS 180
Db 507 TNDKGRLSKDDIDEMVQEAERYKSEANRDRVAAKNAVESYTNIKQTVEDEKLKGKIS 566

Qy 181 EADKKVLDKQEVISWLDANTLAEKDFEPHKRKELRQVNCNPIISGLYQAGAGGPGGFG 240
Db 567 DQDKNKILDKQEVINWLDNRQNAEKDEYEHKQELERVCNPNPIISKLYQG----GPGGGG 622

Qy 241 AQGPKGSGSGPTIEEVD 258
Db 623 GSGSG---GPTIEEVD 636

RESULT 88

Q801X9 PRELIMINARY; PRT; 623 AA.

ID Q801X9 PRELIMINARY; PRT; 623 AA.

AC Q801X9;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Heat shock protein 70 kDa (Fragment).
GN Name:HSP70;
OS Carassius auratus (Goldfish).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Carassius.
OX NCBI_TaxID=7957;
PI [1]
RN SEQUENCE FROM N.A.
RP Watabe S., Kondo H., Hashimoto S.;
RA Submitted (Oct-2002) to the EMBL/GenBank/DBJ databases.
RL -1- SIMILARITY: Belongs to the heat shock protein 70 family.
CC EMBL; AB092839; BAC67184.1; -.
DR HSPSP; P08107; IS3X.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0006457; P:protein folding; IEA.
DR GO; GO:0006986; P:response to unfolded protein; IEA.
DR InterPro; IPR001023; Hsp70.
DR Pfam; PF00012; HSP70; 1.
DR PRINTS; PR00301; HEATSHOCK70.
DR ProDom; PD000089; Hsp70_1.
DR PROSITE; PS00329; HSP70_2; 1.
DR PROSITE; PS01036; HSP70_3; 1.
KW ATP-binding; Heat shock.
FT NON_TER 1
SQ SEQUENCE 623 AA; 69781 MW; 7A3756151749BC56 CRC64;

Query Match 79.9%; Score 1050; DB 2; Length 623;
Best Local Similarity 80.0%; Pred. No. 8.1e-57;
Matches 208; Conservative 26; Mismatches 20; Indels 6; Gaps 3

Qy 2 SENVDLLLDVAPLSIGLETAGGVMTALIKRNSTPTKQTQIFTTYSNDQPGVLIOVY 61

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Db 367 SGNVQDLLLLDVARLSGLIETAGGVMTALIKENTTIPTKQTCTSTYSNDQPGVLIQVYE 426
QY 62 GERAMTKDNLLGRPELSGIPPPAPRGVPOIEVTFDIDANGILNVATDKSTGKANKITIT 121
Db 427 GERAMTKDNLLGKPELTGIPPPAPRGVPOIEVTFDIDANGILNVSAVDKSTGKANKITIT 486
QY 122 NDKGRLSKEETRMVQAEKKAEDVORERSVAKNALESVAFNMKSAVEDGLKGIKISE 181
Db 487 NDKGRLSKDEETRMVQAEKKAEDVORERSVAKNALESVAFNMKSAVEDGLKGIKISE 546
QY 182 ADKKKVLDCOEVISWLDANTLAEDFEHKKRKELEQVNCNPIISGLYQAGGPGPGGFGA 241
Db 547 DDKKKVIEKNEAVSLENNQLADKEEYEHHLKELEKVCNPIITKLYQ--GGMPAGGGA 604
QY 242 QGPKGGSG---SGPTIEVD 258
Db 605 Q-TRGSGPVLRGPTIEVD 623

RESULT 89
HS70_CHICK
ID HS70_CHICK STANDARD; PRT; 634 AA.
AC P08106;
DT 01-AUG-1988 (Rel. 08, Created)
DT 01-AUG-1988 (Rel. 08, Last sequence update)
DT 01-FEB-1994 (Rel. 28, Last annotation update)
DE Heat shock 70 kDa protein (HSP70).
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]_TaxID=9031;
RP SEQUENCE FROM N.A.
RX MEDLINE=86304452; PubMed=3017985;
RA Morimoto R.I., Hunt C., Huang S.-Y., Berg K.L., Banerji S.S.;
RT "Organization, nucleotide sequence, and transcription of the chicken
HSP70 gene.";
RL J. Biol. Chem. 261:12692-12699 (1986).
CC -!- SIMILARITY: Belongs to the heat shock protein 70 family.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; J02579; AAA48825.1; -.
DR PIR; A25646; A25646.
DR HSP; P08109; 1CKR.
DR InterPro; IPR001023; Hsp70.
DR Pfam; PF00012; HSP70; 1.
DR PRINTS; PR00301; HEATSHOCK70.
DR ProDom; PD000089; Hsp70; 1.
DR TIGRFAMs; TIGR01991; HscA; 1.
DR PROSITE; PS00297; HSP70_1; 1.
DR PROSITE; PS00329; HSP70_2; 1.
DR PROSITE; PS01036; HSP70_3; 1.
DR ATP-binding; Heat shock; Multigene family.
KW ATP-binding; Heat shock; Multigene family.
SQ SEQUENCE 634 AA; 69750 MW; 4270F7F08D365AEB.CRC64;

Query Match 79.9%; Score 1050; DB 1; Length 634;
Best Local Similarity 79.1%; Pred. No. 8.2e-57;
Matches 204; Conservative 23; Mismatches 21; Indels 10; Gaps 1;

QY 1 KSENVQDLLLLDVAPLSGLIETAGGVMTALIKRNTSTPTKQTCTSTYSNDQPGVLIQVYE 60
Db 387 KSENVQDLLLLDVAPLSGLIETAGGVMTALIKRNTSTPTKQTCTSTYSNDQSSVLIQVY 446
QY 61 EGERAMTKDNLLGRFELSGLIPPPAPRGVPOIEVTFDIDANGILNVATDKSTGKANKITIT 120

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Db 447 EGERAMTKDNLLGKFDLTGIPPPAPRGVPOIEVTFDIDANGILNVSAVDKSTGKANKITIT 506
QY 121 TNDKGRLSKEETRMVQAEKKAEDVORERSVAKNALESVAFNMKSAVEDGLKGIKISE 180
Db 507 TNDKGRLSKODIDRMVQAEKKAEDVORERSVAKNALESVAFNMKSAVEDGLKGIKISE 566
QY 181 EADKKKVLDCOEVISWLDANTLAEDFEHKKRKELEQVNCNPIISGLYQAGGPGPGGFG 240
Db 567 DQDKQKVLDCOEVISWLDANTLAEDFEHKKRKELEQVNCNPIISGLYQAGGPGPGGFG 626
QY 241 AQGPKGGSGSGPTIEVD 258
Db 627 -----GPTIEVD 634

RESULT 90
O93240
ID O93240 PRELIMINARY; PRT; 640 AA.
AC O93240;
DT 01-NOV-1998 (TReMBLrel. 08, Created)
DT 01-NOV-1998 (TReMBLrel. 08, Last sequence update)
DT 01-MAR-2004 (TReMBLrel. 26, Last annotation update)
DE HSP70.
OS Paralicthys olivaceus (Japanese flounder).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Pleuronectiformes;
OC Pleuronectoidae; Paralicthyidae; Paralicthys.
OX NCBI_TaxID=8255;
RN [1]_TaxID=8255;
RP SEQUENCE FROM N.A.
RA Yokoyama Y., Hashimoto H., Kubota S., Kinoshita M., Toyohara H.,
RA Sakaguchi M., Tanaka M., Seikai T., Kanamori M.;
RT "cDNA cloning of heat-inducible HSP70, a 70.6 kDa heat shock protein,
RT in Japanese flounder Paralicthys olivaceus.";
RL Fisheries Sci. 64:964-968 (1998).
CC -!- SIMILARITY: Belongs to the heat shock protein 70 family.
DR EMBL; AB010871; BAA31697.1; -.
DR PIR; T43724; T43724.
DR HSP; P08107; 1HJO.
DR GO; GO:0005524; F:ATP binding; IEA.
DR InterPro; IPR001023; Hsp70.
DR Pfam; PF00012; HSP70; 1.
DR PRINTS; PR00301; HEATSHOCK70.
DR ProDom; PD000089; Hsp70; 1.
DR PROSITE; PS00297; HSP70_1; 1.
DR PROSITE; PS00329; HSP70_2; 1.
DR PROSITE; PS01036; HSP70_3; 1.
DR ATP-binding.
KW ATP-binding.
SQ SEQUENCE 640 AA; 70608 MW; 9C8E65738F0CF705.CRC64;

Query Match 79.9%; Score 1049.5; DB 2; Length 640;
Best Local Similarity 77.8%; Pred. No. 8.9e-57;
Matches 200; Conservative 33; Mismatches 21; Indels 3; Gaps 2;

QY 2 SENVQDLLLLDVAPLSGLIETAGGVMTALIKRNTSTPTKQTCTSTYSNDQPGVLIQVYE 61
Db 387 SENVQDLLLLDVAPLSGLIETAGGVMTALIKRNTSTPTKQTCTSTYSNDQPGVLIQVYE 446
QY 62 GERAMTKDNLLGRFELSGLIPPPAPRGVPOIEVTFDIDANGILNVATDKSTGKANKITIT 121
Db 447 GERAMTKDNLLGKFDLTGIPPPAPRGVPOIEVTFDIDANGILNVSAVDKSTGKANKITIT 506
QY 122 NDKGRLSKEETRMVQAEKKAEDVORERSVAKNALESVAFNMKSAVEDGLKGIKISE 181
Db 507 NDKGRLSKEETRMVQAEKKAEDVORERSVAKNALESVAFNMKSAVEDGLKGIKISE 566
QY 182 ADKKKVLDCOEVISWLDANTLAEDFEHKKRKELEQVNCNPIISGLYQAGGPGPGGFGA 241
Db 567 EDKKVIDKNCQTISWLENNQLAEKDEYEHQKLEKVCNPIITKLYQGA-APPPG--GS 623
QY 242 QGPKGGSGSGPTIEVD 258

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Db 624 SCHAGNAOQPTIEVD 640
RESULT 91
Q8AYL6 PRELIMINARY; PRT; 634 AA.
AC Q8AYL6
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Heat shock protein.
GN Name=hsp70;
OS Numida meleagris (Helmeted guinea fowl).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Numididae; Numida.
OX NCBI_TaxID=8996;
RN [1]
RP SEQUENCE FROM N.A.
RA Koike Y., Hanzawa K., Hara H., Hosomichi K., Yoshida Y., Watanabe S.;
RL Submitted (NOV-2002) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: Belongs to the heat shock protein 70 family.
DR EMBL; AB096696; BAC24791.1; -.
DR HSP; P19120; 3HSC.
DR GO; GO:0005524; P:ATP binding; IEA.
DR GO; GO:0006457; P:protein folding; IEA.
DR GO; GO:0006986; P:response to unfolded protein; IEA.
DR InterPro; IPR001023; Hsp70.
DR Pfam; PF00012; HSP70_1.
DR PRINTS; PR00301; HEATSHOCK70.
DR ProDom; PD000089; Hsp70_1.
DR PROSITE; PS00297; HSP70_1; 1.
DR PROSITE; PS00329; HSP70_2; 1.
DR PROSITE; PS01036; HSP70_3; 1.
DR ATP-binding; Heat shock.
KW ATP-binding; Heat shock.
SQ SEQUENCE 634 AA; 69874 MW; 5D84DC80CF407F0C CRC64;

Query Match 79.8%; Score 1049; DB 2; Length 634;
Best Local Similarity 78.3%; Pred. No. 9.5e-57;
Matches 202; Conservative 25; Mismatches 21; Indels 10; Gaps 1;

QY 1 KSENVQDILLDLVAPLSGLTAGVMTALIKRNTIPTKQTQITTTSDNQPGVLQVY 60
DB 387 KSENVQDILLDLVTPLSGLTAGVMTALIKRNTIPTKQTQITTTSDNQSSVLQVY 446
QY 61 EGERAMTKDNNLGRFELSGIPPAQPGVPQIEVTDFIDANGILNVATDKSTGKANKITI 120
DB 447 EGERAMTKDNNLGRFELDTGIPPAQPGVPQIEVTDFIDANGILNVSAVDKSTGKANKITI 506
QY 121 TNDKRLSKDEIERMVQAEKYKAEDVQVRERVSANNALESYAFNMKSAVEDGLKKGKIS 180
DB 507 TNDKRLSKDDIDRMVQAEKYKAEDANRDVGAKNLSLEYTYNNKQTVEDDKLKGKIS 566
QY 181 EADKKKVLKCOEVLISWLDANTLAEKDFEHRKELEQVNCPIISGLYQAGGPGPGFG 240
DB 567 QDQKQKVLKCOEVLISWLDNRNQMAEKEHYHKKQLEKLCNPIVTKLYQAGGAGGSGG 626
QY 241 AQGPKGSGSGPTIEVD 258
DB 627 -----GPTIEVD 634

RESULT 92
Q86MC3 PRELIMINARY; PRT; 649 AA.
AC Q86MC3
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE 70kDa heat shock protein.
GN Balanus amphitrite (Barnacle).
OC Eukaryota; Metazoa; Arthropoda; Crustacea; Maxillopoda; Cirripedia;
OC Thoracica; Sessilia; Balanidae; Balanus.
OX NCBI_TaxID=32267;

RN [1]
RP SEQUENCE FROM N.A.
RA Cheng S.H., So C.H., Chan P.K., Cheng C.W., Wu R.S.;
RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: Belongs to the heat shock protein 70 family.
DR EMBL; AY150182; AAN74984.1; -.
DR HSP; P19120; 3HSC.
DR GO; GO:0005524; P:ATP binding; IEA.
DR GO; GO:0006457; P:protein folding; IEA.
DR GO; GO:0006986; P:response to unfolded protein; IEA.
DR InterPro; IPR001023; Hsp70.
DR Pfam; PF00012; HSP70_1.
DR PRINTS; PR00301; HEATSHOCK70.
DR ProDom; PD000089; Hsp70_1.
DR PROSITE; PS00297; HSP70_1; 1.
DR PROSITE; PS00329; HSP70_2; 1.
DR PROSITE; PS01036; HSP70_3; 1.
DR ATP-binding; Heat shock.
KW ATP-binding; Heat shock.
SQ SEQUENCE 649 AA; 70737 MW; 4C2475790382C721 CRC64;

Query Match 79.8%; Score 1048; DB 2; Length 649;
Best Local Similarity 76.8%; Pred. No. 1.1e-56;
Matches 205; Conservative 21; Mismatches 31; Indels 10; Gaps 2;

QY 1 KSENVQDILLDLVAPLSGLTAGVMTALIKRNTIPTKQTQITTTSDNQPGVLQVY 60
DB 384 KSENVQDILLDLVTPLSGLTAGVMTAPIKRNTIPTKQTQITTTSDNQPGVLQVY 443
QY 61 EGERAMTKDNNLGRFELSGIPPAQPGVPQIEVTDFIDANGILNVATDKSTGKANKITI 120
DB 444 EGERAMTKDNNLGRFELTGIPPAQPGVPQIEVTDFIDANGILNVSAADKSTGKASNTI 503
QY 121 TNDKRLSKDEIERMVQAEKYKAEDVQVRERVSANNALESYAFNMKSAVEDGLKKGKIS 180
DB 504 TNDKRLTKETIERMVNEAEQFNQDEQREKISPKNALESYCFNMKSTVEDDKVKDKIS 563
QY 181 EADKKKVLKCOEVLISWLDANTLAEKDFEHRKELEQVNCPIISGLYQAGGPGPGFP- 239
DB 564 ESDKTTIIDKNCNTIKWLDGNQLAEKDFEHRKELEQVNCPIISGLYQAGGAAFGGMP 623
QY 240 -----GAQPKGSGSGPTIEVD 258
DB 624 GMPGMPGGAPKGGAG-GPTIEVD 649

RESULT 93
HS72_RAT
ID HS72_RAT STANDARD; PRT; 633 AA.
AC P14659;
DT 01-APR-1990 (Rel. 14, Created)
DT 01-APR-1990 (Rel. 14, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Heat shock-related 70 kDa protein 2 (Heat shock protein 70.2) (Testis-
DE specific heat shock protein-related) (HST).
GN Name=Hsp2; Synonyms=Hsp70;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN=Sprague-Dawley; TISSUE=Liver;
RX MEDLINE=90122930; PubMed=1688714; DOI=10.1016/0167-4781(90)90027-Y;
RA Wisniewski J., Kordula T., Krawczyk Z.;
RT "Isolation and nucleotide sequence analysis of the rat testis-specific
RT major heat-shock protein (HSP70)-related gene.";
RL Biochim. Biophys. Acta 1048:93-99(1990).
CC -1- FUNCTION: In cooperation with other chaperones, Hsp70s stabilize
CC of newly translated polypeptides in the cytosol as well as within
CC organelles. These chaperones participate in all these processes
CC through their ability to recognize nonnative conformations of
CC other proteins. They bind extended peptide segments with a net
```

hydrophobic character exposed by polypeptides during translation and membrane translocation, or following stress-induced damage.

-!- SIMILARITY: Belongs to the heat shock protein 70 family.

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EMBL; X15705; CAA33735.1; --

HSSP; P19120; 3HSC.

InterPro; IPR001023; Hsp70.

Pfam; PF00012; HSP70; 1.

PRINTS; P00301; HEATSHOCK70.

ProDom; PD000089; Hsp70; 1.

TIGRFAMs; TIGR01991; HsGA; 1.

PROSITE; PS00297; HSP70_1; 1.

PROSITE; PS00329; HSP70_2; 1.

PROSITE; PS01036; HSP70_3; 1.

ATP-binding; Chapterone; Heat shock; Multigene family; Spermatogenesis.

SEQUENCE 633 AA; 69528 MW; 6878CA5C2EEBF7DA CRC64;

Query Match 79.7%; Score 1047.5; DB 1; Length 633;
Best Local Similarity 78.7%; Pred. No. 1.2e-56;
Matches 203; Conservative 23; Mismatches 26; Indels 11; Gaps 2;

QY 1 KSENVQDLLLLDVAPLSGLGTAGGVTALIKRNSTIPTKTQTFITTSYDNPQGVLIQVY 60
Db 387 KSENVQDLLLLDVAPLSGLGTAGGVTALIKRNSTIPTKTQTFITTSYDNPQGVLIQVY 446

QY 61 EGERAMTKDNLGKLFELSGIPAPRGVQPIEVTFDIDANGILNVTATDKSTGKANKITI 120
Db 447 EGERAMTKDNLGKLFELSGIPAPRGVQPIEVTFDIDANGILNVTATDKSTGKANKITI 506

QY 121 TNDKGRLSKEEIERMVOEAEKYKAEDVQRRVSAKNALESYAFNMKSAVEDEGLKGKIS 180
Db 507 TNDKGRLSKDDIDRMVQVQADGKYSDEANRVAANKAVESYTNIKQTVEDEKLKGKIS 566

QY 181 EADKKVLDKQEVISWLDANTLAEKDFEHRKLEQVNCNPIISGLYQAGGPGPGFG 240
Db 567 EQDKNKLIDKQEVINWLDNRQMAEKDEYEHKQELERVCNPIISGLYQAGGPGPGFG 620

QY 241 AQGPKGGSGSGPTIEVD 258
Db 621 -----GGSGSGGPTIEVD 633

RESULT 94

Q7PYR5 PRELIMINARY; PRT; 656 AA.

ID Q7PYR5

AC Q7PYR5

DT 01-MAR-2004 (Tremblrel. 26, Created)

DT 01-MAR-2004 (Tremblrel. 26, Last sequence update)

DT 01-MAR-2004 (Tremblrel. 26, Last annotation update)

DE AGC12309

GN Name=agc949697; ORFNames=ENSAAGG00000017398;

OS Anopheles gambiae str. PEST.

OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;

OC Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Anopheles.

OX NCBI_TaxID=180454;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=PEST;

RA Anopheles Genome Sequencing Consortium;

RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.

CC -!- SIMILARITY: Belongs to the heat shock protein 70 family.

CC -!- CAUTION: The sequence shown here is derived from an EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is preliminary data.

CC EMBL; AAA01008987; EAA01046.1; --

HSSP; P19120; LATR.

GO; GO:0005524; F-ATP binding; IEA.

InterPro; IPR001023; Hsp70.

Pfam; PF00012; HSP70; 1.

PRINTS; P00301; HEATSHOCK70.

ProDom; PD000089; Hsp70; 1.

PROSITE; PS00297; HSP70_1; 1.

PROSITE; PS00329; HSP70_2; 1.

PROSITE; PS01036; HSP70_3; 1.

ATP-binding.

SEQUENCE 656 AA; 71375 MW; 0CBCFD5FC07B894A CRC64;

Query Match 79.6%; Score 1045.5; DB 2; Length 656;
Best Local Similarity 77.1%; Pred. No. 1.6e-56;
Matches 209; Conservative 22; Mismatches 27; Indels 13; Gaps 4;

QY 1 KSENVQDLLLLDVAPLSGLGTAGGVTALIKRNSTIPTKTQTFITTSYDNPQGVLIQVY 60
Db 386 KSENVQDLLLLDVAPLSGLGTAGGVTALIKRNSTIPTKTQTFITTSYDNPQGVLIQVY 445

QY 61 EGERAMTKDNLGKLFELSGIPAPRGVQPIEVTFDIDANGILNVTATDKSTGKANKITI 120
Db 446 EGERAMTKDNLGKLFELSGIPAPRGVQPIEVTFDIDANGILNVTATDKSTGKANKITI 505

QY 121 TNDKGRLSKEEIERMVOEAEKYKAEDVQRRVSAKNALESYAFNMKSAVEDEGLKGKIS 180
Db 506 TNDKGRLSKEDIERMVQVQADGKYSDEANRVAANKAVESYTNIKQTVEDEKLKGKIS 565

QY 181 EADKKVLDKQEVISWLDANTLAEKDFEHRKLEQVNCNPIISGLYQAGGPGPGFG 235
Db 566 DSDKTLVLDKCNDRITKWLDAQNLADKEEYEHKQELERVCNPIISGLYQAGGPGPGFG 625

QY 236 -PGSGF-GAQQPKG-----GSGSGGPTIEVD 258
Db 626 PFGGAPGAGGAAGGAGGSGSGPTIEVD 656

RESULT 95

HS7D MANSE STANDARD; PRT; 652 AA.

ID HS7D MANSE

AC Q90639;

DT 16-OCT-2001 (Rel. 40, Created)

DT 16-OCT-2001 (Rel. 40, Last sequence update)

DT 28-FEB-2003 (Rel. 41, Last annotation update)

DE Heat shock 70 kDa protein cognate 4 (Hsc 70-4).

OS Manduca sexta (Tobacco hawkmoth) (Tobacco hornworm).

OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;

OC Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia; Sphingioidea;

OC Sphingidae; Sphinginae; Manduca.

OX NCBI_TaxID=7130;

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE=Prothoracic gland;

RX MEDLINE=20304587; PubMed=10844250; DOI=10.1016/S0965-1748(00)00031-X;

RA Rybczynski R., Gilbert L.I.;

RT "cDNA cloning and expression of a hormone-regulated heat shock protein (hsc 70) from the prothoracic gland of Manduca sexta.";

RL Insect Biochem. Mol. Biol. 30:579-589(2000).

CC -!- SUBCELLULAR LOCATION: Nuclear (By similarity).

CC -!- DEVELOPMENTAL STAGE: Heat shock cognate proteins are expressed constitutively during normal development.

CC -!- SIMILARITY: Belongs to the heat shock protein 70 family.

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CC EMBL; AF194819; AAF09496.1; --

DR HSSP; P19120; 3HSC.

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DR InterPro; IPR001023; Hsp70.
DR Pfam; PF00012; Hsp70; 1.
DR PRINTS; PR00301; HEATSHOCK70.
DR ProDom; PD000089; Hsp70; 1.
DR TIGRFAMs; TIGR01991; Hsca; 1.
DR PROSITE; PS00297; Hsp70_1; 1.
DR PROSITE; PS00329; Hsp70_2; 1.
DR PROSITE; PS01036; Hsp70_3; 1.
DR ATP-binding; Heat shock; Multigene family; Nuclear protein.
SQ SEQUENCE 652 AA; 71431 MW; F5DBPEA4FEP76E3E CRC64;

Query Match 79.4%; Score 1043.5; DB 1; Length 652;
Best Local Similarity 76.2%; Pred. No. 2.2e-56;
Matches 205; Conservative 24; Mismatches 29; Indels 11; Gaps 3;

Qy 1 KSENVQDLLLDVAPLSGLTETAGGVMTALIKRNSTIPTKQTQITFTTYSNDQPGVLIQVY 60
Db 384 KSENVQDLLLDVAPLSGLTETAGGVMTALIKRNSTIPTKQTQITFTTYSNDQPGVLIQV 443

Qy 61 EGERAMTKNNLLGRFELSGIPAPRGVQPIEVTFDIDANGILNVATDKSTGKANKITI 120
Db 444 EGERAMTKNNLLGRFELSGIPAPRGVQPIEVTFDIDANGILNVATDKSTGKANKITI 503

Qy 121 TNDKGRLSKEIERMVQAEKYKAEDVQERVSANNALESYAFNMKSAVEDGLKGKIS 180
Db 504 TNDKGRLSKEIERMVQAEKYKAEDVQERVSANNALESYAFNMKSTMEDEKLKOKIS 563

Qy 181 EADKKVKLDKQCEVISWLDANTLAEKDFEHRKELEQVNCPIISGLYQAGG-PG--PG 237
Db 564 DSDKQTLKNCNDIKWLDLSQNLADKEIEYHKELEGICNPIITKLYQAGGPGGMPG 623

Qy 238 GF-----GAQGPFGGSGSGPTIEVD 258
Db 624 GMPGPGGAPGAGGAAPGGGAGPTIEVD 652

RESULT 96
HS73_BOVIN STANDARD; PRT; 631 AA.
AC P34933;
DT 01-FEB-1994 (Rel. 28, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Heat shock 70 kDa protein 3.
GN Name=Hsp70-3;
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=9312795; PubMed=1478667;
RT "Synthetic conservation of HSP70 genes in cattle and humans.";
RL Genomics 14:863-868(1992).
CC -1- FUNCTION: In cooperation with other chaperones, Hsp70s stabilize
CC preexistent proteins against aggregation and mediate the folding
CC of newly translated polypeptides in the cytosol as well as within
CC organelles. These chaperones participate in all these processes
CC through their ability to recognize nonnative conformations of
CC other proteins. They bind extended peptide segments with a net
CC hydrophobic character exposed by polypeptides during translation
CC and membrane translocation, or following stress-induced damage.
CC -1- SIMILARITY: Belongs to the heat shock protein 70 family.
CC
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CC or send an email to license@isb-sib.ch).
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CC EMBL; L10428; AAA30569.1; -.
DR HSP; P19120; 3HSC.
DR InterPro; IPR001023; Hsp70.
DR Pfam; PF00012; Hsp70; 1.
DR PRINTS; PR00301; HEATSHOCK70.
DR ProDom; PD000089; Hsp70; 1.
DR TIGRFAMs; TIGR01991; Hsca; 1.
DR PROSITE; PS00297; Hsp70_1; 1.
DR PROSITE; PS00329; Hsp70_2; 1.
DR PROSITE; PS01036; Hsp70_3; 1.
DR ATP-binding; Chaperone; Heat shock; Multigene family.
KW SEQUENCE 631 AA; 69199 MW; 01ACA20600C9322F CRC64;

Query Match 79.4%; Score 1043; DB 1; Length 631;
Best Local Similarity 78.3%; Pred. No. 2.2e-56;
Matches 202; Conservative 24; Mismatches 24; Indels 8; Gaps 2;

Qy 1 KSENVQDLLLDVAPLSGLTETAGGVMTALIKRNSTIPTKQTQITFTTYSNDQPGVLIQVY 60
Db 382 KSENVQDLLLDVAPLSGLTETAGGVMTALIKRNSTIPTKQTQITFTTYSNDQSSVLQVY 441

Qy 61 EGERAMTKNNLLGRFELSGIPAPRGVQPIEVTFDIDANGILNVATDKSTGKANKITI 120
Db 442 EGERAMTKNNLLGRFELSGIPAPRGVQPIEVTFDIDANGILNVATDKSTGKANKITI 501

Qy 121 TNDKGRLSKEIERMVQAEKYKAEDVQERVSANNALESYAFNMKSAVEDGLKGKIS 180
Db 502 TNDKGRLSKEIERMVQAEKYKAEDVQERVSANNALESYAFNMKSTMEDEKLKOKIS 561

Qy 181 EADKKVKLDKQCEVISWLDANTLAEKDFEHRKELEQVNCPIISGLYQAGGPGGPGFG 240
Db 562 DQDKNKILDKQCEVINWLDNRQNAEKDEYHKELEQVNCPIISGLYQG---GPGGG 617

Qy 241 AQGPFGGSGSGPTIEVD 258
Db 618 GSGASG----GPTIEVD 631

RESULT 97
HS73_BOVIN PRELIMINARY; PRT; 639 AA.
AC O73922;
DT 01-AUG-1998 (TrEMBLrel. 07, Created)
DT 01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Heat shock protein 70.
GN Name=Hsp70;
OS Oreochromis mossambicus (Mozambique tilapia) (Tilapia mossambica).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Perciformes; Labroidae;
OC Cichlidae; Oreochromis.
OX NCBI_TaxID=8127;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=20291068; PubMed=10828441; DOI=10.1016/S0014-5793(00)01538-6;
RT "Cloning and expression analysis of an inducible HSP70 gene from
RT tilapia fish.";
RL FEBS Lett. 474:5-10(2000).
RN [2]
RP SEQUENCE FROM N.A.
RA Molina A.I.;
RL Submitted (AUG-1997) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: Belongs to the heat shock protein 70 family.
DR EMBL; AJ001312; CAA04673.1; -.
DR HSP; P08107; IHJO.
DR GO; GO:0005524; P:ATP binding; IEA.
DR GO; GO:0006457; P:protein folding; IEA.
DR GO; GO:0006986; P:response to unfolded protein; IEA.
DR InterPro; IPR001023; Hsp70.
```

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DR Pfam: PF00012; HSP70_1.
DR PRINTS: PR00301; HEATSHOCK70.
DR ProDom: PD000089; HSP70_1.
DR PROSITE: PS00297; HSP70_1; 1.
DR PROSITE: PS00329; HSP70_2; 1.
DR PROSITE: PS01036; HSP70_3; 1.
KW ATP-binding; Heat shock_
SQ SEQUENCE 639 AA; 70292 MW; B296FA98407BD4AE CRC64;

Query Match
Best Local Similarity 79.3%; Score 1042.5; DB 2; Length 639;
Matches 203; Conservative 28; Mismatches 23; Indels 3; Gaps 2;

QY 2 SENVQDLLLLDVAPLSGLGLETAGGVTALIKENSTIPTKQTQIFFTYSNQGVLIOYVE 61
DB 386 SGNVQDLLLLDVAPLSGLGLETAGGVTALIKRNTTPTKQTQIFFTYSNQGVLIOYVE 445

QY 62 GERAMTKNNLLGRFELSGIPAPRGVPOIEVTFDIDANGILNVATDKSTGKANKITIT 121
DB 446 GERAMTKNNLLGKFLTGIPAPRGVPOIEVTFDIDANGILNVSAVDKSTGKANKITIT 505

QY 122 NDKGRLSKEEIERMVOEAEKYKADEVQVRVSAKNALESYAFNMKSAYEDELGKGIKISE 181
DB 506 NDKGRLSKEEIERMVOEAEKYKAEDDLDQDKIAAKNSLESYAFNMKSAYEDELGKGIKISE 565

QY 182 ADKKKVLKQCVISWLDANTLAEDKDFEKKKELEQVNCNPIISGLYQAGGPGFGA 241
DB 566 EDKKKVLKQCVISWLDANTLAEDKDFEKKKELEQVNCNPIISGLYQAGGPGFGA 241

QY 242 QGPKGGSGSGPTIEVD 258
DB 625 QARAG-SQGPTIEVD 639

RESULT 98
HS70 ONCTS
ID HS70 ONCTS STANDARD; PRT; 644 AA.
AC Q91233;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DE 05-JUL-2004 (Rel. 44, Last annotation update)
DE Heat shock 70 kDa protein (HSP70).
GN Name=HSP70;
OS Oncorhynchus tshawytscha (Chinook salmon) (King salmon).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
OC Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
OX NCBI_TaxID=74940;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC CRL-1681;
RA Hargis M.T., Goff H., Dauble D.D., Howard S., Candido P., Hickey E.,
RA Weber L.A.;
RL Submitted (OCT-1995) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: Belongs to the heat shock protein 70 family.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC
CC EMBL; U35064; AAA78276.1; -.
DR HSP; F08109; ICRK.
DR InterPro; IPR001023; Hsp70.
DR Pfam; PF00012; HSP70; 1.
DR PRINTS; PR00301; HEATSHOCK70.
DR ProDom; PD000089; HSP70_1.
DR TIGRFAMs; TIGR01991; Hsca; 1.
DR PROSITE; PS00297; HSP70_1; 1.
DR PROSITE; PS00329; HSP70_2; 1.

DR PROSITE; PS01036; HSP70_3; 1.
KW ATP-binding; Heat shock; Multigene family.
SQ SEQUENCE 644 AA; 70976 MW; 25DSC8AA2464B939 CRC64;

Query Match
Best Local Similarity 77.6%; Pred. No. 2.4e-56;
Matches 201; Conservative 30; Mismatches 27; Indels 1; Gaps 1;

QY 1 KSENVQDLLLLDVAPLSGLGLETAGGVTALIKENSTIPTKQTQIFFTYSNQGVLIOYV 60
DB 386 KSENVQDLLLLDVAPLSGLGLETAGGVTALIKRNTTPTKQTQIFFTYSNQGVLIOYV 445

QY 61 EGERAMTKNNLLGRFELSGIPAPRGVPOIEVTFDIDANGILNVATDKSTGKANKITIT 120
DB 446 EGERAMTKNNLLGKFLTGIPAPRGVPOIEVTFDIDANGILNVSAVDKSTGKANKITIT 505

QY 121 TNDKGRLSKEEIERMVOEAEKYKADEVQVRVSAKNALESYAFNMKSAYEDELGKGIKISE 180
DB 506 TNDKGRLSKEEIERMVOEAEKYKAEDDQAEKIAAKNSLESYAFNMKSAYEDELGKGIKISE 565

QY 181 EADKKKVLKQCVISWLDANTLAEDKDFEKKKELEQVNCNPIISGLYQAGGPGFGA 239
DB 566 QEDKKKVLKQCVISWLDANTLAEDKDFEKKKELEQVNCNPIISGLYQAGGPGFGA 239

QY 240 GAQPKGGSGSGPTIEVD 258
DB 626 QARTSSGDSGSGPTIEVD 644

RESULT 99
Q17310
ID Q17310 PRELIMINARY; PRT; 653 AA.
AC Q17310;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DE 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Ceratitis capitata heat shock-like protein.
OS Ceratitis capitata (Mediterranean fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Tephritidae; Tephritidae; Ceratitis.
OX NCBI_TaxID=7213;
RN [1]
RP SEQUENCE FROM N.A.
RC MEDLINE=98119518; PubMed=9459430;
RA Thanaphum S., Haymer D.S.;
RT "A member of the hsp70 gene family from the Mediterranean fruit fly,
RT Ceratitis capitata."
RL Insect Mol. Biol. 7:63-72(1998).
CC -!- SIMILARITY: Belongs to the heat shock protein 70 family.
CC EMBL; U20256; AAC23392.1; -.
DR HSP; P19120; IBA1
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0006457; P:protein folding; IEA.
DR GO; GO:0006986; P:response to unfolded protein; IEA.
DR InterPro; IPR001023; Hsp70.
DR Pfam; PF00012; HSP70; 1.
DR PRINTS; PR00301; HEATSHOCK70.
DR PROSITE; PS00297; HSP70_1; 1.
DR PROSITE; PS00329; HSP70_2; 1.
DR PROSITE; PS01036; HSP70_3; 1.
KW ATP-binding; Heat shock.
SQ SEQUENCE 653 AA; 71194 MW; 0745A6AC1041FAPC CRC64;

Query Match
Best Local Similarity 75.6%; Pred. No. 2.7e-56;
Matches 204; Conservative 29; Mismatches 25; Indels 12; Gaps 4;

QY 1 KSENVQDLLLLDVAPLSGLGLETAGGVTALIKENSTIPTKQTQIFFTYSNQGVLIOYV 60
DB 384 KSQEVQDLLLLDVAPLSGLGLETAGGVTALIKRNTTPTKQTQIFFTYSNQGVLIOYV 443

QY 61 EGERAMTKNNLLGRFELSGIPAPRGVPOIEVTFDIDANGILNVATDKSTGKANKITIT 120
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Db 623 NFGAPGAGGPTFGAGSGSGPTIEVD 650

Search completed: April 6, 2005, 17:24:15
Job time : 205 secs

Db 444 EGERAMTKDNLLGKFEISGIPPAAPRGVPQIEVTFDIDANGILNVTALERTNKENKITI 503
QY 121 TNDKGRLSKEETERNVQAEKYKASDEVQERVSNAKNALESYAFNMKSAVEDGLKKGKIS 180
Db 504 TNDKGRLSKEEDIERMVNAEAKYRSDEKQETIAAKNSLESYCFNMKATLDBENKTKIS 563
QY 181 EADKKKVLKDCQEVISWLDANTLAEKDFEHRKELEQVCMNPISGLYQAGG-----PG 235
Db 564 ESDRTTILDKCNETIKWLDANQLAEKEEYEHKQKELESVCNPIITKLYQAGGAPGGMPP 623
QY 236 --PGGF-----GAQPGKG--GSGSGPTIEVD 258
Db 624 GIPGFPAGGAGGAGGAGTGAGPTIEVD 653

RESULT 100

Q8ITL5 PRELIMINARY; PRT; 650 AA.
AC Q8ITL5
DT 01-MAR-2003 (TRENBLrel. 23, Created)
DT 01-MAR-2003 (TRENBLrel. 23, Last sequence update)
DT 01-MAR-2004 (TRENBLrel. 26, Last annotation update)
DE Heat shock cognate 70.
OS Chironomus tentans (Widge).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Nematocera; Chironomidae;
OC Chironomidae; Chironominae; Chironomus.
OX NCBI_TaxID=7153;
RN [1]
SEQUENCE FROM N.A.
RX MEDLINE=22431718; PubMed=12542632;
RA Karouna-Renier N.K., Yang W.-J., Rao K.R.;
RT "Cloning and characterization of a 70 kDa heat shock cognate gene.
RT (HSC70) from two species of Chironomus.";
RL Insect Mol. Biol. 12:19-26(2003).
CC -1- SIMILARITY: Belongs to the heat shock protein 70 family.
DR EMBL; AF448433; AAN14525.1; -.
DR HSSP; P19120; IBA1.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0006457; P:protein folding; IEA.
DR GO; GO:0006986; P:response to unfolded protein; IEA.
DR InterPro; IPR001023; Hsp70.
DR Pfam; PF00012; HSP70; 1.
DR PRINTS; PR00301; HEATSHOCK70.
DR PROSITE; PS00297; HSP70_1; 1.
DR PROSITE; PS00329; HSP70_2; 1.
DR PROSITE; PS01036; HSP70_3; 1.
KW ATP-binding; Heat shock.
SQ SEQUENCE 650 AA; 71340 MW; F826AAEA0228C18A CRC64;

Query Match 79.3%; Score 1041.5; DB 2; Length 650;
Best Local Similarity 76.1%; Pred No. 2.8e-56;
Matches 204; Conservative 24; Mismatches 29; Indels 11; Gaps 3;
QY 1 KSENVQDLLLDVAPLSGLTAGGVMITALIKRNTIPTKTQIPTTYSNDQPGVLIQVY 60
Db 384 KSEEVQDLLLDVTPLSGLTAGGVMVLKRNITPTKTQIPTTYSNDQPGVLIQV 443
QY 61 EGERAMTKDNLLGKFEISGIPPAAPRGVPQIEVTFDIDANGILNVTATDKSTGKANKITI 120
Db 444 EGERAMTKDNLLGKFEISGIPPAAPRGVPQIEVTFDIDANGILNVTALERTNKENKITI 503
QY 121 TNDKGRLSKEETERNVQAEKYKASDEVQERVSNAKNALESYAFNMKSAVEDGLKKGKIS 180
Db 504 TNDKGRLSKEEDIERMVNAEAKYRNEDDAQKERITAKNGLESYCFNMKSTMEDEKLKDKIS 563
QY 181 EADKKKVLKDCQEVISWLDANTLAEKDFEHRKELEQVCMNPISGLYQAGGFPGPGF- 239
Db 564 ESDKKIINDKCNETIKWLDANQLAEKEEYEHKQKELEGICNPIITKLYQSAGG-APGGM 622
QY 240 ---GAQG-----PKGGSGSGPTIEVD 258

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Result No.	Query			DB	ID	Description
	Score	Match	Length			
1	1314	100.0	641	2	A45871	dnaK-type molecule
2	1298.5	98.8	640	2	A29160	dnaK-type molecule
3	1295	98.6	641	2	S53357	dnaK-type molecule
4	1279.5	97.4	638	2	S31766	dnaK-type molecule
5	1279	97.3	641	2	S35718	dnaK-type molecule
6	1258	95.7	641	2	I54542	dnaK-type molecule
7	1228.5	93.5	642	2	JH0095	dnaK-type molecule
8	1216	92.5	420	2	A26283	dnaK-type molecule
9	1100.5	83.8	646	2	S31716	dnaK-type molecule
10	1100.5	83.8	646	2	A35922	dnaK-type molecule
11	1100.5	83.8	646	2	JC4853	dnaK-type molecule
12	1100.5	83.8	646	2	S07197	dnaK-type molecule
13	1099	83.6	641	2	B45871	dnaK-type molecule
14	1097.5	83.5	646	2	A27077	dnaK-type molecule
15	1094.5	83.3	646	2	A45935	dnaK-type molecule
16	1092	83.1	641	2	I49761	dnaK-type molecule
17	1091.5	83.1	650	2	S11456	dnaK-type molecule
18	1087	82.7	641	2	S41415	dnaK-type molecule
19	1084	82.5	651	2	S21175	dnaK-type molecule
20	1083	80.9	335	2	A45805	dnaK-type molecule
21	1063	80.9	644	2	A45635	dnaK-type molecule
22	1059.5	80.6	639	2	A55719	dnaK-type molecule
23	1058	80.5	645	2	I51129	dnaK-type molecule
24	1054.5	80.3	633	2	S10859	dnaK-type molecule
25	1050	79.9	634	2	A25646	dnaK-type molecule
26	1049.5	79.9	640	2	A23724	dnaK-type molecule
27	1047.5	79.7	633	2	S08211	dnaK-type molecule
28	1036.5	78.9	647	1	HXL70	dnaK-type molecule
29	1034	78.7	640	2	T21394	hypothetical prote

ALIGNMENTS

RESULT 1

A45871
dnaK-type molecular chaperone HSP70-1 - human
N:Alternate names: heat shock protein HSP70-1
C:Species: Homo sapiens (man)
C>Date: 03-Mar-1994 #sequence_revision 03-Mar-1994 #text_change 09-Jul-2004
C:Accession: A45871
R:Milner, C.M.; Campbell, R.D.
Immunogenetics 32, 242-251, 1990
A:Title: Structure and expression of the three MHC-linked HSP70 genes.
A:Reference number: A45871; MUID:91055806; PMID:1700760
A:Accession: A45871
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-641 <ML>
A:CROSS-references: UNIPROT:P08107; GB:M59828; GB:M34267; NID:g188487; PIDN:AAA63226.1;
C:Superfamily: involved in protein folding and assembling/disassembling of protein comp
C:Keywords: ATP; molecular chaperone

Query Match	100.0%;	Score 1314;	DB 2;	Length 641;
Best Local Similarity	100.0%;	Pred. No. 1.2e-77;		
Matches	258;	Conservative 0;	Mismatches 0;	Indels 0; Gaps 0;

QY 1 KSENVQDLLLDVAPLSGLTAGVMTALIKRNSTIPTKQTQIFTTYSNDQPGVLIQVY 60
DB 384 KSENVQDLLLDVAPLSGLTAGVMTALIKRNSTIPTKQTQIFTTYSNDQPGVLIQVY 443

QY 61 EGERAMTKONNLGRFELSGIPAPRGVPOIEVTFDIDANGILNVATDSTGKANKITI 120
DB 444 EGERAMTKONNLGRFELSGIPAPRGVPOIEVTFDIDANGILNVATDSTGKANKITI 503

QY 121 TNDKGRLSKEIERMVQEAQKAEDEVQERVSANNALESYAFNMKSAVEDEGLKGKIS 180
DB 504 TNDKGRLSKEIERMVQEAQKAEDEVQERVSANNALESYAFNMKSAVEDEGLKGKIS 563

QY 181 EADKKVLDKQEVISWLDANTLAEKDFEHKKELEQVNCNPIISGLYQAGGPGGFG 240
DB 564 EADKKVLDKQEVISWLDANTLAEKDFEHKKELEQVNCNPIISGLYQAGGPGGFG 623

QY 241 AQGPKGSGSGPTIEVD 258
DB 624 AQGPKGSGSGPTIEVD 641

RESULT 2

A29160
dnaK-type molecular chaperone HSPALL - human
N:Alternate names: heat shock protein, 70K
C:Species: Homo sapiens (man)
C>Date: 16-Aug-1988 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004
C:Accession: A29160; I37561; I37562
R:Hunt, C.; Morimoto, R.I.
Proc. Natl. Acad. Sci. U.S.A. 82, 6455-6459, 1985
A:Title: Conserved features of eukaryotic hsp70 genes revealed by comparison with the nu
A:Reference number: A29160; MUID:86016721; PMID:3931075
A:Accession: A29160
A:Molecule type: DNA
A:Residues: 1-640 <HUN>
A:Note: the authors mistranslated residues 463, 491, and 492
R:Drabent, B.; Genthe, A.; Benecke, B.J.
Nucleic Acids Res. 14, 8933-8948, 1986
A:Title: In vitro transcription of a human hsp 70 heat shock gene by extracts prepared f
A:Reference number: I37561; MUID:87066768; PMID:3786141
A:Accession: I37561
A:Status: translation not shown; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-22 <RES>

A:CROSS-references: EMBL:X04676; NID:g32480; PIDN:CAA28381.1; PID:g32481
A:Accession: I37562
A:Status: translation not shown; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 616-640 <RE2>
A:CROSS-references: EMBL:X04677; NID:g32482; PIDN:CAA28382.1; PID:g32483
C:Genetics:
A:Gene: GDB:HSPALL; HSP70-HOM
A:CROSS-references: GDB:120058; OMIM:140559
A:Map position: 6p21.3-6p21.3
A:Introns: #status absent
C:Function:
A:Description: involved in protein folding and assembling/disassembling of protein comp
C:Superfamily: heat shock protein 70
C:Keywords: ATP; molecular chaperone

Query Match	98.8%;	Score 1298.5;	DB 2;	Length 640;
Best Local Similarity	99.8%;	Pred. No. 1.2e-76;		
Matches	257;	Conservative 0;	Mismatches 0;	Indels 1; Gaps 1;

QY 1 KSENVQDLLLDVAPLSGLTAGVMTALIKRNSTIPTKQTQIFTTYSNDQPGVLIQVY 60
DB 384 KSENVQDLLLDVAPLSGLTAGVMTALIKRNSTIPTKQTQIFTTYSNDQPGVLIQVY 443

QY 61 EGERAMTKONNLGRFELSGIPAPRGVPOIEVTFDIDANGILNVATDSTGKANKITI 120
DB 444 EGERAMTKONNLGRFELSGIPAPRGVPOIEVTFDIDANGILNVATDSTGKANKITI 502

QY 121 TNDKGRLSKEIERMVQEAQKAEDEVQERVSANNALESYAFNMKSAVEDEGLKGKIS 180
DB 503 TNDKGRLSKEIERMVQEAQKAEDEVQERVSANNALESYAFNMKSAVEDEGLKGKIS 562

QY 181 EADKKVLDKQEVISWLDANTLAEKDFEHKKELEQVNCNPIISGLYQAGGPGGFG 240
DB 563 EADKKVLDKQEVISWLDANTLAEKDFEHKKELEQVNCNPIISGLYQAGGPGGFG 622

QY 241 AQGPKGSGSGPTIEVD 258
DB 623 AQGPKGSGSGPTIEVD 640

RESULT 3

S53357
dnaK-type molecular chaperone hsp70 - bovine
N:Alternate names: 70K heat shock protein
C:Species: Bos primigenius taurus (cattle)
C>Date: 05-Dec-1998 #sequence_revision 05-Dec-1998 #text_change 09-Jul-2004
C:Accession: S53357
R:Gutierrez, J.A.; Guerriero Jr., V.
Biochem. J. 305, 197-203, 1995
A:Title: Chemical modifications of a recombinant bovine stress-inducible 70 kDa heat-sho
A:Reference number: S53357; MUID:95126904; PMID:7826329
A:Accession: S53357
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-641 <GT>
A:CROSS-references: UNIPROT:Q27975; EMBL:U09861; NID:g497937; PIDN:AAA73914.1; PID:g49793
C:Genetics:
A:Gene: hsp70
C:Function:
A:Description: involved in protein folding and assembling/disassembling of protein comp
C:Superfamily: heat shock protein 70
C:Keywords: ATP; molecular chaperone

Query Match	98.6%;	Score 1295;	DB 2;	Length 641;
Best Local Similarity	98.8%;	Pred. No. 2.1e-76;		
Matches	255;	Conservative 1;	Mismatches 2;	Indels 0; Gaps 0;

QY 1 KSENVQDLLLDVAPLSGLTAGVMTALIKRNSTIPTKQTQIFTTYSNDQPGVLIQVY 60
DB 384 KSENVQDLLLDVAPLSGLTAGVMTALIKRNSTIPTKQTQIFTTYSNDQPGVLIQVY 443

QY 61 EGERAMTKONNLGRFELSGIPAPRGVPOIEVTFDIDANGILNVATDSTGKANKITI 120

Db 444 EGERAMTRDNNLLGRFELSGIPAPRGVPQIEVTFDIDANGILNVTATDKSTGKANKITI 503
Qy 121 TNDKGRLSKEIERMVOEAEKYKAEDVQERVRSAKNALESYAFNMKSAVEDEGLKGKIS 180
Db 504 TNDKGRLSKEIERMVOEAEKYKAEDVQERVRSAKNALESYAFNMKSAVEDEGLKGKIS 563
Qy 181 EADKKKVLDKCOEIVSWLDANTLAEKDFEHRKELEQVNCNPIISGLYQAGAGGPGGFG 240
Db 564 EADKKKVLDKCOEIVSWLDANTLAEKDFEHRKELEQVNCNPIISGLYQAGAGGPGGFG 623
Qy 241 AQPKGGSGSGPTTIEVD 258
Db 624 AQPKGGSGSGPTTIEVD 641

RESULT 4
S31766
dnaK-type molecular chaperone hsp70 - green monkey
N;Alternate names: heat shock protein 70
C;Species: Cercopithecus aethiops (green monkey, grivet)
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 09-Jul-2004
C;Accession: S31766; I36927
R;Sainis, I.; Angelidis, C.; Pagoulatos, G.; Lazaridis, I.
submitted to the EMBL Data Library, January 1993
A;Description: Nucleotide sequence of the cDNA encoding a monkey 70kd heat shock protein
A;Reference number: S31766
A;Accession: S31766
A;Molecule type: mRNA
A;Residues: 1-638 <SAI>
A;Cross-references: UNIPROT:Q28222
R;Sainis, I.; Angelidis, C.; Pagoulatos, G.; Lazaridis, I.
FEBS Lett. 355, 282-286, 1994
A;Title: The hsc70 gene which is slightly induced by heat is the main virus inducible me
A;Reference number: I36927; MUID:95080396; PMID:7988690
A;Accession: I36927
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-638 <RES>
A;Cross-references: EMBL:X70684; NID:g22781; PIDN:CAA50019.1; PID:g22782
A;Experimental source: kidney; cell line COS-1
C;Genetics:
A;Gene: hsp70
C;Function:
A;Description: involved in protein folding and assembling/disassembling of protein comp
C;Superfamily: heat shock protein 70
C;Keywords: ATP; molecular chaperone

Query Match 97.4%; Score 1279.5; DB 2; Length 638;
Best Local Similarity 98.1%; Pred. No. 2.1e-75;
Matches 253; Conservative 1; Mismatches 3; Indels 1; Gaps 1;
Qy 1 KSENVQDLLLLDVAPLSIGLETAGVMTALIKRNSTIPTKTQTQITFTYSDNQPGVLQVY 60
Db 382 KSENVQDLLLLDVAPLSIGLETAGVMTALIKRNSTIPTKTQTQITFTYSDNQPGVLQVY 441
Qy 61 EGERAMTKDNNLLGRFELSGIPAPRGVPQIEVTFDIDANGILNVTATDKSTGKANKITI 120
Db 442 EGERAMTKDNNLLGRFELSGIPAPRGVPQIEVTFDIDANGILNVTATDKSTGKANKITI 500
Qy 121 TNDKGRLSKEIERMVOEAEKYKAEDVQERVRSAKNALESYAFNMKSAVEDEGLKGKIS 180
Db 501 TNDKGRLSKEIERMVOEAEKYKAEDVQERVRSAKNALESYAFNMKSAVEDEGLKGKIS 560
Qy 181 EADKKKVLDKCOEIVSWLDANTLAEKDFEHRKELEQVNCNPIISGLYQAGAGGPGGFG 240
Db 561 EADKKKVLDKCOEIVSWLDANTLAEKDFEHRKELEQVNCNPIISGLYQAGAGGPGGFG 620
Qy 241 AQPKGGSGSGPTTIEVD 258
Db 621 AQPKGGSGSGPTTIEVD 638

RESULT 5
S35718
dnaK-type molecular chaperone hsp70 - pig
N;Alternate names: heat shock protein hsp70
C;Species: Sus scrofa domestica (domestic pig)
C;Date: 09-Dec-1993 #sequence_revision 28-May-1995 #text_change 09-Jul-2004
C;Accession: S35718
R;Peelman, L.J.; van de Weghe, A.R.; Coppieters, W.R.; Van Zeveren, A.J.; Bouquet, Y.H.
Immunogenetics 35, 286-289, 1992
A;Title: Complete nucleotide sequence of a porcine HSP70 gene.
A;Reference number: S35718; MUID:92175874; PMID:1339404
A;Accession: S35718
A;Status: translation not shown
A;Molecule type: DNA
A;Residues: 1-641 <PBE>
A;Cross-references: UNIPROT:P34930; EMBL:M69100
C;Genetics:
A;Gene: hsp70
C;Function:
A;Description: involved in protein folding and assembling/disassembling of protein compl
C;Superfamily: heat shock protein 70
C;Keywords: ATP; molecular chaperone

Query Match 97.3%; Score 1279; DB 2; Length 641;
Best Local Similarity 97.3%; Pred. No. 2.3e-75;
Matches 251; Conservative 2; Mismatches 5; Indels 0; Gaps 0;
Qy 1 KSENVQDLLLLDVAPLSIGLETAGVMTALIKRNSTIPTKTQTQITFTYSDNQPGVLQVY 60
Db 384 KSENVQDLLLLDVAPLSIGLETAGVMTALIKRNSTIPTKTQTQITFTYSDNQPGVLQVY 443
Qy 61 EGERAMTKDNNLLGRFELSGIPAPRGVPQIEVTFDIDANGILNVTATDKSTGKANKITI 120
Db 444 EGERAMTKDNNLLGRFELSGIPAPRGVPQIEVTFDIDANGILNVTATDKSTGKANKITI 503
Qy 121 TNDKGRLSKEIERMVOEAEKYKAEDVQERVRSAKNALESYAFNMKSAVEDEGLKGKIS 180
Db 504 TNDKGRLSKEIERMVOEAEKYKAEDVQERVRSAKNALESYAFNMKSAVEDEGLKGKIS 563
Qy 181 EADKKKVLDKCOEIVSWLDANTLAEKDFEHRKELEQVNCNPIISGLYQAGAGGPGGFG 240
Db 564 EADKKKVLDKCOEIVSWLDANTLAEKDFEHRKELEQVNCNPIISGLYQAGAGGPGGFG 623
Qy 241 AQPKGGSGSGPTTIEVD 258
Db 624 APDLKGGSGSGPTTIEVD 641

RESULT 6
I54542
dnaK-type molecular chaperone HSP70 - rat
N;Alternate names: dnaK-type molecular chaperone HSP70ib; heat shock protein 70
C;Species: Rattus norvegicus (Norway rat)
C;Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 09-Jul-2004
C;Accession: I54542; I68986; S43388; S47522; I56574; S35955; S38199; S41413; S41414
R;Walter, L.; Rauh, F.; Gunther, E.
Immunogenetics 40, 325-330, 1994
A;Title: Comparative analysis of the three major histocompatibility complex-linked heat
A;Reference number: I54542; MUID:95012453; PMID:7927536
A;Accession: I54542
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-641 <WAL1>
A;Cross-references: UNIPROT:Q07439; UNIPROT:Q63256; EMBL:X77207; NID:g1814000; PIDN:CAA5
A;Experimental source: HSP70.1
A;Genetics: HSP1
A;Accession: I68986
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-641 <WAL2>
A;Cross-references: EMBL:X77208; NID:g927512; PIDN:CAA54423.1; PID:g450932
A;Experimental source: HSP70.2
A;Genetics: HSP2

R;Meistril, R.; Chi, S.H.; Sayen, M.R.; Dillmann, W.H.
Biochem. J. 298, 561-569, 1994
A>Title: Isolation of a novel inducible rat heat-shock protein (HSP70) gene and its expression
A;Reference number: S43388; MUID:94190258; PMID:8141767
A;Accession: S43388
A;Molecule type: DNA
A;Residues: 1-70, 'NG', 73-109, 'K', 111-203, 'R', 205-261, 'P', 263, 'ADGV', 268-641 <MES>
A;Cross-references: EMBL:X75357; NID:9407163; PIDN:CAA53140.1; PID:9407164
A;Experimental source: ischaemic rat heart
R;Lisowska, K.; Widlak, W.; Krawczyk, Z.; Wolniczek, P.; Wisniewski, J.
Biochim. Biophys. Acta 1219, 64-72, 1994
A>Title: Cloning, nucleotide sequence and expression of rat heat inducible hsp70 gene.
A;Reference number: S47522; MUID:94368874; PMID:8086479
A;Accession: S47522
A;Molecule type: DNA
A;Residues: 1-70, 'NG', 73-407, 'A', 409-641 <LIS>
A;Cross-references: EMBL:X74271; NID:93413499; PIDN:CAA52328.1; PID:9396270
A;Note: the authors translated the codon CCG for residue 365 as Asp
R;Longo, F.M.; Wang, S.; Narasimhan, P.; Zhang, J.S.; Chen, J.; Massa, S.M.; Sharp, F.R.
J. Neurosci. Res. 36, 325-335, 1993
A>Title: cDNA cloning and expression of stress-inducible rat hsp70 in normal and injured
A;Reference number: I56574; MUID:94096443; PMID:8271311
A;Accession: I56574
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-226, 'D', 228-641 <LON>
A;Cross-references: GB:L16764; NID:9294567; PIDN:AAA17441.1; PID:9294568
A;Genetics: <HSP1>
A;Gene: hsp70.1
C;Genetics: <HSP2>
A;Gene: hsp70.2
C;Function:
A;Description: involved in protein folding and assembling/disassembling of protein comp
A;Superfamily: heat shock protein 70
C;Keywords: ATP; heat shock; molecular chaperone; stress-induced protein

Query Match 95.7%; Score 1258; DB 2; Length 641;
Best Local Similarity 95.3%; Pred. No. 5.2e-74;
Matches 246; Conservative 7; Mismatches 5; Indels 0; Gaps 0;
Qy 1 KSENVQDLLLLDVAPLSGLGTAGVMTALIKRNTSTPTKTQTQTFYTSNQPGLVQY 60
Db 384 KSENVQDLLLLDVAPLSGLGTAGVMTALIKRNTSTPTKTQTQTFYTSNQPGLVQY 443
Qy 61 EGERAMTKNNLLGRFELSGIPPPAPRGVQPIEVTFDANGILNVTATDKSTGKANKITI 120
Db 444 EGERAMTRDNNLLGRFELSGIPPPAPRGVQPIEVTFDANGILNVTATDKSTGKANKITI 503
Qy 121 TNDKGRLSKEIERMWQEAERYKAEDVQRRVSAKNALSYAFNMKSAVEDEGLGKGIS 180
Db 504 TNDKGRLSKEIERMWQEAERYKAEDVQRRVSAKNALSYAFNMKSAVEDEGLGKGIS 563
Qy 181 EADKKKVLDCQEVISWLDANTLAEDFEHKKELQVNCNPIISGLYQAGGPGGFG 240
Db 564 EADKKKVLDCQEVISWLDNTLAEDFEHKKELQVNCNPIISGLYQAGGPGGFG 623
Qy 241 AQPKGGSGSGPTIEVD 258
Db 624 AQAPKGGSGSGPTIEVD 641
RESULT 7
JH0095
dnak-type molecular chaperone hsp70 - mouse
N;Alternate names: heat shock protein 70
C;Species: Mus musculus (house mouse)
C;Date: 31-Dec-1990 #sequence_revision 31-Dec-1990 #text_change 20-Aug-1999
A;Accession: JH0095
R;Hunt, C.; Calderwood, S.
Gene 87, 199-204, 1990
A>Title: Characterization and sequence of a mouse hsp70 gene and its expression in mouse
A;Reference number: JH0095; MUID:90236310; PMID:2332169
A;Accession: JH0095

A;Molecule type: DNA
A;Residues: 1-642 <HUN>
A;Cross-references: GB:M35021; NID:9194022; PIDN:AAA37864.1; PID:9387211
A;Experimental source: strain A7
C;Function:
A;Description: involved in protein folding and assembling/disassembling of protein comp
A;Superfamily: heat shock protein 70
C;Keywords: ATP; molecular chaperone

Query Match 93.5%; Score 1228.5; DB 2; Length 642;
Best Local Similarity 93.1%; Pred. No. 4.2e-72;
Matches 241; Conservative 11; Mismatches 6; Indels 1; Gaps 1;
Qy 1 KSENVQDLLLLDVAPLSGLGTAGVMTALIKRNTSTPTKTQTQTFYTSNQPGLVQY 60
Db 384 KSENVQDLLLLDVAPLSGLGTAGVMTALIKRNTSTPTKTQTQTFYTSNQPGLVQY 443
Qy 61 EGERAMTKNNLLGRFELSGIPPPAPRGVQPIEVTFDANGILNVTATDKSTGKANKITI 120
Db 444 EGERAMTRDNNLLGRFELSGIPPPAPRGVQPIEVTFDANGILNVTATDKSTGKANKITI 503
Qy 121 TNDKGRLSKEIERMWQEAERYKAEDVQRRVSAKNALSYAFNMKSAVEDEGLGKGIS 180
Db 504 TNDKGRLSKEIERMWQEAERYKAEDVQRRVSAKNALSYAFNMKSAVEDEGLGKGIS 563
Qy 181 EADKKKVLDCQEVISWLDANTLAEDFEHKKELQVNCNPIISGLYQAGGPGGFG 240
Db 564 EADKKKVLDCQEVISWLDNTLAEDFEHKKELQVNCNPIISGLYQAGGPGGFG 623
Qy 241 AQPKGGSGSGPTIEVD 258
Db 624 AQAPKGGSGSGPTIEVD 642
RESULT 8
A26283
dnak-type molecular chaperone - mouse (fragment)
N;Alternate names: heat shock protein 68
C;Species: Mus musculus (house mouse)
C;Date: 19-Nov-1988 #sequence_revision 19-Nov-1988 #text_change 09-Jul-2004
A;Accession: A26283
R;Lowe, D.G.; Moran, L.A.
J. Biol. Chem. 261, 2102-2112, 1986
A>Title: Molecular cloning and analysis of DNA complementary to three mouse Mr=68,000 he
A;Reference number: A26283; MUID:86111900; PMID:2868009
A;Accession: A26283
A;Molecule type: mRNA
A;Residues: 1-420 <LOW>
A;Cross-references: UNIPROT:Q61696; GB:M12571; NID:9194014; PIDN:AAA57234.1; PID:9387208
A;Note: the authors translated the codon CTG for residue 173 as Val and CGC for residue
C;Function:
A;Description: involved in protein folding and assembling/disassembling of protein comp
A;Superfamily: heat shock protein 70
C;Keywords: ATP; molecular chaperone

Query Match 92.5%; Score 1216; DB 2; Length 420;
Best Local Similarity 91.9%; Pred. No. 1.6e-71;
Matches 237; Conservative 12; Mismatches 9; Indels 0; Gaps 0;
Qy 1 KSENVQDLLLLDVAPLSGLGTAGVMTALIKRNTSTPTKTQTQTFYTSNQPGLVQY 60
Db 163 KSENVQDLLLLDVAPLSGLGTAGVMTALIKRNTSTPTKTQTQTFYTSNQPGLVQY 222
Qy 61 EGERAMTKNNLLGRFELSGIPPPAPRGVQPIEVTFDANGILNVTATDKSTGKANKITI 120
Db 223 EGERAMTRDNNLLGRFELSGIPPPAPRGVQPIEVTFDANGILNVTATDKSTGKANKITI 282
Qy 121 TNDKGRLSKEIERMWQEAERYKAEDVQRRVSAKNALSYAFNMKSAVEDEGLGKGIS 180
Db 283 TNDKGRLSKEIERMWQEAERYKAEDVQRRVSAKNALSYAFNMKSAVEDEGLGKGIS 342
Qy 181 EADKKKVLDCQEVISWLDANTLAEDFEHKKELQVNCNPIISGLYQAGGPGGFG 240
Db 624 AQAPKGGSGSGPTIEVD 642


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Db 444 EGERAMTKDNLLGKFEUTGTPAPRGVPPQIEVTFDIDANGILNVSAVDKSTGKKNKITI 503
Qy 121 TNDKGRLSKEEIERMVQEAERYKAEDEVQRRVSAKNALESYAFNMKSAVEDEGLKKGKIS 180
Db 504 TNDKGRLSKEDIERMVQEAERYKAEDEKQDKVSSKNSLESYAFNMKATVEDEKLQKIN 563
Qy 181 BADKKVLDKQCVISWLDANTLAERKDEFEHKELEKQVNCNPIISGLYQAGG-PG--PG 237
Db 564 DEDKQKILDKNETIINWLDKNQTAKEBEFEHQKELEKVCNPIITKLYQSAGGMPGMPG 623
Qy 238 GF--GAQGPKGSGSGPTIEVD 258
Db 624 GPGGGAPPSCGASSGPTIEVD 646

RESULT 15
A45935
dnak-type molecular chaperone hsc70 - mouse
N;Alternate names: heat shock cognate protein hsc70
C;Species: Mus musculus (house mouse)
C;Date: 30-Sep-1993 #sequence_revision 26-May-1994 #text_change 09-Jul-2004
C;Accession: A45935; S12830; S12831; S12832
R;Giebel, L.B.; Dworniczak, B.P.; Bautz, E.K.F.
Dev. Biol. 125, 200-207, 1988
A;Title: Developmental regulation of a constitutively expressed mouse mRNA encoding a 72
A;Reference number: A45935; MUID:88055872; PMID:3334718
A;Accession: A45935
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-646 <GB>
A;Cross-references: UNIPROT:P08109; GB:M19141; NID:g194034; PIDN:AAA37869.1; PID:g309319
A;Note: the authors translated the codon GAT for residue 97 as Asn
R;Imamoto, N.; Matsuoka, Y.; Kurihara, T.; Kohno, K.; Miyagi, M.; Sakiyama, F.; Okada, Y.
J. Cell Biol. 119, 1047-1061, 1992
A;Title: Antibodies against 70-kD heat shock cognate protein inhibit mediated nuclear in
A;Reference number: A44262; MUID:93077667; PMID:1332978
A;Accession: A44262
A;Molecule type: protein
A;Residues: 89-102;160-167;272-282;575-583;610-638 <IMA>
R;Maxwell, E.S.
submitted to the EMBL Data Library, August 1990
A;Reference number: S50895
A;Accession: S50895
A;Molecule type: DNA
A;Residues: 438-452 <MAX>
A;Cross-references: EMBL:X54402; NID:G55073; PIDN:CAA38268.1; PID:g55074
R;Liu, J.; Maxwell, E.S.
Nucleic Acids Res. 18, 6565-6571, 1990
A;Title: Mouse U14 snRNA is encoded in an intron of the mouse cognate hsc70 heat shock g
A;Reference number: S12830; MUID:91067440; PMID:2251119
A;Accession: S12830
A;Molecule type: DNA
A;Residues: 333-383;438-452;580-587 <LIU>
A;Cross-references: EMBL:X54401
C;Genetics:
A;Gene: hsc70
C;Function:
A;Description: involved in protein folding and assembling/diseassembling of protein comp
A;Superfamily: heat shock protein 70
C;Keywords: ATP; molecular chaperone

Query Match 83.3%; Score 1094.5; DB 2; Length 646;
Best Local Similarity 81.4%; Pred. No. 2e-63;
Matches 214; Conservative 23; Mismatches 21; Indels 5; Gaps 3;

Qy 1 KSENVQDLLLDVAPLSLGLETAGVMTALIKRNSTIPTKTQTFTTYSNQPGLVQVY 60
Db 384 KSENVQDLLLDVTPLSLGIETAGVMTVLIKRNTIPTKTQTTLTYSNQPGLVQVY 443
Qy 61 EGERAMTKDNLLGRFELSGIPAPRGVPPQIEVTFDIDANGILNVATDSTGKANKITI 120
Db 444 EGERAMTKDNLLGKFEUTGTPAPRGVPPQIEVTFDIDANGILNVSAVDKSTGKKNKITI 503

RESULT 16
A49761
dnak-type molecular chaperone hsc70t - mouse
N;Alternate names: heat shock protein 70
C;Species: Mus musculus (house mouse)
C;Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 09-Jul-2004
C;Accession: I49761
R;Shoek, M.; Olavessen, M.G.; van Vugt, H.; Milner, C.M.; Teuscher, C.; Campbell, R.D.
Immunogenetics 40, 159-162, 1994
A;Title: Coding sequences and levels of expression of Hsc70t are identical in mice with
A;Reference number: I49761; MUID:94299288; PMID:8026864
A;Accession: I49761
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-641 <RES>
A;Cross-references: UNIPROT:P16627; GB:L27086; NID:g457299; PIDN:AAA59362.1; PID:g457300
C;Genetics:
A;Gene: Hsc70t
C;Function:
A;Description: involved in protein folding and assembling/diseassembling of protein comp
C;Superfamily: heat shock protein 70
C;Keywords: ATP; molecular chaperone

Query Match 83.1%; Score 1092; DB 2; Length 641;
Best Local Similarity 84.5%; Pred. No. 2.9e-63;
Matches 218; Conservative 17; Mismatches 21; Indels 2; Gaps 2;

Qy 1 KSENVQDLLLDVAPLSLGLETAGVMTALIKRNSTIPTKTQTFTTYSNQPGLVQVY 60
Db 386 KSENVQDLLLDVAPLSLGLETAGVMTVLIKRNSTIPTKTQTFTTYSNQPGLVQVY 445
Qy 61 EGERAMTKDNLLGRFELSGIPAPRGVPPQIEVTFDIDANGILNVATDSTGKANKITI 120
Db 446 EGERAMTKDNLLGRFOLTGIPAPRGVPPQIEVTFDIDANGILNVATDSTGKANKITI 505
Qy 121 TNDKGRLSKEEIERMVQEAERYKAEDEVQRRVSAKNALESYAFNMKSAVEDEGLKKGKIS 180
Db 506 TNDKGRLSKEEIERMVQEAERYKAEDEGQREKIAAKNALESYAFNMKSAVGEGLKDKIS 565
Qy 181 BADKKVLDKQCVISWLDANTLAERKDEFEHKELEKQVNCNPIISGLYQAGGPGPGFG 240
Db 566 ESDKKKILDKNETIINWLDKNQTAKEBEFEHQKELEKVCNPIITKLYQ-SGCTGPTCTP 624
Qy 241 AQGPKGSGSGSGPTIEVD 258
Db 625 GYTP-GRATGPTIEVD 641

RESULT 17
S11456
dnak-type molecular chaperone hsc70 - bovine
N;Alternate names: heat shock cognate protein, 79K
C;Species: Bos primigenius taurus (cattle)
C;Date: 21-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 09-Jul-2004
C;Accession: S11456
R;DeLuca-Flaherty, C.; McKay, D.B.
Nucleic Acids Res. 18, 5569, 1990
A;Title: Nucleotide sequence of the cDNA of a bovine 70 kilodalton heat shock cognate pr
A;Reference number: S11456; MUID:91016866; PMID:2216746
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Db 444 EGERAMTKDNLLGKFEUTGTPAPRGVPPQIEVTFDIDANGILNVSAVDKSTGKKNKITI 503
Qy 121 TNDKGRLSKEEIERMVQEAERYKAEDEVQRRVSAKNALESYAFNMKSAVEDEGLKKGKIS 180
Db 504 TNDKGRLSKEDIERMVQEAERYKAEDEKQDKVSSKNSLESYAFNMKATVEDEKLQKIN 563
Qy 181 BADKKVLDKQCVISWLDANTLAERKDEFEHKELEKQVNCNPIISGLYQAGG-PG--PG 237
Db 564 DEDKQKILDKNETIINWLDKNQTAKEBEFEHQKELEKVCNPIITKLYQSAGGMPGMPG 623
Qy 238 GF--GAQGPKGSGSGPTIEVD 258
Db 624 GPGGGAPPSCGASSGPTIEVD 646

RESULT 15
A45935
dnak-type molecular chaperone hsc70 - mouse
N;Alternate names: heat shock cognate protein hsc70
C;Species: Mus musculus (house mouse)
C;Date: 30-Sep-1993 #sequence_revision 26-May-1994 #text_change 09-Jul-2004
C;Accession: A45935; S12830; S12831; S12832
R;Giebel, L.B.; Dworniczak, B.P.; Bautz, E.K.F.
Dev. Biol. 125, 200-207, 1988
A;Title: Developmental regulation of a constitutively expressed mouse mRNA encoding a 72
A;Reference number: A45935; MUID:88055872; PMID:3334718
A;Accession: A45935
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-646 <GB>
A;Cross-references: UNIPROT:P08109; GB:M19141; NID:g194034; PIDN:AAA37869.1; PID:g309319
A;Note: the authors translated the codon GAT for residue 97 as Asn
R;Imamoto, N.; Matsuoka, Y.; Kurihara, T.; Kohno, K.; Miyagi, M.; Sakiyama, F.; Okada, Y.
J. Cell Biol. 119, 1047-1061, 1992
A;Title: Antibodies against 70-kD heat shock cognate protein inhibit mediated nuclear in
A;Reference number: A44262; MUID:93077667; PMID:1332978
A;Accession: A44262
A;Molecule type: protein
A;Residues: 89-102;160-167;272-282;575-583;610-638 <IMA>
R;Maxwell, E.S.
submitted to the EMBL Data Library, August 1990
A;Reference number: S50895
A;Accession: S50895
A;Molecule type: DNA
A;Residues: 438-452 <MAX>
A;Cross-references: EMBL:X54402; NID:G55073; PIDN:CAA38268.1; PID:g55074
R;Liu, J.; Maxwell, E.S.
Nucleic Acids Res. 18, 6565-6571, 1990
A;Title: Mouse U14 snRNA is encoded in an intron of the mouse cognate hsc70 heat shock g
A;Reference number: S12830; MUID:91067440; PMID:2251119
A;Accession: S12830
A;Molecule type: DNA
A;Residues: 333-383;438-452;580-587 <LIU>
A;Cross-references: EMBL:X54401
C;Genetics:
A;Gene: hsc70
C;Function:
A;Description: involved in protein folding and assembling/diseassembling of protein comp
A;Superfamily: heat shock protein 70
C;Keywords: ATP; molecular chaperone

Query Match 83.3%; Score 1094.5; DB 2; Length 646;
Best Local Similarity 81.4%; Pred. No. 2e-63;
Matches 214; Conservative 23; Mismatches 21; Indels 5; Gaps 3;

Qy 1 KSENVQDLLLDVAPLSLGLETAGVMTALIKRNSTIPTKTQTFTTYSNQPGLVQVY 60
Db 384 KSENVQDLLLDVTPLSLGIETAGVMTVLIKRNTIPTKTQTTLTYSNQPGLVQVY 443
Qy 61 EGERAMTKDNLLGRFELSGIPAPRGVPPQIEVTFDIDANGILNVATDSTGKANKITI 120
Db 444 EGERAMTKDNLLGKFEUTGTPAPRGVPPQIEVTFDIDANGILNVSAVDKSTGKKNKITI 503
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A:Accession: S11456
A:Status: preliminary; translation not shown
A:Molecule type: mRNA
A:Residues: 1-650
A:Cross-references: UNIPROT:P19120; EMBL:X53827; NID:g427; PIDN:CAA37823.1; PID:g428
C:Genetics:
A:Gene: hsc70
C:Function:
A:Description: involved in protein folding and assembling/disassembling of protein complex
A:Superfamily: heat shock protein 70
C:Keywords: ATP; molecular chaperone

Query Match 83.1%; Score 1091.5; DB 2; Length 650;
Best Local Similarity 79.8%; Pred. No. 3.2e-63;
Matches 213; Conservative 25; Mismatches 20; Indels 9; Gaps 3;

Qy 1 KSENVQDLLLLDVAPLSGLGLETAGGVMTVLIKRNTIPTKTQTFTTYSNQPGVLIQVY 60
Db 384 KSENVQDLLLLDVTPLSGLIETAGGVMTVLIKRNTIPTKTQTFTTYSNQPGVLIQVY 443

Qy 61 EGERAMTKDNNLLGRFELSGIPAPRGVPQIEVTFDIDANGILNVATDKSTGKANKITI 120
Db 444 EGERAMTKDNNLLGKFLTGIPAPRGVPQIEVTFDIDANGILNVSAVDKSTGKANKITI 503

Qy 121 TNDKGRLSKEIEIEMVQEAERKAEDEQVQERVSAAKNALESYAFNMKSAVEDEGLKQKIS 180
Db 504 TNDKGRLSKEDIEMVQEAERKAEDEQVQERVSAAKNALESYAFNMKATVEDEKLQKIN 563

Qy 181 EADKKVLDKCOEIVSWLDANTLAEDFEHKKLEQVNCNPIISGLYQ-QAGGP-----PG 235
Db 564 DEDKQKILDKCNKINWLDKNTAEKEFEHQKELEKVCNPIITKLYQSAGGMPGMPG 623

Qy 236 --PGGP--GAQPGKGGSGPTIEVD 258
Db 624 GMPGGFPGGAPPSSGASGPTIEVD 650

RESULT 18
S41415
dnak-type molecular chaperone Hsp70.3 - rat
N:Alternate names: heat shock protein 70
C:Species: Rattus norvegicus (Norway rat)
C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 09-Jul-2004
C:Accession: S41415; I68987
R:Lutz, W.
submitted to the EMBL Data Library, January 1994
A:Reference number: S41413
A:Accession: S41415
A:Molecule type: DNA
A:Residues: 1-641 <LUT>
A:Cross-references: UNIPROT:P55063; EMBL:X77209; NID:g1814002; PIDN:CAA54424.1; PID:g450
R:Walter, L.; Rauh, F.; Gunther, E.
Immunogenetics 40, 325-330, 1994
A:Title: Comparative analysis of the three major histocompatibility complex-linked heat
A:Reference number: 154542; MUID:95012453; PMID:7927536
A:Accession: I68987
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-641 <RES>
A:Cross-references: EMBL:X77209; NID:g1814002; PIDN:CAA54424.1; PID:g450934
C:Genetics:
A:Gene: Hsp70-3
C:Function:
A:Description: involved in protein folding and assembling/disassembling of protein complex
A:Superfamily: heat shock protein 70
C:Keywords: ATP; molecular chaperone

Query Match 82.7%; Score 1087; DB 2; Length 641;
Best Local Similarity 83.5%; Pred. No. 6.1e-63;
Matches 218; Conservative 17; Mismatches 19; Indels 8; Gaps 3;

Qy 1 KSENVQDLLLLDVAPLSGLGLETAGGVMTVLIKRNTIPTKTQTFTTYSNQPGVLIQVY 60
Db 384 KSENVQDLLLLDVTPLSGLIETAGGVMTVLIKRNTIPTKTQTFTTYSNQPGVLIQVY 443

Qy 61 EGERAMTKDNNLLGRFELSGIPAPRGVPQIEVTFDIDANGILNVATDKSTGKANKITI 120
Db 444 EGERAMTKDNNLLGKFLTGIPAPRGVPQIEVTFDIDANGILNVSAVDKSTGKANKITI 503

Qy 121 TNDKGRLSKEIEIEMVQEAERKAEDEQVQERVSAAKNALESYAFNMKSAVEDEGLKQKIS 180
Db 504 TNDKGRLSKEDIEMVQEAERKAEDEQVQERVSAAKNALESYAFNMKATVEDEKLQKIN 563

Qy 181 EADKKVLDKCOEIVSWLDANTLAEDFEHKKLEQVNCNPIISGLYQ-QAGGP-----PG 235
Db 564 DEDKQKILDKCNKINWLDKNTAEKEFEHQKELEKVCNPIITKLYQSAGGMPGMPG 623

Qy 236 --PGGP--GAQPGKGGSGPTIEVD 258
Db 624 GMPGGFPGGAPPSSGASGPTIEVD 650

Db 386 KSEKVDLLLLDVAPLSGLGLETAGGVMTVLIKRNTIPTKTQTFTTYSNQPGVLIQVY 445
Qy 61 EGERAMTKDNNLLGRFELSGIPAPRGVPQIEVTFDIDANGILNVATDKSTGKANKITI 120
Db 446 EGERAMTRDNNLLGRFDLTGIPAPRGVPQIEVTFDIDANGILNVATDKSTGKANKITI 505
Qy 121 TNDKGRLSKEIEIEMVQEAERKAEDEQVQERVSAAKNALESYAFNMKSAVEDEGLKQKIS 180
Db 506 TNDKGRLSKEIEIEMVQEAERKAEDEQVQERVSAAKNALESYAFNMKSAVGDGLKQKIS 565
Qy 181 EADKKVLDKCOEIVSWLDANTLAEDFEHKKLEQVNCNPIISGLYQ-QAGGP--GPG 237
Db 566 ESDKKILDKCSEVLWLANLAKEEFDHKKELENMCNPIITKLYQSCTGPTCAPG 625

Qy 238 GFGAQPCKGSGSGPTIEVD 258
Db 626 -----YTPGRARTGPTIEVD 641

RESULT 19
S21175
dnak-type molecular chaperone hsc71 - rainbow trout
N:Alternate names: heat shock cognate protein 71
C:Species: Oncorhynchus mykiss (rainbow trout)
C:Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 09-Jul-2004
C:Accession: S21175
R:Zafarullah, M.; Wisniewski, J.; Shworak, N.W.; Schieman, S.; Misra, S.; Gedamu, L.
Eur. J. Biochem. 204, 893-900, 1992
A:Title: Molecular cloning and characterization of a constitutively expressed heat-shock
A:Reference number: S21175; MUID:92174952; PMID:1371753
A:Accession: S21175
A:Molecule type: DNA
A:Residues: 1-651 <ZAF>
A:Cross-references: UNIPROT:P08108; EMBL:S85730; NID:g246718; PIDN:AAB21658.1; PID:g24671
C:Genetics:
A:Gene: hsc71
A:Introns: 69/1; 137/3; 188/3; 374/1; 441/3; 508/1; 585/3
C:Function:
A:Description: involved in protein folding and assembling/disassembling of protein complex
A:Superfamily: heat shock protein 70
C:Keywords: ATP; molecular chaperone

Query Match 82.5%; Score 1084; DB 2; Length 651;
Best Local Similarity 79.5%; Pred. No. 9.7e-63;
Matches 213; Conservative 21; Mismatches 24; Indels 10; Gaps 3;

Qy 1 KSENVQDLLLLDVAPLSGLGLETAGGVMTVLIKRNTIPTKTQTFTTYSNQPGVLIQVY 60
Db 384 KSENVQDLLLLDVTPLSGLIETAGGVMTVLIKRNTIPTKTQTFTTYSNQPGVLIQVY 443

Qy 61 EGERAMTKDNNLLGRFELSGIPAPRGVPQIEVTFDIDANGILNVATDKSTGKANKITI 120
Db 444 EGERAMTKDNNLLGKFLTGIPAPRGVPQIEVTFDIDANGILNVSAADKSTGKANKITI 503

Qy 121 TNDKGRLSKEIEIEMVQEAERKAEDEQVQERVSAAKNALESYAFNMKSAVEDEGLKQKIS 180
Db 504 TNDKGRLSKEDIEMVQEAERKAEDEQVQERVSAAKNALESYAFNMKSTVEDEKLQKIS 563

Qy 181 EADKKVLDKCOEIVSWLDANTLAEDFEHKKLEQVNCNPIISGLYQ-QAGG--PG---- 235
Db 564 DEDTKILEKCNKINWLDKNTAEKEFEHKKLEKVCNPIITKLYQAGGMPGMPG 623

Qy 236 --PGGP--GAQPGKGGSGPTIEVD 258
Db 624 GMAGGFPAGGAAPGGGSGPTIEVD 651

RESULT 20
A45805
dnak-type molecular chaperone - nematode (Brugia pahangi) (fragment)
N:Alternate names: heat shock cognate protein 70
C:Species: Brugia pahangi
C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 09-Jul-2004

C;Accession: A45805
J;Selkirk, M.E.; Denham, D.A.; Partono, F.; Maizels, R.M.
J. Immunol. 143, 299-308, 1989
A;Title: Heat shock cognate 70 is a prominent immunogen in brugian filariasis.
A;Reference number: A45805; MUID:89278663; PMID:2659668
A;Accession: A45805
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-335 <SEL>
A;Cross-references: UNIPROT:Q17267; GB:M26191
A;Note: the authors translated the codon CTG for residue 1 as Arg
C;Function:
A;Description: involved in protein folding and assembling/diseassembling of protein comp
C;Superfamily: heat shock protein 70
C;Keywords: ATP; molecular chaperone

Query Match 80.9%; Score 1063; DB 2; Length 335;
Best Local Similarity 79.8%; Pred. No. 9.9e-62; Mismatches 29; Indels 4; Gaps 3;
Matches 209; Conservative 20; Mismatches 29; Indels 4; Gaps 3;

Qy 1 KSENVQDLLLDVAPLSGLTAGVMTALIKRNSTIPTKTQTQFTTYSNQPGLVQVY 60
Db 74 KSEAVQDLLLDVAPLSGLTAGVMTALIKRNTIPTKTSTQFTTYSNQPGLVQVY 133

Qy 61 EGERAMTKNNLLGRFELSGIPPPAPRGVPOIEVTFDIDANGILNVATDSTGKANKITI 120
Db 134 EGERALTKNNLLGKFLSGIPPPAPRGVPEIEVTFDIDANGILNVSAQDKSTGKQNKITI 193

Qy 121 TNDKGRSLKKEIERMVQEAERYKAEDVQREVRSKNALESYAFNMKSAVEDEGLKGKIS 180
Db 194 TNDKGRSLKKEIERMVQEAERYKADDEAQRDIAAKNALESYAFNMKQTIIEDEKLKDKIS 253

Qy 181 EADKKVKLDKQEVISWLDANTLAEDKDFEHRKKELEQVNCNPIISGLYQAGG-PG--PG 237
Db 254 EEDKKIKQEKDEIVRWLDGNQTAEDKDFEHRQKELESVCNPIITKLYQSAGGMPGMPG 313

Qy 238 GFAGQAGPKGGS-GSGPTIEVD 258
Db 314 GMPGAPGAGSTGGPTIEVD 335

RESULT 21
A45635
dnak-type molecular chaperone BmhsA - nematode (Brugia malayi)
N;Alternate names: heat shock protein homolog BmhsA
C;Species: Brugia malayi
C;Date: 22-Apr-1993 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
C;Accession: A45635
R;Rothstein, N.; Rajan, T.V.
Mol. Biochem. Parasitol. 49, 229-237, 1991
A;Title: Characterization of an hsp70 gene from the human filarial parasite, Brugia mala
A;Reference number: A45635; MUID:92131059; PMID:1775166
A;Accession: A45635
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-644 <ROT>
A;Cross-references: UNIPROT:P27541; GB:M68933; NID:g156069; PIDN:AAC17926.1; PID:g156070
A;Note: sequence extracted from NCBI backbone (NCBIN:77613, NCBI:P:77616)
C;Genetics:
A;Gene: BmhsA
C;Function:
A;Description: involved in protein folding and assembling/diseassembling of protein comp
C;Superfamily: heat shock protein 70
C;Keywords: ATP; molecular chaperone

Query Match 80.9%; Score 1063; DB 2; Length 644;
Best Local Similarity 79.8%; Pred. No. 2.2e-61; Mismatches 29; Indels 4; Gaps 3;
Matches 209; Conservative 20; Mismatches 29; Indels 4; Gaps 3;

Qy 1 KSENVQDLLLDVAPLSGLTAGVMTALIKRNSTIPTKTQTQFTTYSNQPGLVQVY 60
Db 383 KSEAVQDLLLDVAPLSGLTAGVMTALIKRNTIPTKTSTQFTTYSNQPGLVQVY 442

Qy 61 EGERAMTKNNLLGRFELSGIPPPAPRGVPOIEVTFDIDANGILNVATDSTGKANKITI 120
Db 443 EGERALTKNNLLGKFLSGIPPPAPRGVPOIEVTFDIDANGILNVSAQDKSTGKQNKITI 502

Qy 121 TNDKGRSLKKEIERMVQEAERYKAEDVQREVRSKNALESYAFNMKSAVEDEGLKGKIS 180
Db 503 TNDKGRSLKKEIERMVQEAERYKADDEAQRDIAAKNALESYAFNMKQTIIEDEKLKDKIS 562

Qy 181 EADKKVKLDKQEVISWLDANTLAEDKDFEHRKKELEQVNCNPIISGLYQAGG-PG--PG 237
Db 563 EEDKKIKQEKDEIVRWLDGNQTAEDKDFEHRQKELESVCNPIITKLYQSAGGMPGMPG 622

Qy 238 GFAGQAGPKGGS-GSGPTIEVD 258
Db 623 GMPGAPGAGSTGGPTIEVD 644

RESULT 22
A55719
dnak-type molecular chaperone HSPA2 - human
N;Alternate names: heat shock protein A2
C;Species: Homo sapiens (man)
C;Date: 23-Mar-1995 #sequence_revision 23-Mar-1995 #text_change 09-Jul-2004
C;Accession: A55719
R;Bonnycastle, L.L.C.; Yu, C.B.; Hunt, C.R.; Trask, B.J.; Clancy, K.P.; Weber, J.L.; Pat
Genomics 23, 85-93, 1994
A;Title: Cloning, sequencing, and mapping of the human chromosome 14 heat shock protein
A;Reference number: A55719; MUID:95130116; PMID:7829106
A;Accession: A55719
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-639 <BON>
A;Cross-references: UNIPROT:P54652; GB:L26336; NID:g476704; PIDN:AAA52698.1; PID:g476705
C;Genetics:
A;Gene: GDB:HSPA2
A;Cross-references: GDB:120059; OMIM:140560
A;Map position: 14q22-14q22
A;Introns: #status absent
C;Function:
A;Description: involved in protein folding and assembling/diseassembling of protein comp
C;Superfamily: heat shock protein 70
C;Keywords: ATP; molecular chaperone

Query Match 80.6%; Score 1059.5; DB 2; Length 639;
Best Local Similarity 79.1%; Pred. No. 3.7e-61; Mismatches 25; Indels 5; Gaps 1;
Matches 204; Conservative 24; Mismatches 25; Indels 5; Gaps 1;

Qy 1 KSENVQDLLLDVAPLSGLTAGVMTALIKRNSTIPTKTQTQFTTYSNQPGLVQVY 60
Db 387 KSENVQDLLLDVTPLSGLTAGVMTPLIKRNTIPTKTQTQFTTYSNQSGLVQVY 446

Qy 61 EGERAMTKNNLLGRFELSGIPPPAPRGVPOIEVTFDIDANGILNVATDSTGKANKITI 120
Db 447 EGERAMTKNNLLGKFLDTGTGIPPPAPRGVPOIEVTFDIDANGILNVTAADSTGKANKITI 506

Qy 121 TNDKGRSLKKEIERMVQEAERYKAEDVQREVRSKNALESYAFNMKSAVEDEGLKGKIS 180
Db 507 TNDKGRSLKDDIDRMVQEAERYKSEDEANRDRVAAKNALESYTYNIQTVEDEKLKGKIS 566

Qy 181 EADKKVKLDKQEVISWLDANTLAEDKDFEHRKKELEQVNCNPIISGLYQAGGPGPGG 240
Db 567 EQDKNKILDKQEVINWLDNMAEKDEYEHKQELERVNCNPIITSLKYQGGPGGGGGG 626

Qy 241 AQGPKGSGSGPTIEVD 258
Db 627 S-----GASGPTIEVD 639

RESULT 23
I51129
dnak-type molecular chaperone hsp70 - Iberian ribbed newt
N;Alternate names: heat shock protein HSP70
C;Species: Pleurodeles waltlii (Iberian ribbed newt)

C;Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 09-Jul-2004
C;Accession: I51129
R;Billoud, B.; Rodriguez-Martin, M.L.; Berard, L.; Moreau, N.; Angelier, N.
Development 119, 921-932, 1993
A;Title: Constitutive expression of a somatic heat-inducible hsp70 gene during amphibian
A;Reference number: I51129; MUID:94244484; PMID:8187647
A;Accession: I51129
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-645 <BL>
A;Cross-references: UNIPROT:Q91291; EMBL:X71951; NID:9431200; PIDN:CAA50749.1; PID:94312
C;Genetics:
A;Gene: hsp70
C;Function:
A;Description: involved in protein folding and assembling/disassembling of protein comp
C;Superfamily: heat shock protein 70
C;Keywords: ATP; molecular chaperone

Query Match 80.5%; Score 1058; DB 2; Length 645;
Best Local Similarity 79.6%; Pred. No. 4.6e-61;
Matches 207; Conservative 24; Mismatches 27; Indels 2; Gaps 1;

Qy 1 KSENVQDLLLDVAPLSLGLETAGGVTALIKRNTTPTKQTQTFITYSDNQSGVLQVY 60
Db 386 KSENVQDLLLDVAPLSLGLETAGGVTALIKRNTTPTKQTQTFITYSDNQSGVLQVY 445

Qy 61 EGERAMTKNNLLGRFELSGIPAPRGVPOIEVTFDIDANGILNVATATDKSTGKANKITI 120
Db 446 EGERAMTKNNLLGRFELSGIPAPRGVPOIEVTFDIDANGILNVATATDKSTGKANKITI 505

Qy 121 TNDKGRLSKEIERMVQEAERYKAEDVQERVSNAKNALESYAFNMKSAVEDGLKGKIS 180
Db 446 EGERAMTKNNLLGRFELSGIPAPRGVPOIEVTFDIDANGILNVATATDKSTGKANKITI 505

Qy 121 TNDKGRLSKEIERMVQEAERYKAEDVQERVSNAKNALESYAFNMKSAVEDGLKGKIS 180
Db 506 TNDKGRLSKEIERMVQEAERYKAEDVQERVSNAKNALESYAFNMKSTVEGDNLDKIS 565

Qy 181 EADKKVLDKQCVISWLDANTLAEDFEHKELEQVNCNPIISGLYQAGGPGGFG 238
Db 566 EDDRKKIVDKQNTISWNNMAEKEEYEHQKELEKVCNIIITLYQGMPGMPGSGS 625

Qy 239 FGAQPKGGSGSGPTIEVD 258
Db 626 SGAQARQSSSTGTIEVD 645

RESULT 24
S10859
dnak-type molecular chaperone HSP70.2 - mouse
N;Alternate names: heat shock protein 70.2
C;Species: Mus musculus (house mouse)
C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 30-Jan-1998
C;Accession: S10859
R;Zakeri, Z.F.; Wolgemuth, D.J.; Hunt, C.R.
Mol. Cell. Biol. 8, 2925-2932, 1988
A;Title: Identification and sequence analysis of a new member of the mouse HSP70 gene fa
A;Reference number: S10859; MUID:98302212; PMID:3405224
A;Accession: S10859
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-633 <ZAK>
A;Cross-references: EMBL:M20567
C;Genetics:
A;Gene: HSP70.2
C;Function:
A;Description: involved in protein folding and assembling/disassembling of protein comp
C;Superfamily: heat shock protein 70
C;Keywords: ATP; molecular chaperone

Query Match 80.3%; Score 1054.5; DB 2; Length 633;
Best Local Similarity 79.1%; Pred. NO. 7.6e-61;
Matches 204; Conservative 23; Mismatches 20; Indels 11; Gaps 2;

Qy 1 KSENVQDLLLDVAPLSLGLETAGGVTALIKRNTTPTKQTQTFITYSDNQSGVLQVY 60

Db 387 KSENVQDLLLDVTPLSLGIETAGGVTPLIKRNTTPTKQTQTFITYSDNQSVLVQVY 446
Qy 61 EGERAMTKNNLLGRFELSGIPAPRGVPOIEVTFDIDANGILNVATATDKSTGKANKITI 120
Db 447 EGERAMTKNNLLGRFELSGIPAPRGVPOIEVTFDIDANGILNVATADKSTGKANKITI 506
Qy 121 TNDKGRLSKEIERMVQEAERYKAEDVQERVSNAKNALESYAFNMKSAVEDGLKGKIS 180
Db 507 TNDKGRLSKDDIDRMVQEAERYKSEDEANRDRVAKNVAVSYTYNIKQTVEDEKLGKIS 566

Qy 181 EADKKVLDKQCVISWLDANTLAEDFEHKELEQVNCNPIISGLYQAGGPGGFG 240
Db 567 EQDNKILDKQCVINWLDNRNMAEKEEYEHQKELEKVCNPIISKLQYQ-----GPGG-- 620

Qy 241 AQGPKGGSGSGPTIEVD 258
Db 621 -----GSSGSGPTIEVD 633

RESULT 25
A25646
dnak-type molecular chaperone - chicken
N;Alternate names: heat shock protein 70
C;Species: Gallus gallus (chicken)
C;Date: 19-Nov-1998 #sequence_revision 19-Nov-1998 #text_change 09-Jul-2004
C;Accession: A25646
R;Morimoto, R.I.; Hunt, C.; Huang, S.Y.; Berg, K.L.; Banerji, S.S.
J. Biol. Chem. 261, 12692-12699, 1986
A;Title: Organization, nucleotide sequence, and transcription of the chicken HSP70 gene.
A;Reference number: A25646; MUID:86304452; PMID:3017985
A;Accession: A25646
A;Molecule type: DNA
A;Residues: 1-634 <MOR>
A;Cross-references: UNIPROT:P08106; GB:J02579; NID:G211940; PIDN:AAA48825.1; PID:G211941
A;Note: the authors translated the codon TCG for residue 583 as TTP
C;Function:
A;Description: involved in protein folding and assembling/disassembling of protein comp
C;Superfamily: heat shock protein 70
C;Keywords: ATP; molecular chaperone

Query Match 79.9%; Score 1050; DB 2; Length 634;
Best Local Similarity 79.1%; Pred. No. 1.5e-60;
Matches 204; Conservative 23; Mismatches 21; Indels 10; Gaps 1;

Qy 1 KSENVQDLLLDVAPLSLGLETAGGVTALIKRNTTPTKQTQTFITYSDNQSGVLQVY 60
Db 387 KSENVQDLLLDVTPLSLGIETAGGVTPLIKRNTTPTKQTQTFITYSDNQSVLVQVY 446

Qy 61 EGERAMTKNNLLGRFELSGIPAPRGVPOIEVTFDIDANGILNVATATDKSTGKANKITI 120
Db 447 EGERAMTKNNLLGRFELSGIPAPRGVPOIEVTFDIDANGILNVATADKSTGKANKITI 506

Qy 121 TNDKGRLSKEIERMVQEAERYKAEDVQERVSNAKNALESYAFNMKSAVEDGLKGKIS 180
Db 507 TNDKGRLSKDDIDRMVQEAERYKAEDVQERVSNAKNALESYAFNMKSTVEDEKLGKIS 566

Qy 181 EADKKVLDKQCVISWLDANTLAEDFEHKELEQVNCNPIISGLYQAGGPGGFG 240
Db 567 DQDKQVLDKQCVISWLDNRNMAEKEEYEHQKELEKVCNPIVTKLYQAGGAGAGGSG 625

Qy 241 AQGPKGGSGSGPTIEVD 258
Db 627 -----GPTIEVD 634

RESULT 26
T43724
dnak-type molecular chaperone [imported] - Japanese flounder
N;Alternate names: HSP70
C;Species: Paralichthys olivaceus (Japanese flounder)
C;Date: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 09-Jul-2004
C;Accession: T43724
R;Yokoyama, Y.; Hashimoto, H.; Kubota, S.; Kinoshita, M.; Toyohara, H.; Sakaguchi, M.; T

submitted to the EMBL Data Library, January 1998
A;Description: cDNA cloning of heat-inducible HSP70, a 70.6 kDa heat shock protein, in 3
A;Reference number: Z22648
A;Accession: T43724
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-640 <YOK>
A;Cross-references: UNIPROT:O93240; EMBL:AB010871; PIDN:BAA31697.1
C;Superfamily: heat shock protein 70

Query Match 79.9%; Score 1049.5; DB 2; Length 640;
Best Local Similarity 77.8%; Pred. No. 1.6e-60;
Matches 200; Conservative 33; Mismatches 20; Indels 3; Gaps 2;

Qy 2 SENVQDLLLDVAPLSGLGLETAGVMTALIKRNSTIPTKTQITFTTSDNQPGVLIQVY 61
Db 387 SENVQDLLLDVAPLSGLGLETAGVMTPLIKRNTIPTKTQITFTTSDNQPGVLIQVY 446

Qy 62 GERAMTKDNLLGRFELSGIPAPRGVPQIEVTFDIDANGILNVTATDKSTGKANKITIT 121
Db 447 GERAMTKDNLLGRFELSGIPAPRGVPQIEVTFDIDANGILNVTATDKSTGKANKITIT 506

Qy 122 NDKGRLSKEEIERMVOAEKYKAEDEVQRRVSAKNALESYAFNMKSAVEDEGLKGKIS 181
Db 507 NDKGRLSKEEIERMVOAEKYKAEDEVQRRVSAKNALESYAFNMKSAVEDEGLKGKIS 566

Qy 182 ADKKKVLDDKQEVISWLDANTLAEDKDEFEHKKRKELEQVNCNPIISGLYQAGGPGPGFGA 241
Db 567 EDKKIVIDKCNQITISWLENNQAEKDEYEHQKLEKVCNPIIVTKLQGA-APPG--GS 623

Qy 242 QGPKGSGSGPTIEVD 258
Db 624 SGHAGGNAQGPPTIEVD 640

RESULT 27
S08211
dnak-type molecular chaperone hsp70 - rat
N;Alternate names: heat shock protein 70.2; heat shock protein, testis-specific
C;Species: Rattus norvegicus (Norway rat)
C;Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 30-Jan-1998
C;Accession: S08211
R;Wisniewski, J.; Kordula, T.; Krawczyk, Z.
Biochim. Biophys. Acta 1048, 93-99, 1990
A;Title: Isolation and nucleotide sequence analysis of the rat testis-specific major hea
A;Reference number: S08211; MUID:90122930; PMID:1688714
A;Accession: S08211
A;Molecule type: DNA
A;Residues: 1-633 <WIS>
A;Cross-references: EMBL:X15705
A;Note: the authors translated the codon GAG for residue 217 as Asp
C;Genetics:
A;Gene: hsp70
C;Function:
A;Description: involved in protein folding and assembling/diseassembling of protein compl
A;Superfamily: heat shock protein 70
C;Keywords: ATP; molecular chaperone

Query Match 79.7%; Score 1047.5; DB 2; Length 633;
Best Local Similarity 78.7%; Pred. No. 2.2e-60;
Matches 203; Conservative 23; Mismatches 21; Indels 11; Gaps 2;

Qy 1 KSENVQDLLLDVAPLSGLGLETAGVMTALIKRNSTIPTKTQITFTTSDNQPGVLIQVY 60
Db 387 KSENVQDLLLDVAPLSGLGLETAGVMTPLIKRNTIPTKTQITFTTSDNQPGVLIQVY 446

Qy 61 EGERAMTKDNLLGRFELSGIPAPRGVPQIEVTFDIDANGILNVTATDKSTGKANKITIT 120
Db 447 EGERAMTKDNLLGRFELSGIPAPRGVPQIEVTFDIDANGILNVTATDKSTGKANKITIT 506

Qy 121 TNDKGRLSKEEIERMVOAEKYKAEDEVQRRVSAKNALESYAFNMKSAVEDEGLKGKIS 180
Db 507 TNDKGRLSKEEIERMVOAEKYKAEDEVQRRVSAKNALESYAFNMKSAVEDEGLKGKIS 566

Qy 181 EADKKKVLDDKQEVISWLDANTLAEDKDEFEHKKRKELEQVNCNPIISGLYQAGGPGPGFG 240
Db 567 EADKKKVLDDKQEVISWLDANTLAEDKDEFEHKKRKELEQVNCNPIISGLYQAGGPGPGFG 620

Qy 241 AQGPKGSGSGPTIEVD 258
Db 621 -----GGSGGPTIEVD 633

RESULT 28
HXKL70
dnak-type molecular chaperone - African clawed frog
N;Alternate names: heat shock protein 70; heat shock protein X16
C;Species: Xenopus laevis (African clawed frog)
C;Date: 28-May-1986 #sequence_revision 28-May-1986 #text_change 09-Jul-2004
C;Accession: A03310; A22175
R;Bienz, M.
EMBO J. 3, 2477-2483, 1984
A;Title: Xenopus hsp 70 genes are constitutively expressed in injected oocytes.
A;Reference number: A09993; MUID:85076567; PMID:6510409
A;Accession: A03310
A;Molecule type: DNA
A;Residues: 1-647 <BIE>
A;Cross-references: UNIPROT:P02827; GB:X01102; GB:M11915; NID:964795; PIDN:CAA25576.1; P
R;Bienz, M.
Proc. Natl. Acad. Sci. U.S.A. 81, 3138-3142, 1984
A;Title: Developmental control of the heat shock response in Xenopus.
A;Reference number: A22175; MUID:84221917; PMID:6203112
A;Accession: A22175
A;Molecule type: mRNA
A;Residues: 81-120 <BIE>
A;Cross-references: GB:X02307; NID:g214271; PIDN:AAA49759.1; PID:g214272
C;Comment: This protein is expressed constitutively in oocytes, disappears after fertili
C;Function:
A;Description: involved in protein folding and assembling/diseassembling of protein compl
A;Superfamily: heat shock protein 70
C;Keywords: ATP; heat shock; molecular chaperone; stress-induced protein

Query Match 78.9%; Score 1036.5; DB 1; Length 647;
Best Local Similarity 78.1%; Pred. No. 1.1e-59;
Matches 207; Conservative 27; Mismatches 22; Indels 9; Gaps 4;

Qy 1 KSENVQDLLLDVAPLSGLGLETAGVMTALIKRNSTIPTKTQITFTTSDNQPGVLIQVY 60
Db 385 KSENVQDLLLDVAPLSGLGLETAGVMTPLIKRNTIPTKTQITFTTSDNQPGVLIQVY 444

Qy 61 EGERAMTKDNLLGRFELSGIPAPRGVPQIEVTFDIDANGILNVTATDKSTGKANKITIT 120
Db 445 EGERAMTKDNLLGRFELSGIPAPRGVPQIEVTFDIDANGILNVTATDKSTGKANKITIT 504

Qy 121 TNDKGRLSKEEIERMVOAEKYKAEDEVQRRVSAKNALESYAFNMKSAVEDEGLKGKIS 180
Db 505 TNDKGRLSKEEIERMVOAEKYKAEDEVQRRVSAKNALESYAFNMKSAVEDEGLKGKIS 564

Qy 181 EADKKKVLDDKQEVISWLDANTLAEDKDEFEHKKRKELEQVNCNPIISGLYQAGGPG--PG 238
Db 565 DEDKRTISEKTQIVISWLENNQAEKAEYAFQKDEKVCPIITTKLYQG-GVPGGVP 623

Qy 239 F-----GAQPKGSGSGPTIEVD 258
Db 624 MFGSSCGAQAQGGN-SGPTIEVD 647

RESULT 29
T21394
hypothetical protein F26D10.3 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T21394
R;Baaham, V.; Ainscough, R.
submitted to the EMBL Data Library, September 1996
A;Reference number: Z19417

A;Accession: T21394
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-640 <Wt>
A;Cross-references: UNIPROT:Q93601; EMBL:Z80223; PIDN:CA02319.1; GSPDB:GN00022; CESP:F2
A;Experimental source: clone F26D10
C;Genetics:
A;Gene: CESP:F26D10.3
A;Map position: 4
A;Introns: 69/1; 331/3; 558/3
C;Superfamily: heat shock protein 70

Query Match 78.7%; Score 1034; DB 2; Length 640;
Best Local Similarity 77.9%; Pred. No. 1.6e-59;
Matches 201; Conservative 21; Mismatches 34; Indels 2; Gaps 1;

Qy 1 KSENVQDLLLLDVAPLSGLGTAGVMTALIKRNSTIPTKTQTFTTYSNQPGLVLIQVY 60
Db 385 KSEAVQDLLLLDVAPLSGLGTAGVMTALIKRNSTIPTKTQTFTTYSNQPGLVLIQVY 444

Qy 61 EGERAMTKDNNLLGRFELSGIPAPRGVQIETVTFDIDANGILNVATDSTGKANKITI 120
Db 445 EGERAMTKDNNLLGRFELSGIPAPRGVQIETVTFDIDANGILNVATDSTGKANKITI 504

Qy 121 TNDKGRLSKEIEIRWQEAKEYKAEDVQERVSANAKLESYAFNMKSAVEDEGLKGKIS 180
Db 505 TNDKGRLSKODIERWVNEAEKYKADDEAQAQDRIGAKNGLESYAFNLKQTIDEKLDKIS 564

Qy 181 EADKKVLDKQEVISWLDANTLAEDKDEFEHKKELQVNCNPIISGLYQAGGPG 240
Db 565 PEDKKIEDKDEILKWLDSNQTAEKEFEHQKLEGLANFIISKLYQAGGAPPG--A 622

Qy 241 AQGPKGGSGSGPTIEVD 258
Db 623 APGGAAGAGGPTIEVD 640

RESULT 30
A36333
dnak-type molecular chaperone Hsc70-4 - fruit fly (Drosophila melanogaster)
N;Alternate names: heat shock cognate protein 70
C;Species: Drosophila melanogaster
C;Date: 25-Jan-1991 #sequence_revision 25-Jan-1991 #text_change 09-Jul-2004
C;Accession: A36333
R;Perkins, L.A.; Doctor, J.S.; Zhang, K.; Stinson, L.; Perrimon, N.; Craig, E.A.
Mol. Cell. Biol. 10, 3232-3238, 1990
A;Title: Molecular and developmental characterization of the heat shock cognate 4 gene c
A;Reference number: A36333; MUID:90258915; PMID:2111451
A;Accession: A36333
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-651 <PER>
A;Cross-references: UNIPROT:P11147; GB:M36114; NID:gl57663; PIDN:AAA28627.1; PID:gl57665
C;Genetics:
A;Gene: FlyBase:Hsc70-4
A;Cross-references: FlyBase:FBgn0001219
C;Function:
A;Description: involved in protein folding and assembling/disassembling of protein comp
C;Superfamily: heat shock protein 70
C;Keywords: ATP; molecular chaperone; nucleus

Query Match 77.9%; Score 1023; DB 2; Length 651;
Best Local Similarity 73.5%; Pred. No. 8.7e-59;
Matches 197; Conservative 28; Mismatches 33; Indels 10; Gaps 1;

Qy 1 KSENVQDLLLLDVAPLSGLGTAGVMTALIKRNSTIPTKTQTFTTYSNQPGLVLIQVY 60
Db 384 KSEVQDLLLLDVAPLSGLGTAGVMTALIKRNSTIPTKTQTFTTYSNQPGLVLIQVY 443

Qy 61 EGERAMTKDNNLLGRFELSGIPAPRGVQIETVTFDIDANGILNVATDSTGKANKITI 120
Db 444 EGERAMTKDNNLLGRFELSGIPAPRGVQIETVTFDIDANGILNVATDSTGKANKITI 503

Qy 121 TNDKGRLSKEIEIRWQEAKEYKAEDVQERVSANAKLESYAFNMKSAVEDEGLKGKIS 180
Db 504 TNDKGRLSKEDIERWVNEAEKYKADDEAQAQDRIGAKNGLESYAFNLKQTIDEKLDKIS 563

Qy 181 EADKKVLDKQEVISWLDANTLAEDKDEFEHKKELQVNCNPIISGLYQAGGPG----- 235
Db 564 DSDRTTILDKCNETIKWLDANQADKEVEHQRKELEGVCNPIITKLYQAGGPPGPGMG 623

Qy 236 -----PGGFGAQGPKGSGSGPTIEVD 258
Db 624 GGGGMPGAAGAAGAGGAGPTIEVD 651

RESULT 31
S09036
dnak-type molecular chaperone HSPA6 - human
N;Alternate names: heat shock protein 70B'
C;Species: Homo sapiens (man)
C;Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 09-Jul-2004
C;Accession: S09036; I37563
R;Leung, T.K.C.; Rajendran, M.Y.; Monfries, C.; Hall, C.; Lim, L.
Biochem. J. 267, 125-132, 1990
A;Title: The human heat-shock protein family. Expression of a novel heat-inducible HSP70
A;Reference number: S09036; MUID:90226304; PMID:2327978
A;Accession: S09036
A;Molecule type: DNA
A;Residues: 1-643 <LEU>
A;Cross-references: UNIPROT:P17066; EMBL:X51757; NID:g35221; PIDN:CAA36061.1; PID:g35222
R;Schiller, P.; Amin, J.; Ananthan, J.; Brown, M.E.; Scott, W.A.; Voellmy, R.
J. Mol. Biol. 193, 97-105, 1988
A;Title: Cis-acting elements involved in the regulated expression of a human HSP70 gene.
A;Reference number: I37563; MUID:89037198; PMID:3184191
A;Accession: I37563
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-6 <RES>
A;Cross-references: EMBL:X13229; NID:g32484; PIDN:CAA31616.1; PID:g579988
C;Genetics:
A;Gene: GDB:HSPA6
A;Cross-references: GDB:127963; OMIM:140555
A;Map position: 1cen-lqter
C;Function:
A;Description: involved in protein folding and assembling/disassembling of protein comp
C;Superfamily: heat shock protein 70
C;Keywords: ATP; molecular chaperone

Query Match 77.0%; Score 1012; DB 2; Length 643;
Best Local Similarity 74.4%; Pred. No. 4.4e-58;
Matches 192; Conservative 33; Mismatches 33; Indels 0; Gaps 0;

Qy 1 KSENVQDLLLLDVAPLSGLGTAGVMTALIKRNSTIPTKTQTFTTYSNQPGLVLIQVY 60
Db 386 KCEKVQDLLLLDVAPLSGLGTAGVMTALIKRNATIPKTQTFTTYSNQPGLVLIQVY 445

Qy 61 EGERAMTKDNNLLGRFELSGIPAPRGVQIETVTFDIDANGILNVATDSTGKANKITI 120
Db 446 EGERAMTKDNNLLGRFELSGIPAPRGVQIETVTFDIDANGILNVATDSTGKANKITI 505

Qy 121 TNDKGRLSKEIEIRWQEAKEYKAEDVQERVSANAKLESYAFNMKSAVEDEGLKGKIS 180
Db 506 TNDKGRLSKEIEIRWVNEAEKYKADDEAQAQDRIVAAKNSLEAHVHVHVKSLQESLRDKIP 565

Qy 181 EADKKVLDKQEVISWLDANTLAEDKDEFEHKKELQVNCNPIISGLYQAGGPGPGFG 240
Db 566 EEDRRKMDKCREVLAWLEHNQLAKEVEYHQRKELEQICRPITFSRLYGGPGVPGGSSCG 625

Qy 241 AQGPKGGSGSGPTIEVD 258
Db 626 TQARQGDPTGTPIIEVD 643

RESULT 32
JC5642

dnak-type molecular chaperone hac70 - Iberian ribbed newt
N;Alternate names: heat shock cognate 70K protein
C;Species: Pleurodeles waltl (Iberian ribbed newt)
C;Date: 28-Oct-1997 #sequence_revision 28-Oct-1997 #text_change 09-Jul-2004
C;Accession: J05642
R;Delellis-Fantien, C.; Penrad-Mobayed, M.; Angelier, N.
Biochem. Biophys. Res. Commun. 238, 159-164, 1997
A;Title: Molecular cloning of a cDNA encoding the amphibian Pleurodeles waltl 70-kDa heat shock protein
A;Reference number: J05642; MUID:97445144; PMID:9299471
A;Accession: J05642
A;Molecule type: mRNA
A;Residues: 1-645
A;Cross-references: UNIPROT:O13120; GB:Y13661; NID:g2196881; PIDN:CAA74012.1; PID:g219688
A;Experimental source: embryo
A;Note: The sequence of residues 8-17 and 18-27 are interchanged in authors' translation
C;Genetics:
A;Gene: hac70
C;Function:
A;Description: involved in protein folding and assembling/disassembling of protein complex
C;Superfamily: heat shock protein 70
C;Keywords: ATP; molecular chaperone
F;122-264/Domain: ATP-binding #status predicted <ATP>
F;246-262/Region: nuclear location signal
F;521-645/Domain: peptide-binding #status predicted <PEB>

Query Match 76.8%; Score 1009; DB 2; Length 645;
Best Local Similarity 78.5%; Pred. No. 6.9e-58;
Matches 208; Conservative 24; Mismatches 23; Indels 10; Gaps 8;
Qy 1 KSENVQDLLLLLDVAPLSIGLETAGVMTALIKRNSTIPTKTQTFTTYSNDQPGVLIQVY 60
Db KSENVQDLLLLLDVAPLSIGLETAGVMTALIKRNSTIPTKTQTFTTYSNDQPGVLIQVY 60
Qy 384 KSENVQDLLLLLDVAPLSIGLETAGVMTALIKRNSTIPTKTQTFTTYSNDQPGVLIQVY 442
Qy 61 EGERAMTKDNNLLGRFELSGIPPPAPRGVPQIETVFDIDANGILNVATATDKSTGKANKIT 119
Db 443 EGERAMTKDNNLLGRFELSGIPPPAPRGVPQIETVFDIDANGILNVATATDKSTGKANKIT 501
Qy 120 ITNDKGRLSKEIEIRMVQEAQYKAEDVQRRVRSYAKNALESYAFNMKSAVEDEGLKGKI 179
Db 502 ITNDKGRLS-EDIERMVQEAQYKAEDKQRRVRSYAKNALESYAFNMKSAVEDEGLKGKI 560
Qy 180 SEADKKVLDKCOEIVSWLDANTLAKEDEFEHKKELQVNCNPIISGLYQAGG-PG--P 236
Db 561 IDEDKQKILEKNCNIIIAWLDNQTAEDKDEPHQKELQVNCNPIITKLQAGGMPGMP 620
Qy 237 GGFGAQQ--PKG--GSGSGPTIEEVD 258
Db 621 GGFGAQAQAGSGSGSGPTIEEVD 645

RESULT 33
S25585
dnak-type molecular chaperone Hsp70 - pig
N;Alternate names: heat shock protein 70
C;Species: Sus scrofa domestica (domestic pig)
C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 09-Jul-2004
C;Accession: S34625; S25585
R;Dezeure, F.; Vaiman, M.; Chardon, P.
Biochim. Biophys. Acta 1174, 17-26, 1993
A;Title: Characterization of a polymorphic heat shock protein 70 gene in swine outside the pig
A;Reference number: S34625; MUID:93326632; PMID:7687468
A;Accession: S34625
A;Molecule type: mRNA
A;Residues: 1-643 <DEZ>
A;Cross-references: UNIPROT:Q04967; EMBL:X68213; NID:g1977; PIDN:CAA48295.1; PID:g1978
C;Genetics:
A;Gene: Hsp70
C;Function:
A;Description: involved in protein folding and assembling/disassembling of protein complex
C;Superfamily: heat shock protein 70
C;Keywords: ATP; heat shock; molecular chaperone; stress-induced protein

Query Match 76.7%; Score 1008; DB 2; Length 643;

Best Local Similarity 74.4%; Pred. No. 8e-58;
Matches 192; Conservative 32; Mismatches 34; Indels 0; Gaps 0;
Qy 1 KSENVQDLLLLLDVAPLSIGLETAGVMTALIKRNSTIPTKTQTFTTYSNDQPGVLIQVY 60
Db KSENVQDLLLLLDVAPLSIGLETAGVMTALIKRNSTIPTKTQTFTTYSNDQPGVLIQVY 60
Qy 386 KCEKQDLLLLLDVAPLSIGLETAGVMTALIKRNSTIPTKTQTFTTYSNDQPGVLIQVY 445
Db 446 EGERAMTKDNNLLGRFELSGIPPPAPRGVPQIETVFDIDANGILSVTATDRSTGRANKITI 505
Qy 61 EGERAMTKDNNLLGRFELSGIPPPAPRGVPQIETVFDIDANGILNVATATDKSTGKANKITI 120
Db 446 EGERAMTKDNNLLGRFELSGIPPPAPRGVPQIETVFDIDANGILSVTATDRSTGRANKITI 505
Qy 121 TNDKGRLSKEIEIRMVQEAQYKAEDVQRRVRSYAKNALESYAFNMKSAVEDEGLKGKI 180
Db 506 TNDKGRLSKEIEIRMVQEAQYKAEDVQRRVRSYAKNALESYAFNMKSAVEDEGLKGKI 565
Qy 181 EADKKVLDKCOEIVSWLDANTLAKEDEFEHKKELQVNCNPIISGLYQAGGPGPGGFG 240
Db 566 EEDCKVQDCKCOEIVSWLDANTLAKEDEFEHKKELQVNCNPIISGLYQAGGPGPGGFG 625
Qy 241 AQSPKGGSGPTIEEVD 258
Db 626 AQARQAGAPSTGPVIEEVD 643

RESULT 34

S27004
dnak-type molecular chaperone hsp70.1 - Hydra magnipapillata
N;Alternate names: heat shock protein 70.1
C;Species: Hydra magnipapillata
A;Variety: strain 105
C;Date: 07-Apr-1994 #sequence_revision 07-Apr-1994 #text_change 09-Jul-2004
C;Accession: S27004
R;Gellner, K.; Praetzel, G.; Bosch, T.C.G.
Eur. J. Biochem. 210, 683-691, 1992
A;Title: Cloning and expression of a heat-inducible hsp70 gene in two species of Hydra w
A;Reference number: S27004; MUID:93130891; PMID:1483453
A;Accession: S27004
A;Molecule type: DNA
A;Residues: 1-654 <GSL>
A;Cross-references: UNIPROT:Q05944; EMBL:M84019; NID:g159267; PIDN:AAA29213.1; PID:g1592
C;Genetics:
A;Gene: hsp70.1
A;Introns: 69/1; 93/3
C;Function:
A;Description: involved in protein folding and assembling/disassembling of protein compl
C;Superfamily: heat shock protein 70
C;Keywords: ATP; heat shock; molecular chaperone; stress-induced protein

Query Match 76.6%; Score 1007; DB 2; Length 654;
Best Local Similarity 74.0%; Pred. No. 9.5e-58;
Matches 196; Conservative 27; Mismatches 34; Indels 8; Gaps 3;

Qy 1 KSENVQDLLLLLDVAPLSIGLETAGVMTALIKRNSTIPTKTQTFTTYSNDQPGVLIQVY 60
Db 391 KHEAVQDLLLLLDVAPLSIGLETAGVMTALIKRNSTIPTKTQTFTTYSNDQPGVLIQVY 450
Qy 61 EGERAMTKDNNLLGRFELSGIPPPAPRGVPQIETVFDIDANGILNVATATDKSTGKANKITI 120
Db 451 EGERAMTKDNNLLGRFELSGIPPPAPRGVPQIETVFDIDANGILNVATATDKSTGKANKITI 510
Qy 121 TNDKGRLSKEIEIRMVQEAQYKAEDVQRRVRSYAKNALESYAFNMKSAVEDEGLKGKI 180
Db 511 TNDKGRLSKEIEIRMVQEAQYKAEDVQRRVRSYAKNALESYAFNMKSAVEDEGLKGKI 570
Qy 181 EADKKVLDKCOEIVSWLDANTLAKEDEFEHKKELQVNCNPIISGLYQAGG-----PG 235
Db 571 EEDKKTIIKKCNETVWVDKNQTAEDKQYEHKQKELQVNCNPIITKLQAGGMPGMPG 630
Qy 236 --PGFGAQAQPGSGSGPTIEEVD 258
Db 631 GMPGMPGSGSGSKASSG-GPTIEEVD 654

RESULT 35

HKW7A

dnak-type molecular chaperone hsp70A - Caenorhabditis elegans

N/Alternate names: heat shock protein 70 A

C/Species: Caenorhabditis elegans

C/Date: 30-Jun-1989 #sequence_revision 30-Jun-1989 #text_change 09-Jul-2004

C/Accession: J70285

R/Smith, T.P.; Heschl, M.F.P.; Baillie, D.L.

Gene 64, 241-255, 1988

A/Title: The Caenorhabditis elegans hsp70 gene family: a molecular genetic characterization

A/Reference number: J70285; MUID:88297155; PMID:2841196

A/Accession: J70285

A/Molecule type: DNA; mRNA

A/Residues: 1-640 <SNU>

A/Cross-references: UNIPROT:P09446; GB:M18540; NID:g156351; PID:AA28078.1; PID:g156352

A/Note: genomic clones representing six distinct members of the hsp70 gene family were

A/Note: transcripts of hsp70A are abundant in control worms and also increase two- to si

A/Note: one of the three introns in hsp70A is in a position similar to an intron in Dro

C/Genetics:

A/Gene: hsp70A

A/Map position: IV

A/Introns: 69/1; 331/3; 558/3

C/Function:

A/Description: involved in protein folding and assembling/disassembling of protein comp

C/Superfamily: heat shock protein 70

C/Keywords: ATP; heat shock; molecular chaperone; stress-induced protein

Query Match 75.6%; Score 994; DB 1; Length 640;

Best Local Similarity 75.2%; Pred. No. 6.4e-57;

Matches 194; Conservative 23; Mismatches 39; Indels 2; Gaps 1;

Qy 1 KSENVQDLLLLDVAPLSGLTETAGGVMTALIKRNTSTPTKTQTQFTTYSNQPGLVQVY 60

Db 385 KSEAVQDLLLLDVAPLSGLTETAGGVMTALIKRNTSTPTKTQTQFTTYSNQPGLVQVY 444

Qy 61 EGERAMTKDNNLLGRFELSGIPPPAPRGVPOIEVTFDIDANGILNVATDSTGKANKITI 120

Db 445 EGERAMTKDNNLLGRFELSGIPPPAPRGVPOIEVTFDIDANGILNVATDSTGKANKITI 504

Qy 121 TNDKGRLSKEIERMVOEAEKYKAEDVQERVSAKNALESYAFNMKSASVEDGLKGKIS 180

Db 505 TNDKGRLSKEIERMVOEAEKYKAEDVQERVSAKNALESYAFNMKSASVEDGLKGKIS 564

Qy 181 EADKKVLDKQEVISWLDANTLAEDFEHKKRKELEQVNCNPIISGLYQAGGPGPGFG 240

Db 565 PEDKKKIEDKDEILKWLDSNQTAEKEEFESQKDLGLAKPDLKLYQSAGGAPPG--A 622

Qy 241 AQPGKGGSGGPTIEVD 258

Db 623 APGGAAGGAGGPTIEVD 640

RESULT 36

A48469

dnak-type molecular chaperone hsp70 - fluke (Schistosoma mansoni)

N/Alternate names: heat shock protein hsp70; major surface antigen

C/Species: Schistosoma mansoni

C/Date: 01-Dec-1993 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004

C/Accession: A48469; JQ0314

R/Neumann, S.; Ziv, E.; Lantner, F.; Schechter, I.

Mol. Biochem. Parasitol. 56, 357-360, 1992

A/Title: Cloning and sequencing of an hsp70 gene of Schistosoma mansoni.

A/Reference number: A48469; MUID:93133227; PMID:1484560

A/Accession: A48469

A/Status: preliminary

A/Molecule type: nucleic acid

A/Residues: 1-637 <SNU>

A/Cross-references: UNIPROT:P08418; GB:L02415; NID:L02415; PID:AA29898.1; PID:g552242

A/Note: sequence extracted from NCBI backbone (NCBIN:122799, NCBI:P122802)

R/Hedstrom, R.; Culpepper, J.; Harrison, R.A.; Agabian, N.; Newport, G.

J. Exp. Med. 165, 1430-1435, 1987

A/Title: A major immunogen in Schistosoma mansoni infections is homologous to the heat-s

A/Reference number: JQ0314; MUID:87197073; PMID:3106556

A/Accession: JQ0314

A/Molecule type: mRNA

A/Residues: 19-68, 'T', 70-113, 'P', 115-252, 'FH', 255-288, 'I', 290-299, 'G', 301-326, 'A', 328-38

A/Note: the authors translated the codon GAT for residue 59 as Pro

C/Genetics:

A/Gene: hsp70

C/Function:

A/Description: involved in protein folding and assembling/disassembling of protein comp

C/Superfamily: heat shock protein 70

C/Keywords: ATP; molecular chaperone; surface antigen

Query Match 75.2%; Score 988; DB 2; Length 637;

Best Local Similarity 76.4%; Pred. No. 1.6e-56;

Matches 197; Conservative 23; Mismatches 36; Indels 2; Gaps 2;

Qy 1 KSENVQDLLLLDVAPLSGLTETAGGVMTALIKRNTSTPTKTQFTTYSNQPGLVQVY 60

Db 382 KCEAVQDLLLLDVAPLSGLTETAGGVMTALIKRNTSTPTKTQFTTYSNQPGLVQVY 441

Qy 61 EGERAMTKDNNLLGRFELSGIPPPAPRGVPOIEVTFDIDANGILNVATDSTGKANKITI 120

Db 442 EGERAMTKDNNLLGRFELSGIPPPAPRGVPOIEVTFDIDANGILNVATDSTGKANKITI 501

Qy 121 TNDKGRLSKEIERMVOEAEKYKAEDVQERVSAKNALESYAFNMKSASVEDGLKGKIS 180

Db 502 TNDKGRLSKEIERMVOEAEKYKAEDVQERVSAKNALESYAFNMKSASVEDGLKGKIP 560

Qy 181 EADKKVLDKQEVISWLDANTLAEDFEHKKRKELEQVNCNPIISGLYQAGGPGPGFG 240

Db 561 ESDRQVLIISCEPTISWLDVHSAEKHEYESKRELEKVCAPITTYQAGGMPG-GMHIE 619

Qy 241 AQPGKGGSGGPTIEVD 258

Db 620 ASGAGGSGGKPTIEVD 637

RESULT 37

T45522

heat shock protein HSC70-1, cytosolic [imported] - spinach

C/Species: Spinacia oleracea (spinach)

C/Date: 31-Jan-2000 #sequence_revision 31-Jan-2000 #text_change 09-Jul-2004

C/Accession: T45522

R/Li, Q.B.; Guy, C.L.

A/Description: The organization and evolution of the spinach stress 70 molecular chaperon

A/Reference number: 222998

A/Accession: T45522

A/Status: preliminary; translated from GB/EMBL/DBJ

A/Molecule type: DNA

A/Residues: 1-647 <LIQ>

A/Cross-references: UNIPROT:Q41374; EMBL:AF034618; PIDN:AAB88134.1

C/Genetics:

A/Gene: HSC70-1

A/Introns: 72/1

C/Superfamily: heat shock protein 70

Query Match 73.4%; Score 964; DB 2; Length 647;

Best Local Similarity 71.6%; Pred. No. 5.7e-55;

Matches 184; Conservative 31; Mismatches 42; Indels 0; Gaps 0;

Qy 2 SENVDQLLLDVAPLSGLTETAGGVMTALIKRNTSTPTKTQFTTYSNQPGLVQVYE 61

Db 391 NEKVQDLLLLDVTPLSGLTETAGGVMTALIPRNTTPTTKEQVFTSYSDNQPGLVQVYE 450

Qy 62 GERAMTKDNNLLGRFELSGIPPPAPRGVPOIEVTFDIDANGILNVATDSTGKANKITI 121

Db 451 GERTRDNNLLGRFELSGIPPPAPRGVPOINVCFDIDANGILNVSAEDKTTGQKNKITI 510

Qy 122 NDKGRLSKEIERMVOEAEKYKAEDVQERVSAKNALESYAFNMKSASVEDGLKGKISE 181

Db 511 NDKGRLSKEIERMVOEAEKYKAEDVQERVSAKNALENYAYNMRTVYKDEIGAKLSE 570

Qy 182 ADKKKVLDKQEVISWLDANTLAEDFEHKKRKELEQVNCNPIISGLYQAGGPGPGFGA 241

R;King, K.
submitted to the EMBL Data Library, January 1994
A;Reference number: S41402
A;Accession: S41402
A:Molecule type: DNA
A;Residues: 15-64,'S','G','V',373-375,'V',377-506,'V',508-651 <KIN>
A;Cross-references: EMBL:X77199; NID:g450879; PIDN:CRA54419.1; PID:g450880
R;Wu, C.H.; Caspar, T.; Browne, J.; Lindquist, S.; Somerville, C.
Plant Physiol. 88, 731-740, 1988
A;Title: Characterization of an HSP70 cognate gene family in Arabidopsis.
A;Reference number: JA0169
A;Accession: JA0169
A:Molecule type: DNA
A;Residues: 1-120 <WUC>
A;Cross-references: GB:M23105
A;Experimental source: leaf
C;Genetics:
A;Gene: HSC70-1
A;Introns: 71/73
C;Function:
A;Description: Involved in protein folding and assembling/disassembling of protein
C;Superfamily: heat shock protein 70
C;Keywords: ATP; molecular chaperone

Query Match 72.7%; Score 955; DB 2; Length 651;
Best Local Similarity 70.1%; Pred. No. 2.2e-54;
Matches 183; Conservative 31; Mismatches 43; Indels 4; Gaps 1;

QY 2 SENVDLLLDVAPLSLGLETAGGVMTALIKRNSTIPTQTQITFTYSNQPGVLIOVYE 61
Db : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| :
391 NEKVQDLLLDVTPLSLGLETAGGVMTTLIPRNTTPTTKKEQVFSTYSNQPGVLIOVYE 450
QY 62 GERAMTKDNMLGRFELSGIPAPRGVPQIETVFDIDANGILNVATDKSTGKANKITIT 121
Db 451 GERARTKNMLLGKFELSGIPAPRGVPQITCFDIDANGILNVSAEDTTTGKANKITIT 510
QY 122 NDGRSLSKSEIERMVOEAKYKAEDVEQRERVSNAKNALESYAFNMKSAYDEGLKGKISE 181
Db : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| :
511 NDGRSLSKSEIERMVOEAKYKSEDEBHKVKYEAKNALENYAVNMRTTIQDEKIGEKLP 570
QY 182 ADKKKVLDCQEVISHLNDANTLAEKDFPHKKELEQVCNPISGLYQG----ACGGPGC 237
Db : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| :
571 ADKKCTIEDSIQAQLWLEGNLAEADPEFKMKELSESICNPITAKMYQAGGAGGPGAS 630
QY 238 GFCAQCPKGGSGSGPTIEVD 258
Db 631 GMDDAPPASGGAGPKIEVD 651

RESULT 40
T48271
dnaK-type molecular chaperone hsc70.1 - Arabidopsis thaliana
N;Alternate names: protein T22P11.90
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 09-Jul-2004
C;Accession: T48271
R;Bevan, M.; Hilbert, H.; Braun, M.; Holzer, E.; Brandt, A.; Duesterhoeft, A.; Ban
submitted to the Protein Sequence Database, April 2000
A;Reference number: Z24490
A;Accession: T48271
A;Status: preliminary
A:Molecule type: DNA
A;Residues: 1-651 <BEV>
A;Cross-references: UNIPROT:P22953; EMBL:AL162971
A;Experimental source: cultivar Columbia; BAC clone T22P11
C;Genetics:
A;Map position: 5
A;Introns: 72/1
A;Note: T22P11.90
C;Superfamily: heat shock protein 70

Query Match 72.7%; Score 955; DB 2; Length 651;
Best Local Similarity 70.1%; Pred. No. 2.2e-54;
Matches 183; Conservative 31; Mismatches 43; Indels 4; Gaps 1;

Db 391 NEKVQDLLLLDVTPLSLGLETAGGVTTLIPRNTTIPTKKEQVSTYSDNQPGVLIQVYE 450
Qy 62 GERAMTKDNLLGRFELSGIPPPAPRGVPOQIEVTFDIDANGILNVTATDKSTGKANKITIT 121
Db 451 GERATRDNNLLGKFLTGIPPA PRGVPOQITVCDFIDANGILNVSADKTTGQKNKITIT 510
Qy 122 NDKGRLSKEEIERMVQAEKKADEQVRERVSNAKNALESYAFNMKSAVEDGLKKGKISE 181
Db 511 NDKGRLSKDETEKVMQAEKKADEEHKKKVEAKNALENAYNNRNTIKDDKTIASKLSP 570
Qy 182 ADKKKVLDDKQEVTSWLDANTLAEKDFEHRKELEQVCPNPIISGLYQAGGPGPGFGA 241
Db 571 DEKKKIEADIASQWLQDGNLADEDFDDKMKLESCNPIIAKMYQAGADMGGMED 630
Qy 241 AQGPKGG---SGSGPTIEVD 258
Db 631 EDGFSAGASSAGAPKIEVD 651
RESULT 44
A42582
dnak-type molecular chaperone SCE70 - spinach
N:Alternate names: heat shock protein SCE70
C:Species: Spinacia oleracea (spinach)
C>Date: 04-Mar-1993 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
C:Accession: A42582; S21943
R:KO, K.; Bornemisz, O.; Kourtz, L.; Ko, Z.W.; Plaxton, W.C.; Cashmore, A.R.
J. Biol. Chem. 267, 2986-2993, 1992
A:Title: Isolation and characterization of a cDNA clone encoding a cognate 70-kDa heat s
A:Reference number: A42582; MUID:92147640; PMID:1371110
A:Accession: A42582
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-653 <K>
A:Cross-references: UNIPROT:P29357; EMBL:X61491; NID:G21337; PIDN:CAA43711.1; PID:G21338
A:Note: sequence extracted from NCBI backbone (NCBIN:80804, NCBI:P:80805)
C:Function:
A:Description: involved in protein folding and assembling/diseassembling of protein comp
C:Superfamily: heat shock protein 70
C:Keywords: ATP; chloroplast; molecular chaperone
Query Match 71.8%; Score 943; DB 2; Length 653;
Best Local Similarity 70.6%; Pred. No. 1.3e-53;
Matches 180; Conservative 31; Mismatches 44; Indels 0; Gaps 0;
Qy 2 SENVQDLLLLDVAPLSLGLETAGGVTALIKRNSTIPTKQTIPTTYSYSDNQPGVLIQVYE 61
Db 391 NEKVQDLLLLDVTPLSLGLETAGGVTTLIPRNTTIPTKKEQVSTYSDNQPGVLIQVYE 450
Qy 62 GERAMTKDNLLGRFELSGIPPPAPRGVPOQIEVTFDIDANGILNVTATDKSTGKANKITIT 121
Db 451 GERATRDNNLLGKFLTGIPPPAPRGVPOQITVCDFIDANGILNVSADKTTGQKNKITIT 510
Qy 122 NDKGRLSKEEIERMVQAEKKADEQVRERVSNAKNALESYAFNMKSAVEDGLKKGKISE 181
Db 511 NDKGRLSKDETEKVMQAEKKADEEHKKKVEAKNALENAYNNRNTIKDDKTIASKLSE 570
Qy 182 ADKKKVLDDKQEVTSWLDANTLAEKDFEHRKELEQVCPNPIISGLYQAGGPGPGFGA 241
Db 571 ADKKKIEADIASQWLQDGNLADEDFDDKMKLESCNPIIAKMYQAGADMGGMED 630
Qy 242 QGPKGGSGPTIEE 256
Db 631 EGPTSGGAGPKIEE 645
RESULT 45
S53126
dnak-type molecular chaperone hap70 - rice (fragment)
N:Alternate names: heat shock cognate protein 70
C:Species: Oryza sativa (rice)
C>Date: 08-Jul-1995 #sequence_revision 21-Jul-1995 #text_change 09-Jul-2004
C:Accession: S53126

R:Qun, W.; Rong-Xiang, F.
submitted to the EMBL Data Library, July 1994
A:Description: Structure and expression of a rice hap 70 cognate gene.
A:Reference number: S53126
A:Accession: S53126
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-649 <Q>
A:Cross-references: UNIPROT:Q40693; EMBL:X67711; NID:G736271; PIDN:CAA47948.1; PID:G7631
C:Genetics:
A:Gene: hap70
A:Introns: 72/1
C:Function:
A:Description: involved in protein folding and assembling/diseassembling of protein comp
C:Superfamily: heat shock protein 70
C:Keywords: ATP; molecular chaperone
Query Match 71.5%; Score 939; DB 2; Length 649;
Best Local Similarity 69.9%; Pred. No. 2.4e-53;
Matches 181; Conservative 31; Mismatches 45; Indels 2; Gaps 1;
Qy 2 SENVQDLLLLDVAPLSLGLETAGGVTALIKRNSTIPTKQTIPTTYSYSDNQPGVLIQVYE 61
Db 391 NEKVQDLLLLDVTPLSLGLETAGGVTTLIPRNTTIPTKKEQVSTYSDNQPGVLIQVYE 450
Qy 62 GERAMTKDNLLGRFELSGIPPPAPRGVPOQIEVTFDIDANGILNVTATDKSTGKANKITIT 121
Db 451 GERATRDNNLLGKFLTGIPPPAPRGVPOQITVCDFIDANGILNVSADKTTGQKNKITIT 510
Qy 122 NDKGRLSKEEIERMVQAEKKADEQVRERVSNAKNALESYAFNMKSAVEDGLKKGKISE 181
Db 511 NDKGRLSKDETEKVMQAEKKADEEHKKKVEAKNALENAYNNRNTIKDDKTIASKLSE 570
Qy 182 ADKKKVLDDKQEVTSWLDANTLAEKDFEHRKELEQVCPNPIISGLYQAGGPGPGFGA 241
Db 571 ADKKKIEADIASQWLQDGNLADEDFDDKMKLESCNPIIAKMYQAGADMGGMED 630
Qy 242 QG--PKGGSGPTIEVD 258
Db 631 DDAPPAGGSGAGPKIEVD 649
RESULT 46
T45517
heat shock protein 70, cytosolic [imported] - spinach
C:Species: Spinacia oleracea (spinach)
C>Date: 31-Jan-2000 #sequence_revision 31-Jan-2000 #text_change 09-Jul-2004
C:Accession: T45517
R:Li, Q.B.; Haskell, D.W.; Guy, C.L.
Plant Mol. Biol. 39, 21-34, 1999
A:Title: Coordinate and non-coordinate expression of the stress 70 family and other mole
A:Reference number: Z16516; MUID:99178791; PMID:10080706
A:Accession: T45517
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-651 <LIQ>
A:Cross-references: UNIPROT:O22664; EMBL:AF033852; NID:G2642647; PIDN:AAB97316.1; PID:G
A:Experimental source: strain Bloomsdale
C:Genetics:
A:Gene: HSC70
C:Superfamily: heat shock protein 70
Query Match 71.4%; Score 938; DB 2; Length 651;
Best Local Similarity 70.6%; Pred. No. 2.8e-53;
Matches 185; Conservative 31; Mismatches 40; Indels 6; Gaps 3;
Qy 2 SENVQDLLLLDVAPLSLGLETAGGVTALIKRNSTIPTKQTIPTTYSYSDNQPGVLIQVYE 61
Db 391 NEKVQDLLLLDVTPLSLGLETAGGVTTLIPRNTTIPTKKEQVSTYSDNQPGVLIQVYE 450
Qy 62 GERAMTKDNLLGRFELSGIPPPAPRGVPOQIEVTFDIDANGILNVTATDKSTGKANKITIT 121
Db 451 GERATRDNNLLGKFLTGIPPPAPRGVPOQITVCDFIDANGILNVSADKTTGQKNKITIT 510

Qy 182 ADKKVLDKCOEVSILWDLANTLAEKDFEHRKLEQVNCNPIISGLYQAGG-----PGPG 237
Db 571 DDKTKIEDAEIQIOWLDGNQLAEAEFEEDKMLESLCNPITAKMYQAGGDMDDRGP- 629
Qy 238 GFAGQGPKGSGSGPTIEEVD 258
Db 630 -----AFSGG-GAGPKIEEVD 644

RESULT 50
A25089
dnak-type molecular chaperone - maize
N/Alternate names: heat shock protein 70
C/Species: Zea mays (maize)
C/Date: 19-Nov-1988 #sequence_revision 19-Nov-1988 #text_change 09-Jul-2004
C/Accession: A25089
R/Rochester, D.E.; Winer, J.A.; Shah, D.M.
EMBO J. 5, 451-458, 1986
A/Title: The structure and expression of maize genes encoding the major heat shock prote
A/Reference number: A25089
A/Accession: A25089
A/Molecule type: DNA
A/Residues: 1-645 <ROC>
A/Cross-references: UNIPROT:P11143
A/Note: the authors translated the codon CTG for residue 22 as Val and GAG for residues
C/Genetics:
A/Introns: 48/1
C/Function:
A/Description: involved in protein folding and assembling/disassembling of protein comp
C/Superfamily: heat shock protein 70
C/Keywords: ATP; molecular chaperone

Qy 7 DLLLLVAPLSGLGLETAGGVTALIKRNSTPTKQTOIFTTYSNQPGLVLIQYGERAM 66
Db 392 DLLLLDVTPLSLGLETAGGVTMLIPRNTTPTKKEQVFSTYSNQPGLVLIQYGERAR 451
Qy 67 TKNNLLGRFELSGIPAPRGVPOIETFTDIDANGILNVATDKSTGKANKITITNDKGR 126
Db 452 TKNNLLGRFELSGIPAPRGVPOITFTDIDVNNILNVSAEDKTTGCKNKITITNDKGR 511
Qy 127 LSKEEIERMVOEAEKYKAEDVQERVSNAKNALESYAFNMKSAAVEDGLKGKISEADKK 186
Db 512 LSKEEIERMVOEAEKYKAEDVQERVSNAKNALENYANNRNTIKDDKIASKLPAEDKK 571
Qy 187 VLDKCOEVSILWDLANTLAEKDFEHRKLEQVNCNPIISGLY--QGAGGPGGFGAQQP 244
Db 572 IEDAVDGAISWLSNQLAEVEEPEDKMLEGICNPITAKMYXGEGAGMGAAAGMDRDP 631
Qy 245 KGGSGSGPTIEEVD 258
Db 632 SGGSGAGPKIEEVD 645

RESULT 51
S51682
dnak-type molecular chaperone hsp70 - Eimeria maxima (fragment)
N/Alternate names: heat shock protein 70
C/Species: Eimeria maxima
C/Date: 07-May-1995 #sequence_revision 01-Sep-1995 #text_change 09-Jul-2004
C/Accession: S51682
R/Dunn, P.P.J.; Billington, K.J.; Bumstead, J.M.; Tomley, F.M.
submitted to the EMBL Data Library, December 1994
A/Description: Isolation and sequences of cDNA clones for cytosolic and organellar hsp70
A/Reference number: S51682
A/Accession: S51682
A/Molecule type: DNA
A/Residues: 1-521 <DUN>
A/Cross-references: UNIPROT:Q24896; EMBL:Z46964; NID:G603811; PIDN:CAA87085.1; PID:G6038
C/Genetics:

A/Gene: hsp70
C/Function:
A/Description: involved in protein folding and assembling/disassembling of protein comp
C/Superfamily: heat shock protein 70
C/Keywords: ATP; molecular chaperone

Query Match 69.5%; Score 913.5; DB 2; Length 521;
Best Local Similarity 66.8%; Pred. No. 8.1e-52;
Matches 179; Conservative 35; Mismatches 43; Indels 11; Gaps 3;

Qy 2 SENVQDLLLDVAPLSGLGLETAGGVTALIKRNSTPTKQTOIFTTYSNQPGLVLIQYVE 61
Db 254 STOVQDLLLDVAPLSGLGLETAGGVTMLIPRNTTPTKKSQFTTADQNPGLVLIQYVE 313
Qy 62 GERAMTKNNLLGRFELSGIPAPRGVPOIETFTDIDANGILNVATDKSTGKANKITIT 121
Db 314 GERAMTKNNLLGRFELSGIPAPRGVPOIETFTDIDANGIMNVATDKSTGKANKITIT 373
Qy 122 NDKGRLSKEEIERMVOEAEKYKAEDVQERVSNAKNALESYAFNMKSAAVEDGLKGKISE 181
Db 374 NDKGRLSQGEIDRMVAEAEKYKAEDVQERVSNAKNALENYANNRNTIKDDKIASKLPA 433
Qy 182 ADKKVLDKCOEVSILWDLANTLAEKDFEHRKLEQVNCNPIISGLYQAGG-----PG- 235
Db 434 EDKDTAAALQKTLDDWLDNQLAEKBEYESKLKEIGVCTPIVTKMTQAAAGAGGMPGA 493
Qy 236 ----PGGF-GAOGPKGSGSGPTIEEVD 258
Db 494 AAGMPGMPDMSGAAAPGAGPTVEEVD 521

RESULT 52
JQ1515
dnak-type molecular chaperone HSP70 - Chlamydomonas reinhardtii
N/Alternate names: heat-shock protein HSP70
C/Species: Chlamydomonas reinhardtii
C/Date: 17-Aug-1992 #sequence_revision 17-Aug-1992 #text_change 09-Jul-2004
C/Accession: JQ1515
R/Mueller, F.W.; Igloi, G.L.; Beck, C.F.
Gene 111, 165-173, 1992
A/Title: Structure of a gene encoding heat-shock protein HSP70 from the unicellular alga
A/Reference number: JQ1515; MUID:92175520; PMID:1541398
A/Accession: JQ1515
A/Molecule type: DNA
A/Residues: 1-649 <MUE>
A/Cross-references: UNIPROT:P25840; GB:M76725; NID:g167420; PIDN:AAB00730.1; PID:g167421
A/Note: the authors translated the codon GAC for residue 371 as Asn
C/Comment: This protein is inducible by light as well as by elevated temperature.
C/Genetics:
A/Introns: 17/2; 59/3; 106/1; 159/3; 193/2; 550/1
C/Function:
A/Description: involved in protein folding and assembling/disassembling of protein comp
C/Superfamily: heat shock protein 70
C/Keywords: ATP; calmodulin binding; molecular chaperone
F/205-213/Region: ATP binding #status predicted
F/222-228/Region: ATP binding #status predicted
F/263-281/Region: calmodulin binding #status predicted

Query Match 69.4%; Score 911.5; DB 2; Length 649;
Best Local Similarity 68.8%; Pred. No. 1.4e-51;
Matches 179; Conservative 33; Mismatches 43; Indels 5; Gaps 3;

Qy 3 ENVQDLLLDVAPLSGLGLETAGGVTALIKRNSTPTKQTOIFTTYSNQPGLVLIQYEG 62
Db 391 EKQVQDLLLDVTPLSGLGLETAGGVTMLIPRNTTPTKKEQVFSTYSNQPGLVLIQYEG 450
Qy 63 ERAMTKNNLLGRFELSGIPAPRGVPOIETFTDIDANGILNVATDKSTGKANKITITN 122
Db 451 ERAMTKNNLLGRFELSGIPAPRGVPOINVIETDIDANGILNVSAEDKTTGCKNKITITN 510
Qy 123 DKGRLSKEEIERMVOEAEKYKAEDVQERVSNAKNALESYAFNMKSAAVEDGLKGKISEA 182
Db 511 DKGRLSKEEIERMVOEAEKYKAEDVQERVSNAKNALENYANNRNTIKDDKIASKLPA 569

Qy 122 NDGRLSKKEIERMVOEAEKYKAEDVQVRSVAKNALESYAFNMKSAVEDGLKGIKE 181
 Db 503 NDGRLSKKEIERMVOEAEKYKAEDVQVRSVAKNALESYAFNMKSAVEDGLKGIKE 562
 Qy 182 ADKKKVLDCQEVISWLDANTLAEDFEHKKKELEQVNCPIISGLYQAGGPG--PGGP 239
 Db 563 SDKAIDKAVKETIEMLDHNTAAKDEYEDKQLEGVANPIMAKIYQAGGAPGGM 622
 Qy 240 --GAQ-GPKGGSGGPTIEVD 258
 Db 623 PGAPGAGGADNGPVEVD 644

RESULT 56
 S14949
 dnak-type molecular chaperone hac-1 - tomato
 N:Alternate names: heat shock cognate protein 70
 C:Species: Lycopersicon esculentum (tomato)
 C>Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 09-Jul-2004
 C:Accession: S14949
 R:Lin, T.Y.; Duck, N.B.; Winter, J.; Folk, W.R.
 Plant Mol. Biol. 16, 475-478, 1991
 A:Title: Sequences of two hac 70 cDNAs from Lycopersicon esculentum.
 A:Reference number: S14949; MUID:91370894; PMID:1893113
 A:Accession: S14949
 A:Molecule type: mRNA
 A:Residues: 1-650 <LIN>
 A:Cross-references: UNIPROT:P24629; EMBL:X54029; NID:g19255; PIDN:CAA37970.1; PID:g19256
 C:Genetics:
 A:Gene: hsc-1
 C:Function:
 A:Description: involved in protein folding and assembling/disassembling of protein comp
 C:Superfamily: heat shock protein 70
 C:Keywords: ATP; molecular chaperone

Query Match 69.2%; Score 909; DB 2; Length 650;
 Best Local Similarity 70.4%; Pred. No. 2.1e-51;
 Matches 183; Conservative 31; Mismatches 42; Indels 4; Gaps 3;

Qy 2 SENVDLLLDVAPLSGLTAGGVTALIKRNSIPTKQTOIFTTYSNQPGLVIOVE 61
 Db 392 NEKVDLLLDVTPUSLGLTAGGVTALIPRNTIPTPKKEQVSTYSNQPGLVIOVE 451
 Qy 62 GE-RAMTKDNLLGRFELSGIPAPRGVPQIEVTFDIDANGILNVATDKSTGKANKITI 120
 Db 452 GERRARTEDNLLGKFLSVIPAPRVQITVCFDIDANGILNVSAEDKTKGQNKITI 511
 Qy 121 TNDKRLSKKEIERMVOEAEKYKAEDVQVRSVAKNALESYAFNMKSAVEDGLKGIKE 180
 Db 512 TNDKRLSKKEIERMVOEAEKYKAEDVQVRSVAKNALESYAFNMKSAVEDGLKGIKE 571
 Qy 181 EADKKVLDCQEVISWLDANTLAEDFEHKKKELEQVNCPIISGLYQAGGPG--PGG 238
 Db 572 SDDKKKIEDAVDQALSWLESQLEAEVDFDKMKELEGICNPITAKMYQAGGAGVPM 631
 Qy 239 FGAQGPKGSGSGPTIEVD 258
 Db 632 DDAP-PSGGSSAGPKIEVD 650

RESULT 57
 S53498
 dnak-type molecular chaperone HSP71.2 - garden pea
 N:Alternate names: heat shock protein HSP71.2
 C:Species: Pisum sativum (garden pea)
 C>Date: 14-Jul-1995 #sequence_revision 21-Jul-1995 #text_change 09-Jul-2004
 C:Accession: S53498
 R:DeRoche, A.; Vierling, E.
 Plant Mol. Biol. 27, 441-456, 1995
 A:Title: Cytoplasmic HSP70 homologues of pea: differential expression in vegetative and
 A:Reference number: S53498; MUID:95201239; PMID:7894010
 A:Accession: S53498

A>Status: nucleic acid sequence not shown
 A:Molecule type: mRNA
 A:Residues: 1-648 <DER>
 A:Cross-references: UNIPROT:Q40980; GB:U08848; NID:g562005; PIDN:AAA82975.1; PID:g562006
 C:Genetics:
 A:Gene: HSP71.2
 C:Function:
 A:Description: involved in protein folding and assembling/disassembling of protein comp
 C:Superfamily: heat shock protein 70
 C:Keywords: ATP; heat shock; molecular chaperone; stress-induced protein

Query Match 68.9%; Score 906; DB 2; Length 648;
 Best Local Similarity 69.0%; Pred. No. 3.2e-51;
 Matches 178; Conservative 33; Mismatches 45; Indels 2; Gaps 2;

Qy 3 ENVODLLLDVAPLSGLTAGGVTALIKRNSIPTKQTOIFTTYSNQPGLVIOVE 62
 Db 391 EKVDLLLDVTPUSLGLTAGGVTALIPRNTIPTPKKEQVSTYSNQPGLVIOVE 450
 Qy 63 ERAMTKDNLLGRFELSGIPAPRGVPQIEVTFDIDANGILNVATDKSTGKANKITI 122
 Db 451 ERARTKDNLLGKFLSVIPAPRGVPQVNVCFDIDANGILNVSAEDKTKGQNKITI 510
 Qy 123 DKGRLSKEIERMVOEAEKYKAEDVQVRSVAKNALESYAFNMKSAVEDGLKGIKE 182
 Db 511 DKGRLSKEIERMVOEAEKYKAEDVQVRSVAKNALESYAFNMKSAVEDGLKGIKE 570
 Qy 183 DKKVLDCQEVISWLDANTLAEDFEHKKKELEQVNCPIISGLYQAGGPGGPGGA 241
 Db 571 DREKIEKAVEAIOQLGQVLEVEFEDKQLEGVNCPITAKMYQAGGAGVPMGDGM 630
 Qy 242 Q-GPKGGSGSGPTIEVD 258
 Db 631 PGGGSSAGPKIEVD 648

RESULT 58
 S14992
 dnak-type molecular chaperone hsp70 - soybean
 N:Alternate names: heat shock protein, 70K
 C:Species: Glycine max (soybean)
 C>Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 09-Jul-2004
 C:Accession: S14992
 R:Roberts, J.K.; Key, J.L.
 Plant Mol. Biol. 16, 671-683, 1991
 A:Title: Isolation and characterization of a soybean hsp70 gene.
 A:Reference number: S14992; MUID:91329700; PMID:1714321
 A:Accession: S14992
 A:Molecule type: DNA
 A:Residues: 1-645 <PLA>
 A:Cross-references: UNIPROT:P26413; EMBL:X62799; NID:g18662; PIDN:CAA44620.1; PID:g18663
 C:Genetics:
 A:Gene: hsp70
 A:Introns: #status absent
 C:Function:
 A:Description: involved in protein folding and assembling/disassembling of protein comp
 C:Superfamily: heat shock protein 70
 C:Keywords: ATP; heat shock; molecular chaperone; stress-induced protein

Query Match 68.8%; Score 904.5; DB 2; Length 645;
 Best Local Similarity 68.1%; Pred. No. 4e-51;
 Matches 175; Conservative 38; Mismatches 41; Indels 3; Gaps 2;

Qy 3 ENVODLLLDVAPLSGLTAGGVTALIKRNSIPTKQTOIFTTYSNQPGLVIOVE 62
 Db 391 EKVDLLLDVTPUSLGLTAGGVTALIPRNTIPTPKKEQVSTYSNQPGLVIOVE 450
 Qy 63 ERAMTKDNLLGRFELSGIPAPRGVPQIEVTFDIDANGILNVATDKSTGKANKITI 122
 Db 451 ERARTKDNLLGKFLSVIPAPRGVPQVNVCFDIDANGILNVSAEDKTKGQNKITI 510
 Qy 123 DKGRLSKEIERMVOEAEKYKAEDVQVRSVAKNALESYAFNMKSAVEDGLKGIKE 182
 Db 511 DKGRLSKEIERMVOEAEKYKAEDVQVRSVAKNALESYAFNMKSAVEDGLKGIKE 182

Db 511 DKGRSLKEELKVMYKAEDYKAEDEEVKKVKAENSLNAYNNRNTIKDEKIGKLSPD 570
Qy 183 DKKKVLDKQEVISWLDANTLAEDFEHKKRKELEQVNCNPIISGLYQAGGPGPG-GFGA 241
Db 571 EKQIERKAVEDAIQWLEGNOVAEVEDPEKQKELEGICNPFIIAKMYQGAAGPGDPMGA 630
Qy 242 QGPKGGSGGPTIEVD 258
Db 631 DMP--AAAGAGPKIEVD 645

RESULT 59
JC7132
heat shock protein 70 - Rhizopus nigricans
C:Species: Rhizopus nigricans
C:Date: 19-May-2000 #sequence_revision 19-May-2000 #text_change 09-Jul-2004
C:Accession: JC7132
R:Cernila, B.; Cresnar, B.; Brekvar, K.
Biochem. Biophys. Res. Commun. 265, 494-498, 1999
A:Title: Induction of Hsp70 in the fungus Rhizopus nigricans.
A:Reference number: JC7132; MUID:20025372; PMID:10558896
A:Accession: JC7132
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-651 <CER>
A:Cross-references: UNIPROT:Q9UVM1; GB:AF188288
C:Superfamily: heat shock protein 70

Query Match 68.8%; Score 904; DB 2; Length 651;
Best Local Similarity 66.3%; Pred. No. 4.4e-51;
Matches 177; Conservative 36; Mismatches 44; Indels 10; Gaps 3;

Qy 2 SENVDQLLLDVAPLSGLTAGVMTALIKRNSIPTKQTIPTTYSNDQPGVLIQVYE 61
Db 385 SEKTQDLLLDVAPLSGLTAGVMTALIKRNTVPTKSEVSTYADNQPGLIQVFE 444

Qy 62 GERAMTKDNLLGRFELSGIPAPRGVPQIEVTFDIDANGILNVTATDKSTGKANKITIT 121
Db 445 GERAMTKDNLLGRFELSGIPAPRGVPQIEVTFDIDANGILNVSALDKTKGSKNITIT 504

Qy 122 NDGRLSKKEETRMVQEAQKAEDEVQVRVSAKNALESYAFNMKSAVEDGLKGKISE 181
Db 505 NDGRLSKKEETRMVQEAQKAEDEAAASIAQKNGLESYAVNLTLDERSVGALPE 564

Qy 182 ADKKVLDKQEVISWLDANTLAEDFEHKKRKELEQVNCNPIISGLYQAGG----PG- 235
Db 565 EDTKLNAAVDESIAKWLDESQAESEYSEKQKELEETANFIMMKFYQAGGAPGGAPGA 624

Qy 236 -PGGFGAGQPKGGS---GSGPTIEVD 258
Db 625 AFGGPPGAGAPGSDTDTGFSIEVD 651

RESULT 60
T43730
dnaK-type molecular chaperone 70A2 [imported] - Anopheles albimanus
N:Alternate names: heat shock protein hsp70A2
C:Species: Anopheles albimanus
C:Date: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 09-Jul-2004
C:Accession: T43730; T43729
R:Benedict, M.Q.; Cockburn, A.F.; Seawright, J.A.
Insect Mol. Biol. 2, 93-102, 1993
A:Title: The Hsp70 heat-shock gene family of the mosquito Anopheles albimanus.
A:Reference number: Z22652; MUID:97242549; PMID:9087548
A:Accession: T43730
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-640 <BEN>
A:Cross-references: UNIPROT:P41827; EMBL:M96661; NID:g159591; PIDN:AAC41543.1; PID:g159591
A:Accession: T43729
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-502 <BE2>

A:Cross-references: EMBL:M96661; NID:g159591; PIDN:AAC41542.1; PID:g159592
C:Genetics:
A:Gene: hsp70
C:Superfamily: heat shock protein 70

Query Match 68.7%; Score 903; DB 2; Length 640;
Best Local Similarity 65.6%; Pred. No. 5e-51;
Matches 170; Conservative 43; Mismatches 44; Indels 2; Gaps 2;

Qy 1 KSENVQDLLLDVAPLSGLTAGVMTALIKRNSIPTKQTIPTTYSNDQPGVLIQVY 60
Db 383 KDDKIQDVLVDVAPLSGLTAGVMTALIKRNSIPCKQKQIFSTYADNQPGLIQVFE 442

Qy 61 EGERAMTKDNLLGRFELSGIPAPRGVPQIEVTFDIDANGILNVTATDKSTGKANKITIT 120
Db 443 EGERAMTKDNLLGRFELSGIPAPRGVPQIEVTFDIDANGILNVAEKSTGKKNITIT 502

Qy 121 TNDKRLSKKEETRMVQEAQKAEDEVQVRVSAKNALESYAFNMKSAVEDGLKGKIS 180
Db 503 KNDKRLSQADIDRMVSEAEKFEDEKQERISARNQLEAYCFNLKSLDGGG-ASKLS 561

Qy 181 EADKKVLDKQEVISWLDANTLAEDFEHKKRKELEQVNCNPIISGLY-QGAGGPGPGGF 239
Db 562 DADRKTVDRCETLRWDGNTWADKEEFHKKMQLTKACSPIMTKLHQQAAGGPGSPSSC 621

Qy 240 GAQPKGKGSGGPTIEVD 258
Db 622 AQAAGGFGGTGPTVEVD 640

RESULT 61
T41121
heat shock protein 70 - fission yeast (Schizosaccharomyces pombe)
C:Species: Schizosaccharomyces pombe
C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
C:Accession: T41121; T43342
R:Lyne, M.; Rajandream, M.A.; Barrell, B.G.; Murphy, L.; Harris, D.
submitted to the EMBL Data Library, September 1998
A:Reference number: Z21969
A:Accession: T41121
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-647 <LYN>
A:Cross-references: UNIPROT:O59855; EMBL:AL031540; PIDN:CAA20787.1; GSPDB:GN00068; SPDB:8
A:Experimental source: strain 972h-; cosmid c1739
R:Kawamukai, M.
submitted to the EMBL Data Library, March 1998
A:Description: S.pombe heat shock protein of HSP70 family.
A:Reference number: Z22442
A:Accession: T43342
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-647 <KAW>
A:Cross-references: EMBL:AB012387; PIDN:BAA25322.1
C:Genetics:
A:Gene: SPCC1739.13
A:Map position: 3
C:Superfamily: heat shock protein 70

Query Match 68.6%; Score 902; DB 2; Length 647;
Best Local Similarity 66.8%; Pred. No. 5.9e-51;
Matches 177; Conservative 34; Mismatches 46; Indels 8; Gaps 2;

Qy 2 SENVDQLLLDVAPLSGLTAGVMTALIKRNSIPTKQTIPTTYSNDQPGVLIQVYE 61
Db 383 SEKTQDLLLDVAPLSGLTAGVMTALIKRNTVPTKSEIFSTYSDNQPGLIQVFE 442

Qy 62 GERAMTKDNLLGRFELSGIPAPRGVPQIEVTFDIDANGILNVTATDKSTGKANKITIT 121
Db 443 GERARTKCNLLKGFELSGIPAPRGVPQIEVTFDIDANGILNVSALKEGFGTKITIT 502

Qy 122 NDKRLSKKEETRMVQEAQKAEDEVQVRVSAKNALESYAFNMKSAVEDGLKGKISE 181
A:Residues: 1-502 <BE2>

[illegible]

DB 501 TNDKGRLSKEDIERMVAEAEFKNEEDERESQRTASKNQLESATSLKNIISEAG--DNLE 338

Qy 181 EADKKVLDKQEVISWLDANTLAKEDEFEHKKLEQVNCNPIISGLYQAGGPG----- 235
Db 559 QADKDTVTTKAETISWLDNSTASKBFDKLEQDIANPIMSKLYQAGGAPGGAAG 618
Qy 236 -PGGFGAQQPKGSGSGPTIEVD 258
Db 619 APGGFPGGAPPAEAGTVEVD 642

RESULT 67
B36590
dnak-type molecular chaperone SSA4 - yeast (Saccharomyces cerevisiae)
N:Alternate names: heat shock protein SSA4; protein YER103w
C:Species: Saccharomyces cerevisiae
C:Date: 12-Apr-1991 #sequence_revision 12-Apr-1991 #text_change 09-Jul-2004
A:Accession: B36590; S50606
R:Boorstein, W.R.; Craig, E.A.
J. Biol. Chem. 265, 18912-18921, 1990
A:Title: Structure and regulation of the SSA4 HSP70 gene of Saccharomyces cerevisiae.
A:Reference number: A36590; MUID:91035412; PMID:2121731
A:Accession: B36590
A:Molecule type: DNA
A:Residues: 1-642 <BOO>
A:Cross-references: UNIPROT:P22202; EMBL:J05637; NID:gl171726; PIDN:AAA63574.1; PID:gl1717
R:Dietrich, F.S.
submitted to the EMBL Data Library, December 1994
A:Description: The sequence of S. cerevisiae cosmids 9747, 8198, 9781, and lambda clones
A:Reference number: S50606
A:Accession: S50606
A:Molecule type: DNA
A:Residues: 1-642 <DIE>
A:Cross-references: EMBL:U18839; NID:9603313; PIDN:AAB64658.1; PID:G603341; MIPS:YER103w
C:Genetics:
A:Gene: SGD:SSA4
A:Cross-references: MIPS:YER103w; SGD:S0000905
A:Map position: 5R
C:Function:
A:Description: involved in protein folding and assembling/disassembling of protein comp
C:Superfamily: heat shock protein 70
C:Keywords: ATP; molecular chaperone; stress-induced protein

Query Match 67.8%; Score 891.5; DB 2; Length 642;
Best Local Similarity 66.4%; Pred. No. 2.8e-50;
Matches 174; Conservative 38; Mismatches 45; Indels 5; Gaps 3;

Qy 1 KSENVQDLLLDVAPLSIGLETAGVMTALIKRNSTIPTKTQTQITFTYSDNPGVLIQVY 60
Db 382 QSSTQDLLLLLDVAPLSIGLETAGIMTKLIPRNSTIPTKSEVFSTYADNPGVLIQVY 441
Qy 61 EGERAMTKDNNLLGRFELSGIPAPRGVPQIEVTFDIDANGILNVTATDKSTGKANKITI 120
Db 442 EGERTRYKNNLLGKFLSGIPAPRGVPQIEVTFDIDANGILNVSAREKGTGSKNKITI 501
Qy 121 TNDKGRLSKEIERMVOEAEKYKAEDVQVRRVSAKNALESYAFNMKSAVEDEGLKGGKIS 180
Db 502 TNDKGRLSKEDIKWAEEAEKFAEDEQEAQVQAKQKLESYAFTLKNSVSENNFKKVG 561
Qy 181 EADKKVLDKQEVISWLDANTLAKEDEFEHKKLEQVNCNPIISGLYQAGG--PGPG-- 237
Db 562 EEDARKLEAAQDAINWLDASQNSTEYKEREKELEGVNPIMSKFYGAAGGAPGAGPV 621
Qy 238 -GFGAQQPKGSGSGPTIEVD 258
Db 622 PGAGA-GTGA PDNGPTVEVD 642

RESULT 68
S11448
dnak-type molecular chaperone hac70 - Leishmania donovani
N:Alternate names: heat shock cognate protein 70
C:Species: Leishmania donovani
C:Date: 07-Apr-1994 #sequence_revision 07-Apr-1994 #text_change 09-Jul-2004
C:Accession: S11448; S11572

R:MacFarlane, J.; Blaxter, M.L.; Bishop, R.P.; Miles, M.A.; Kelly, J.M.
Eur. J. Biochem. 190, 377-384, 1990
A:Title: Identification and characterisation of a Leishmania donovani antigen belonging
A:Reference number: S11448; MUID:90306037; PMID:2163842
A:Accession: S11448
A:Molecule type: DNA
A:Residues: 1-653 <MAC1>
A:Cross-references: UNIPROT:P17804; EMBL:X52314
R:MacFarlane, J.
submitted to the EMBL Data Library, April 1990
A:Reference number: S11572
A:Accession: S11572
A:Molecule type: DNA
A:Residues: 1-208,'S',210-653 <MAC2>
A:Cross-references: EMBL:X52314; NID:g9495; PIDN:CAA36551.1; PID:g9496
C:Genetics:
A:Gene: hac70
C:Function:
A:Description: involved in protein folding and assembling/disassembling of protein comp
A:Superfamily: heat shock protein 70
C:Keywords: ATP; molecular chaperone

Query Match 67.7%; Score 890; DB 2; Length 653;
Best Local Similarity 63.8%; Pred. No. 3.6e-50;
Matches 171; Conservative 42; Mismatches 45; Indels 10; Gaps 2;

Qy 1 KSENVQDLLLDVAPLSIGLETAGVMTALIKRNSTIPTKTQTQITFTYSDNPGVLIQVY 60
Db 386 KSKQTEGLLDLDDVTPFLTGIEAGVMTALIKRNTIPTKSKQISFYADNPGVLIQVY 445
Qy 61 EGERAMTKDNNLLGRFELSGIPAPRGVPQIEVTFDIDANGILNVTATDKSTGKANKITI 120
Db 446 EGERAMTKDCHLLGTGTFDLSGIPAPRGVPQIEVTFDIDANGILNVSAREKGTGKRNOITI 505
Qy 121 TNDKGRLSKEIERMVOEAEKYKAEDVQVRRVSAKNALESYAFNMKSAVEDEGLKGGKIS 180
Db 506 TNDKGRLSKEDIERMVNDAMKYEADRAQDRVAKNGLENAYSMKNTLGDSDNVSGKLD 565
Qy 181 EADKKVLDKQEVISWLDANTLAKEDEFEHKKLEQVNCNPIISGLYQ---GAGGPGPG 237
Db 566 DSDKATLNKEIDVTLEWLSNQENATKEEYEHKQKELESVCNPIMTKYQSMGGAGGMPG 625
Qy 238 GF-----GAQGPKGSGSGPTIEVD 258
Db 626 GMPDMSGMSGAGPAGGAGGSGPKVEVD 653

RESULT 69
I46588
dnak-type molecular chaperone hsp70 - pig (fragment)
N:Alternate names: heat shock protein 70
C:Species: Sus scrofa domestica (domestic pig)
C:Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 09-Jul-2004
C:Accession: I46588
R:Buchanan, T.G.; Cabin, D.E.; Vickers, S.; Deutschan, C.S.; Delgado, E.; Sussman, M.M.;
Surgery 108, 559-566, 1990
A:Title: Molecular biology of circulatory shock. Part II. Expression of four groups of h
A:Reference number: I46588; MUID:90371455; PMID:1697703
A:Accession: I46588
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-379 <BUC>
A:Cross-references: UNIPROT:P34934; GB:M29506; NID:gl64494; PIDN:AAA02938.1; PID:gl64495
C:Function:
A:Description: involved in protein folding and assembling/disassembling of protein comp
C:Superfamily: heat shock protein 70
C:Keywords: ATP; molecular chaperone

Query Match 67.2%; Score 883; DB 2; Length 379;
Best Local Similarity 69.1%; Pred. No. 5.2e-50;
Matches 181; Conservative 33; Mismatches 38; Indels 10; Gaps 5;

Qy 1 KSENVQDLLLDVAPLSIGLETAGVMTALIKRNSTIPTKTQTQIF-TTYSNPGVLIQVY 59

Db 124 KCEVQDLLLLDVAPLSLGLETAGVMTLTIQRTATPTKQTQNFHYLLQNNQGVLIQV 183
Qy 60 YEGERAMTKONNLGRFELSGIPAPRGVPOIEVTFDIDANGILNVTATDKSTGKANKIT 119
Db 184 YEGERAMTRONNLGRFELSGIPPTPGVPOIEVTFDIDANGILNVTATDRSTGRANKMT 243
Qy 120 ITNDKGRLSKEEIERMVQEAQKAEDEQVRYSAKNALESYAFNMKSAAVEDGLKGKI 179
Db 244 LTKDGRLSKEEIERMVQEAQKAEDEQVRYSAKNALESYAFNMKSAAVEDGLKGKI 303
Qy 180 SEADKKVLDKQEV-LSWLDANTLAEDPEHKKRKELEQVCPNPIISGLYQAGGPGPGG 238
Db 304 PEEDRCVKQDKQEVPLWLEHNLQAEKEVEHQRELEQIAS--ISQLL----GPTCWG 357
Qy 239 --FGAOGPKGGSGGPTIEVD 258
Db 358 SSCGAQPKGGPGSTGPTIEVD 379

RESULT 70
PC7036
heat shock protein 70 - Rhizopus nigricans (fragment)
C;Species: Rhizopus nigricans
C;Date: 03-Nov-2000 #sequence_revision 03-Nov-2000 #text_change 09-Jul-2004
C;Accession: PC7036
R;Cernila, B.; Cresnar, B.; Breakvar, K.
Biochem. Biophys. Res. Commun. 265, 494-498, 1999
A;Title: Induction of Hsp70 in the fungus Rhizopus nigricans.
A;Reference number: JC7132; MUID:20025372; PMID:10558896
A;Accession: PC7036
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-641 <CER>
A;Cross-references: UNIPROT:Q9UVM0; GB:AF188289
C;Superfamily: heat shock protein 70

Query Match 67.2%; Score 883; DB 2; Length 641;
Best Local Similarity 64.6%; Pred. No. 9.9e-50;
Matches 170; Conservative 42; Mismatches 45; Indels 6; Gaps 3;

Qy 2 SENVDLLLLDVAPLSLGLETAGVMTALIKRNTIPTKQTQIFTTYSNQPGVLIQVYE 61
Db 379 SEKTDLSLELDVAPLSLGLETAGVMTPLIKRNTIPTKQSEVFTYADNQPGVLIQVYE 438
Qy 62 GERAMTKONNLGRFELSGIPAPRGVPOIEVTFDIDANGILNVTATDKSTGKANKITIT 121
Db 439 GELARTKONNLGRFELSGIPAPRGVPOIEVTFDIDANGILNVTATDKSTGKANKITIT 498
Qy 122 NDKGRLSKEEIERMVQEAQKAEDEQVRYSAKNALESYAFNMKSAAVEDGLKGKISE 181
Db 499 NDKGRLSKEEIERMVQEAQKAEDEQVRYSAKNALESYAFNMKSAAVEDGLKGKISE 558
Qy 182 ADKKKVLKQEV-LSWLDANTLAEDPEHKKRKELEQVCPNPIISGLYQAGG-PPGPGF- 239
Db 559 GDKEKLERAVQAIDWMDNSQASKEVESQKELEEVANPIMMKLYQGGGMPGGGMP 618
Qy 240 --GAOG--PKGGSGGPTIEVD 258
Db 619 GGGAPGGFPGDGTGGEPTIEVD 641

RESULT 71
S52727
dnaK-type molecular chaperone hsp70 - Leishmania donovani infantum (fragment)
N;Alternate names: heat shock protein hsp70; immunodominant antigen
C;Species: Leishmania donovani infantum
C;Date: 19-May-1995 #sequence_revision 21-Jul-1995 #text_change 09-Jul-2004
C;Accession: S52727
R;Quijada, L.; Reguena, J.M.; Soto, M.; Alonso, C.
submitted to the EMBL Data Library, March 1995
A;Description: In canine viscero-cutaneous leishmaniasis the anti-hsp70 antibodies are s
A;Reference number: S52727

A;Accession: S52727
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-653 <QUI>
A;Cross-references: UNIPROT:Q25292; EMBL:X85798; NID:g758135; PIDN:CAAS9793.1; PID:g758135
C;Genetics:
A;Gene: hsp70
C;Function:
A;Description: involved in protein folding and assembling/disassembling of protein complex
C;Superfamily: heat shock protein 70
C;Keywords: ATP; molecular chaperone

Query Match 67.2%; Score 883; DB 2; Length 653;
Best Local Similarity 63.1%; Pred. No. 1e-49;
Matches 169; Conservative 44; Mismatches 45; Indels 10; Gaps 2;

Qy 1 KSENVQDLLLLDVAPLSLGLETAGVMTALIKRNTIPTKQTQIFTTYSNQPGVLIQVY 60
Db 386 KSKQTEGLLELDVAPLSLGLETAGVMTALIKRNTIPTKKSQIFSTYADNQPGVHIQVF 445
Qy 61 EGERAMTKONNLGRFELSGIPAPRGVPOIEVTFDIDANGILNVTATDKSTGKANKITIT 120
Db 446 EGERAMTKONNLGRFELSGIPAPRGVPOIEVTFDIDANGILNVTATDKSTGKANKITIT 505
Qy 121 TNDKGRLSKEEIERMVQEAQKAEDEQVRYSAKNALESYAFNMKSAAVEDGLKGKIS 180
Db 506 TNDKGRLSKEEIERMVQEAQKAEDEQVRYSAKNALESYAFNMKSAAVEDGLKGKIS 565
Qy 181 EADKKVLDKQEV-LSWLDANTLAEDPEHKKRKELEQVCPNPIISGLYQ---GAGGPGPG 237
Db 566 DSDKATLNKEIDVLEWLSNQAEEYEHKKELESVCNPIMTKMYQMGGAAGMPG 625
Qy 238 GF-----GAOGPKGGSGGPTIEVD 258
Db 626 GMPGMSGMSGAGPAGGASGPKVEVD 653

RESULT 72
HHFF72
dnaK-type molecular chaperone Hsp70Bc - fruit fly (Drosophila melanogaster)
N;Alternate names: major heat shock protein 70 2
C;Species: Drosophila melanogaster
C;Date: 31-Dec-1980 #sequence_revision 31-Dec-1980 #text_change 09-Jul-2004
C;Accession: A03307
R;Ingolia, T.D.; Craig, E.A.; McCarthy, B.J.
Cell 21, 669-679, 1980
A;Title: Sequence of three copies of the gene for the major Drosophila heat shock inducer
A;Reference number: A03307; MUID:81064669; PMID:6777045
A;Accession: A03307
A;Molecule type: DNA
A;Residues: 1-641 <ING>
A;Cross-references: UNIPROT:Q9BIR7; GB:J01104; GB:J01105; NID:g157720; PIDN:AAD15226.1; f
C;Comment: Heat shock induces the synthesis of seven proteins at five otherwise inactive
pectively, code for the 70K protein. The function of heat shock proteins is unknown.
C;Genetics:
A;Gene: FlyBase:Hsp70Bc
A;Cross-references: FlyBase:FBgn0013279
C;Function:
A;Description: involved in protein folding and assembling/disassembling of protein complex
C;Superfamily: heat shock protein 70
C;Keywords: ATP; heat shock; molecular chaperone; stress-induced protein

Query Match 67.0%; Score 881; DB 1; Length 641;
Best Local Similarity 65.3%; Pred. No. 1.3e-49;
Matches 175; Conservative 34; Mismatches 41; Indels 18; Gaps 4;

Qy 1 KSENVQDLLLLDVAPLSLGLETAGVMTALIKRNTIPTKQTQIFTTYSNQPGVLIQVY 60
Db 382 QSKQIQDVLLEVDVAPLSLGLETAGVMTALIKRNTIPTKQTKTFSTYSNQPGVSIQVY 441
Qy 61 EGERAMTKONNLGRFELSGIPAPRGVPOIEVTFDIDANGILNVTATDKSTGKANKITIT 120
Db 442 EGERAMTKONNLGRFELSGIPAPRGVPOIEVTFDIDANGILNVTATDKSTGKANKITIT 501

A;Map position: 2L

C;Function:

A;Description: involved in protein folding and assembling/disassembling of protein comp

C;Superfamily: heat shock protein 70

C;Keywords: ATP; heat shock; molecular chaperone; stress-induced protein

Query Match 66.5%; Score 874; DB 2; Length 649;
Best Local Similarity 63.3%; Pred. No. 3.8e-49;
Matches 171; Conservative 37; Mismatches 48; Indels 14; Gaps 3;

Qy 1 KSENVQDLILLIDVAPLSLGLHETAGGVWTLIKRNSTIPTKQTQIFTTYSNDQGVLIQVY 60
Db : |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||: 382 QSTKTOBLLDLVAPLSLGLHETAGGIMTKIIPRNSTIPTKKSETFTYADNPQGVLIQV 441
Qy 61 EGERAMTKNNLLGRFELSGIPAPRGVPOLEVTFDIDANGILNVATDKSTGKANKITI 120
Db |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:||||| 442 EGERTRTKNNLLGKFLSGIPAPRGVPOLDVTFDIDANGILNVSALEKGTGKSNKITI 501
Qy 121 TNDKGRLSKEEIERMVQEAERYKAEDVEQRYERSAKNALESYAFNMKKSAYEDELGKGKIS 180
Db :|||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||: 502 TNDKGRLSKODIDRMVSEAEKYRADDRERAEVQAKNQLESYAFLLKNTINEASFKEKVG 561
Qy 181 EADKKVKYLDKQEVISWLDANTLAEKDPEFHKRKELEQVCNPIISGLYQAGGPGP---- 236
Db :||:||||:||||:||||:||||:||||:||||:||||:||||:||||: 562 EDDAKRLTASQETIDWLDASQAASTDEYKDRQKELEGIANPIWTKFYGAGAGPGPAGE 621
Qy 237 -GGF-----GAQPKGGSGSGPTTIEVD 258
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| 622 SCGFPGSGMPNSGATG--GGEDTGTPTVEVD 649

RESULT 78

A34041

N;Alternate names: mouse
C;Species: Mus musculus (house mouse)
C;Date: 07-Jun-1990 #sequence_revision 07-Jun-1990 #text_change 09-Jul-2004
C;Accession: A34041
R;Matsumoto, M.; Fujimoto, H.
Biochem. Biophys. Res. Commun. 166, 43-49, 1990
A;Title: Cloning of a hsp70-related gene expressed in mouse spermatids.
A;Reference number: A34041; MUID:90147735; PMID:2302214
A;Accession: A34041
A;Molecule type: DNA; mRNA
A;Residues: 1-630 <MAT>
A;Cross-references: UNIPROT:P16627; GB:M32218
C;Function:
A;Description: involved in protein folding and assembling/disassembling of protein comp
C;Superfamily: heat shock protein 70
C;Keywords: ATP; molecular chaperone

Query Match	66.4%;	Score 873;	DB 2;	Length 630;
Best Local Similarity	72.2%;	Pred. No. 4.3e-49;		
Matches 187;	Conservative 17;	Mismatches 45;	Indels 10;	Gaps 5;
Qy	1	KSENVQDLLLLDVAPLSGLGETAGVMTALIKRNSTIPTKOTQFTTYSNDQNPQVLIQVY	60	
Db	381	KSEKVQDLLLLDVAPLSGLGETAGVMTVLIKRNSTIPTKTKTFTTYSNDQNPVLIQC-	439	
Qy	61	EGERAMTKDNNLLGRPELSGIPPAAPRGVQPIEVTFDIDANGILNVATDKSTGKANKITTI	120	
Db	440	--TRQTIIPDNNLVGPFDTLTGIPPAAP-SVPQIEVTFDIARNGILNVATMDKSTGKANKITI	496	
Qy	121	TNDKGRLSKEEIERMVQEAECYKKAEDVQREVRSNAKNALESYAFNMKSAVEDGLGKGIS	180	
Db	497	TNDKGRLSKEEID-SIESRTAYKREDEGQREKIAAKNALESYAFNMKSAACDGEDLKDKIT	555	
Qy	181	EADKKKVLDKQEVYSIWDANTLAEKDFEHRKKELEQVCNPIISGLYQ-GAGGPGPGGF	239	
Db	556	ESDKKKILDKCNVFPFLSQTLAEKVEFDHKRKELENWNCPIITKLYQSCTGPTV---	612	
Qy	240	GAQPGKGGSGSGPTIEVD	258	

Db 613 -RQGIILRQSGTGPTIEVD 630

RESULT 79

A48872

dnaK-type molecular chaperone hsp6b - slime mold (Dictyostelium discoideum) (fragment)

N;Alternate names: 70k heat shock cognate protein aginactin; F-actin capping protein agin

C;Species: Dictyostelium discoideum

C;Date: 19-May-1995 #sequence_revision 19-May-1995 #text_change 09-Jul-2004

C;Accession: A48872

R;Eddy, R.J.; Sauterer, R.A.; Condeelis, J.S.

J. Biol. Chem. 268, 23267-23274, 1993

A;Title: Aginactin, an agonist-regulated F-actin capping activity is associated with an

A;Reference number: A48872; MUID:94043116; PMID:8226849

A;Accession: A48872

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-636 <EDD>

A;Cross-references: UNIPROT:P36415; GB:L22736; NID:G433179; PIDN:AAA33219.1; PID:G433180

A;Note: authors translated the codon ACA for residue 10 as Pro, GCT for residue 60 as Val

C;Function:

A;Description: involved in protein folding and assembling/disassembling of protein complex

C;Superfamily: heat shock protein 70

C;Keywords: ATP; molecular chaperone

Query Match	66.1%;	Score	868.5;	DB	2;	Length	636;
Best Local Similarity	65.9%;	Pred.	No. 8.5e-49;				
Matches	170;	Conservative	35;	Mismatches	46;	Indels	7;
Gaps	2						
Qy	5	VQDILLLDVAPLSLGLETAGVMTALKRSTIPTKQTQIETTYSDNQPGVLIQYEGER	64				
Db	382	VADLLLDVAPLSMGLTAGVMTLIPRNTTIFPKKTQTFTSYSDNQPGVLIQYEGER	441				
Qy	65	AMTKONNLLGRFELSGIPPAPRGVPQIEVTPDIIDANGILNVATDTKSGTKANKITITNDK	124				
Db	442	AMTKONNLLGKFELSGIPPAPRGVPQIEVTPDVDANGILNVASDESKTGNKQKITITNDK	501				
Qy	125	GRLSKEIERMWQEAERYKAEDVEQRBRVSAKNALESYAFNMKSAAVEDGLKGKISEADK	184				
Db	502	GRLSKEIERKWADAERFKQODEOQDRVESKNKLENYAFTVKNSIKDEKYAAKISDSDK	561				
Qy	185	KKVYLDKCQEIVSMILDANTLAKEBFHKKRKELEVCNPIISGLYQGAGGPG----	PGFGF	240			
Db	562	STIESETESVLKWLSEMQTAKEBYEDKMKALEAVVNPIMSKLQEGGMPCGGMPGGMS	621				
Qy	241	AQGPKGSGSGPTEIEVD	258				
Db	622	NDSPK-----SSNNKVVDEL	636				

RESULT 80
S37394
dnak-type molecular chaperone hsc70 - slime mold (Dictyostelium discoideum)
N/Alternate names: heat shock cognate protein 70
C/Species: Dictyostelium discoideum
C/Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 09-Jul-2004
C/Accession: S37394
R/Haus, U.; Trommler, P.; Fisher, P.R.; Hartmann, H.; Lottspeich, F.; Noegel, A.A.; Schli
EMBO J. 12, 3763-3771, 1993
A/Title: The heat shock cognate protein from Dictyostelium affects actin polymerization
A/Reference number: S37394, MUID:94008983; PMID:8404847
A/Accession: S37394
A/Molecule type: mRNA
A/Residues: 1-640 <HAU>
A/Cross-references: UNIPROT:P36415; EMBL:X75263; NID:g433874; PIDN:CAA53039.1; PID:g43333
C/Genetics:
A/Gene: hsc70
C/Function:
A/Description: involved in protein folding and assembling/disassembling of protein comp
C/Superfamily: heat shock protein 70
C/Keywords: ATP; molecular chaperone
Query Match 66.1%; Score 868.5; DB 2; Length 640;

QY 4 NVQDILLDDVAPLSGLGLETAGGWTALIKRNSTIPTKQTQIFTTYSNQPGVLIQVYGE 63
 Db 387 NVKDILLDDVAPLSGLGLETAGGWTALIGRNTTPTKKSQIFTTADNQPGVLIQVYGE 446
 QY 64 RAMTKDNLLGRPELSGIPPAIPRGVPQIETVDFDANGILNVATATDKSTCKANKITITND 123
 Db 447 RSMTKDNHLLGKFNLEGIIPPAIPRGVPQIETVDFDANGILNVSAVDKGTGKINKITITND 506
 QY 124 KGRLSKEEIERMWQAEKYKAEDVQRRERSYAKNNALESYAFNMKSAVEDGLKGKISEAD 183
 Db 507 KGRLSKEEIEKVVNDAEKFGEDKMKRIEAKNSPENYCFQMKNTLNDEKLEKFTEDD 566
 QY 184 KKKVLDKQEVISWLDANTLAEDKDFPHKKELEQVNCNPIISGLYQAGG-----PG--P 236
 Db 567 KKVIEDASKEGLOWLEGNPAEPETIEAKQKEVEAKYNPIMRVYQAAGMPPGMPGMP 626
 QY 237 GGFGAQPCKGSGSGP 252
 Db 627 GGMPPGPGGAGGAAP 642

RESULT 84
 T46650
 heat shock protein 70 [imported] - Neurospora crassa
 C:Species: Neurospora crassa
 C:Date: 18-Feb-2000 #sequence_revision 18-Feb-2000 #text_change 09-Jul-2004
 C:Accession: T46650
 R:Kapoor, M.; Cutler, C.A.; Runham, C.
 J. Bacteriol. 177, 212-221, 1995
 A:Title: The hsp70 gene family of Neurospora crassa: cloning, sequence analysis, expression
 A:Reference number: 223115; MUID:9505970; PMID:7798134
 A:Accession: T46650
 A:Status: preliminary; translated from CB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-646 <KAP>
 A:Cross-references: UNIPROT:Q01233; EMBL:U10443; NID:g607817; PIDN:AAA82183.1; PID:g607817
 C:Genetics:
 A:Gene: hsp70
 A:Map position: LGII
 A:Introns: 23/3; 247/1; 353/1; 360/3
 C:Superfamily: heat shock protein 70

Query Match 65.5%; Score 861; DB 2; Length 646;
 Best Local Similarity 60.5%; Pred. No. 2.6e-48;
 Matches 159; Conservative 48; Mismatches 50; Indels 6; Gaps 1;

QY 2 SENVQDILLDDVAPLSGLGLETAGGWTALIKRNSTIPTKQTQIFTTYSNQPGVLIQVYGE 61
 Db 384 SKSTSETILLDDVAPLSGLGLETAGGWTALKIIPRNTTPTKKSVEVSTFSDNQPGVLIQVYGE 443
 QY 62 GERAMTKDNLLGRPELSGIPPAIPRGVPQIETVDFDANGILNVATATDKSTCKANKITIT 121
 Db 444 GEQRTKDNHLLGKFNLEGIIPPAIPRGVPQIETVDFDANGILNVSALEKGTGKINKITIT 503
 QY 122 NDKGRLSKEEIERMWQAEKYKAEDVQRRERSYAKNNALESYAFNMKSAVEDGLKGKISE 181
 Db 504 NDKGRLSKEEIERMLAEAKFKEDEAEAKVAANKGLESYAYSLRNTLSDSKVDEKLD 563
 QY 182 ADKKVLDKQEVISWLDANTLAEDKDFPHKKELEQVNCNPIISGLYQAGGPG----- 235
 Db 564 ADKEKLKSEIDKIVAWDENQQTREEYERQKELEAIANPIMMKFYGAGGAPGMPGAA 623
 QY 236 PGGFGAQPCKGSGSGPTIEVD 258
 Db 624 PGGFPGAGPGSNDNEGPTVEVD 646

RESULT 85
 A26485
 dnak-type molecular chaperone - malaria parasite (Plasmodium falciparum) (fragments)
 N:Alternate names: cytoplasmic antigen
 C:Species: Plasmodium falciparum

Db 153 TNDKGRSLQDEIDRWVNDAAEKYKAEDENRKRRIEARNLENYCYGVKSSLEDQIKKELQ 212
 Qy 181 EADKKVKLDKQEVISWLDANTLAEKDFEHRKKELEQVNCNPIISGLYQ----GAGG--- 233
 Db 213 PAETCTCKTITTTILEKLNQLAGKDEYERAKQEAESVCAPINISKIYQDRAGAAGGMPG 272
 Qy 234 -----PG-----PGFGAQQPKG--SGSGPTIEVD 258
 Db 273 GMPGMPGMPGMPGMPGMPGMPGMPGMPGMPGMPGMPGMPGMPGMPGMPGMPGMPGMPG 313
 RESULT 87
 T07620
 C:Species: Cyanophora paradoxa
 C>Date: 13-Aug-1999 #sequence_revision 13-Aug-1999 #text_change 09-Jul-2004
 C:Accession: T07620
 R:Rensing, S.A.; Obrdlik, P.; Rober-Kleber, N.; Mueller, S.B.; Hofmann, C.J.; van de Pe
 Eur. J. Phycol. 32, 279-285, 1997
 A:Title: Molecular phylogeny of the stress-70 protein family with certain emphasis on al
 A:Reference number: Z16057
 A:Accession: T07620
 A:Status: translated from GB/EMBL/DDBJ
 A:Molecule type: mRNA
 A:Residues: 1-465 <REN>
 A:Cross-references: UNIPROT:P93662; EMBL:X90949
 C:Genetics:
 A:Gene: hsp70
 C:Function:
 A:Description: involved in protein folding and assembling/diseassembling of protein comp
 C:Superfamily: heat shock protein 70
 C:Keywords: ATP; molecular chaperone

Query Match 65.0%; Score 853.5; DB 2; Length 465;
 Best Local Similarity 66.3%; Pred. No. 5.4e-48;
 Matches 175; Conservative 36; Mismatches 46; Indels 7; Gaps 5;
 Qy 1 KSENVQDLLLDVAPLSGLGTAGVMTALIKRNTIPTKTQIFTYSDNQPGLVQY 60
 Db 203 QSSKVDLLLDVTPSLGLGTAGVMTALIKRNTIPTKTQIFPSYSDNQPGLVQY 262
 Qy 61 EGERAMTKDNNLLGRFELSGIPPPAPRGVPOIEVTFDIDANGILNVTATDKSTGKANKITI 120
 Db 263 EGERAGTKDNNLLGKFLSGIPPPAPR-VPOIEVTFDIDANGILNVSADKTTGNRQKITI 321
 Qy 121 TNDKGRSLKEIERMVAEKYKAEDVQRRVSAKNALESYAFNMKSAVEDGLKGIS 180
 Db 322 TNDKGRSLKDDIERMVAEKYKQDEARDRIEAKNSLENYAYLNRSIREEKVAARME 381
 Qy 181 EADKKVKLDKQEVISWLDANTLAEKDFEHRKKELEQVNCNPII-SGLYQAGG--PGPG 237
 Db 382 EDDKKVIEEVDKAKFLTPNPDADKEFEKVKQKELESKAMPVIMTKLYQSAEAPGAR 441
 Qy 238 GF-GAQQ--PKGSGSGPTIEVD 258
 Db 442 GFPGARPEPSRGKGKGVIEVD 465

RESULT 88
 S06158
 C:Species: Trypanosoma cruzi
 N:Alternate names: heat shock protein 70
 C:Species: Trypanosoma cruzi
 C>Date: 22-Jan-1993 #sequence_revision 22-Jan-1993 #text_change 09-Jul-2004
 C:Accession: S06158; A28531; S25649; A44979
 R:Bedate, C.A.
 submitted to the EMBL Data Library, December 1988
 A:Reference number: S06158
 A:Accession: S06158
 A:Molecule type: DNA
 A:Residues: 1-680 <BED>
 A:Cross-references: UNIPROT:P05456; GB:X07083; EMBL:X13690; NID:g10621; PIDN:CAA30115.1

A:Experimental source: strain Maracai
 R:Queena, J.M.; Lopez, M.C.; Jimenez-Ruiz, A.; de la Torre, J.C.; Alonso, C.
 Nucleic Acids Res. 16, 1393-1406, 1988
 A:Title: A head-to-tail tandem organization of hsp70 genes in Trypanosoma cruzi.
 A:Reference number: A28531; MUID:88157703; PMID:2831499
 A:Accession: A28531
 A:Molecule type: DNA
 A:Residues: 222-473
 A:Cross-references: GB:X07083; GB:X13690; NID:g10621; PIDN:CAA30115.1; PID:g10622
 A:Experimental source: strain Maracai
 A:Note: the sequence is revised in GenBank entry TCHSP70, release 111.0, (PIDN:CAA30115.1)
 R:Yang, S.; Bergman, L.W.; Scholl, D.R.; Rowland, E.C.
 submitted to the EMBL Data Library, August 1992
 A:Description: Cloning and characterization of cDNA encoding glucose-regulated protein 70
 A:Reference number: S25648
 A:Accession: S25649
 A:Molecule type: mRNA
 A:Residues: 1-46, 'T', 48-63, 'T', 65, 'SP', 68-167, 'M', 169-178, 'R', 180-240, 'S', 242-256, 'T', 258
 518-522, 'S', 524-529, 'SQ', 532-533, 'E', 535, 'RER', 539-554, 'T', 556-557, 'E', 559-570, 'N', 572-581, 'Q', 583
 A:Cross-references: EMBL:X67716; NID:g10625; PIDN:CAA47952.1; PID:g10626
 A:Experimental source: strain Brazil
 R:Engman, D.M.; Siag, S.R.; Gabe, J.D.; Donelson, J.E.; Dragon, E.A.
 Mol. Biochem. Parasitol. 37, 285-287, 1989
 A:Title: Comparison of HSP70 genes from two strains of Trypanosoma cruzi.
 A:Reference number: A44979; MUID:90114336; PMID:2691890
 A:Accession: A44979
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-46, 'T', 48-63, 'T', 65-167, 'M', 169-240, 'S', 242-256, 'T', 258, 'SQ', 261-310, 'D', 311
 'SQ', 532-533, 'E', 535, 'RER', 539-554, 'T', 556-557, 'E', 559-570, 'N', 572-581, 'Q', 583
 A:Cross-references: GB:M26595; NID:g162116; PIDN:AAA30205.1; PID:g162117
 A:Experimental source: strain Peru
 C:Genetics:
 A:Gene: hsp70
 C:Function:
 A:Description: involved in protein folding and assembling/diseassembling of protein complex
 C:Superfamily: heat shock protein 70
 C:Keywords: ATP; molecular chaperone

Query Match 64.8%; Score 852; DB 2; Length 680;
 Best Local Similarity 57.8%; Pred. No. 1.1e-47;
 Matches 170; Conservative 40; Mismatches 48; Indels 36; Gaps 3;
 Qy 1 KSENVQDLLLDVAPLSGLGTAGVMTALIKRNTIPTKTQIFTYSDNQPGLVQY 60
 Db 387 KSKQTEGLLLDVTPLTGLTGTAGVMTSLIKRNTIPTKTQIFSTYADNQPGLVQY 446
 Qy 61 EGERAMTKDNNLLGRFELSGIPPPAPRGVPOIEVTFDIDANGILNVTATDKSTGKANKITI 120
 Db 447 EGERAMTKDCHLLGTPLSGIPPPPPRGVPOIEVTFDIDANGILNVSAAEKGTRGNQIVL 506
 Qy 121 TNDKGRSLKEIERMVAEKYKAEDVQRRVSAKNALESYAFNMKSAVEDGLKGIS 180
 Db 507 TNDKGRSLKEIERMVAEKYKAEDVQRRVSAKNALESYAFNMKSAVEDGLKGIS 566
 Qy 181 EADKKVKLDKQEVISWLDANTLAEKDFEHRKKELEQVNCNPIISGLYQ---GAGGPG-- 235
 Db 567 EADKKTITSVAERALEWLNQNNQEAKEEYEHKKELENLCTPMTNMNYQMGAGMPGGM 626
 Qy 236 -----PGFGAQQPKG--SGSGPTIEVD 258
 Db 627 PGMPGMPGMPGMPGMPGMPGMPGMPGMPGMPGMPGMPGMPGMPGMPGMPGMPGMPGMP 680

RESULT 89
 S49303
 N:Alternate names: hsp70 - fungus (Cladosporium herbarum)
 C:Species: Cladosporium herbarum
 C>Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 09-Jul-2004
 C:Accession: S49303
 R:Zhang, L.
 submitted to the EMBL Data Library, September 1994

A;Description: Sequence and IgB-binding sites of an allergen, Cla h IV, of Cladosporium
A;Reference number: S49303
A;Accession: S49303
A:Molecule type: mRNA
A;Residues: 1-643 >SHA>
A;Cross-references: UNIPROT:P40918; EMBL:X81860; NID:g551227; PIDN:CMA57452.1; PID:g551227
A;Experimental source: tissue type mycelia
C;Genetics:
A;Gene: hep70
C;Function:
A;Description: involved in protein folding and assembling/disassembling of protein complex
C;Superfamily: heat shock protein 70
C;Keywords: ATP; heat shock; molecular chaperone; stress-induced protein

Query Match 64.1%; Score 842.5; DB 2; Length 643;
Best Local Similarity 61.7%; Pred. No. 4.1e-47;
Matches 161; Conservative 45; Mismatches 50; Indels 5; Gaps 2;

QY 2 SENVDLLLLLDVAPLSIGLETAGGVTALIKRNSTIPTKTQTFTTYSNDQNPGVLIOVYE 61
Db : : : : :
Dy SKSTKEILLDDVAPLSIGLETAGGVTALIKRNTTIPTKKSETFSTFSNDQNPGVLIOVFE 443

QY 62 GERAMTKDNLLGRFELSGIPPAPRGVPQLEVTFDDANGILNVATDKSTGKANKITIT 121
Db : : : : :
Dy GERARTKDINMGKFELSGIRPARPGVPQLEVTFDDLNGIMVSALEKGSTGTNKIVIT 503

QY 122 NDGRSLSKBEIERMVQAEEKYKAEDVEQRERSVAKNALESYAFAFNMKSAVEDGLKGKISE 181
Db : : : : :
Dy 504 NDGRSLSKBEIERMLADAEEKDEAEAGRIOAKNGLESYAYSLKNTVSDPKVEEKLSA 563

QY 182 ADKKGVLDKCQEVIWILDANTLAOKBFHKHKELEOVCMPIISGLYGAGGGPQGFGA 241
Db : : : : :
Dy 564 EDKETLTGAIDKTVAMDENQATKKEYEAEOQLSEVANPVMMKIY-GAEGGAPGGMPG 622

QY 242 QG----PKGGSQGPTEEVD 258
Db 623 QGAGAPPGGADGDPTVEEVD 643

RESULT 90
A44985
dnaK-type molecular chaperone 70.1 - Theileria annulata
N;Alternate names: heat shock protein 70.1
C;Species: Theileria annulata
C;Date: 28-Apr-1993 #sequence_revision 28-Apr-1993 #text_change_07-May-1999
C;Accession: A44985
R;Mason, P.J.; Shields, B.R.; Tait, A.; Beck, P.; Hall, R.
Mol. Biochem. Parasitol. 37, 27-36, 1989
A;Title: Sequence and expression of a gene from Theileria annulata coding for a 70-kilodalton
A;Reference number: A44985; MUID:90136713; PMID:2515435
A;Accession: A44985
A>Status: preliminary
A:Molecule type: DNA
A;Residues: 1-646 >MAS>
A;Cross-references: GB:J04653
C;Function:
A;Description: involved in protein folding and assembling/disassembling of protein complex
C;Superfamily: heat shock protein 70
C;Keywords: ATP; molecular chaperone

Query Match 64.1%; Score 842; DB 2; Length 646;
Best Local Similarity 62.6%; Pred. No. 4.5e-47;
Matches 164; Conservative 38; Mismatches 56; Indels 4; Gaps 1;

QY 1 KSENVDLLLLLDVAPLSIGLETAGGVTALIKRNSTIPTKTQTFTTYSNDQNPGVLIOVY 60
Db : : : : :
Dy 385 QSEKIQLLEDLVAPLSIGLETAGGVTALIKRNTTIPTKKNOIFTTNDRQEVLIQVF 444

QY 61 EGERAMTKDNLLGRFELSGLPPAPRGVPQLEVTFDDANGILNVATDKSTGKANKITI 120
Db : : : : :
Dy 445 EGERAMTKDNLLGKFLHTGIAPARGVPQLEVTFDDLNGILNVATDKSTGKSEHTI 504

QY 121 TNDKGRSLSKBEIERMVQAEEKYKAEDVEQRERSVAKNALESYAFAFNMKSAVEDGLKGKIS 180

A;Description: involved in protein folding and assembling/disassembling of protein comp
C;Superfamily: heat shock protein 70
C;Keywords: ATP; molecular chaperone

Query Match 63.7%; Score 837; DB 2; Length 651;
Best Local Similarity 63.6%; Pred. No. 9.6e-47;
Matches 168; Conservative 36; Mismatches 50; Indels 10; Gaps 2;

QY 1 KSENVQDLLLLDVAPLSGLGTAGGVTALIKRNTIPTKTQTOIFTTYSNQPGLVQVY 60
DB 392 RNEKQDLLLLDVAPLSGLGTAGGVTALIKRNTIPTKTQTOIFTTYSNQPGLVQVY 451
QY 61 EGERAMTKNNLLGRFELSGIPAPRGVPQIEVTFDIDANGILNVATDKSTGKANKITI 120
DB 452 EGERAMTKNNLLGRFELSGIPAPRGVPQIEVTFDIDANGILNVATDKSTGKANKITI 511
QY 121 TNDKRLSKKEIERMVQAEKYKAEDVQRRVSAKNALSYAFNMKSAVEDGLKQKIS 180
DB 512 TNDKRLSKKEIERMVQAEKYKAEDVQRRVSAKNALSYAFNMKSAVEDGLKQKIS 571
QY 181 EADKKVLDKQEVISWLDANTLAEKDFEHRKKELEQVNCNPIISGLYQAG-----GP 234
DB 572 AEVKKKIDDAWEGAIQWLEAQLAEVDFDCKRRELEGICFVIEKLCQGGIGVIADRWGM 631
QY 235 GPGGFGAQKPGKSGSGPTIEVD 258
DB 632 NEDGTASR----TGGAGPKIEVD 651

RESULT 93
HNUM7B
dnaK-type molecular chaperone - lettuce downy mildew
N;Alternate names: heat shock protein 70
C;Species: Bremia lactucae (lettuce downy mildew)
C;Date: 31-Mar-1990 #sequence_revision 31-Mar-1990 #text_change 09-Jul-2004
C;Accession: J00062
R;Judson, H.S.; Michelmore, R.W.
A;Title: Structure and expression of a gene encoding heat-shock protein Hsp70 from the c
Gene 79, 207-217, 1989
A;Reference number: J00062; MUID:90006750; PMID:2792764
A;Accession: J00062
A;Molecule type: DNA
A;Residues: 1-675 <JUD>
A;Cross-references: UNIPROT:P16394
C;Comment: This fungus causes downy mildew disease in lettuce.
C;Function:
A;Description: involved in protein folding and assembling/disassembling of protein comp
C;Superfamily: heat shock protein 70
C;Keywords: ATP; heat shock; molecular chaperone; stress-induced protein

Query Match 63.0%; Score 827.5; DB 1; Length 675;
Best Local Similarity 57.4%; Pred. No. 4.1e-46;
Matches 166; Conservative 38; Mismatches 52; Indels 33; Gaps 4;

QY 2 SENVQDLLLLDVAPLSGLGTAGGVTALIKRNTIPTKTQTOIFTTYSNQPGLVQVY 61
DB 388 SQKLQDLLLLDVAPLSGLGTAGGVTALIKRNTIPTKTQTOIFTTYSNQPGLVQVY 446
QY 62 GERAMTKNNLLGRFELSGIPAPRGVPQIEVTFDIDANGILNVATDKSTGKANKITI 121
DB 447 GERSMTRNNLLGRFELSGIPAPRGVPQIEVTFDIDANGILNVATDKSTGKANKITI 506
QY 122 NDKRLSKKEIERMVQAEKYKAEDVQRRVSAKNALSYAFNMKSAVEDGLKQKIS 181
DB 507 NDRVVCRRHIDRMVSAEYKSEDEANKIRIEAKGLNYSYNLRTINDEKLDQIPE 566
QY 182 ADKKVLDKQEVISWLDANTLAEKDFEHRKKELEQVNCNPIISGLYQAGGPG----- 235
DB 567 DDKAIEDKVTETINWLDANQSAEKEVEGQKLEGIANFILQKMYAAGAGMPGGM 626
QY 236 ---PGGF-----GAGPKGG-----SGSGPTIEVD 258
DB 627 FGMPGMPGMPGMPGMPGMPGMPGMPGMPGMPGMPGMPGMPGMPGMPGMPGMPGMP 675

RESULT 94

T45471
dnaK-type molecular chaperone hsc70 [imported] - slime mold (Dictyostelium discoideum)
N;Alternate names: heat shock cognate protein 70
C;Species: Dictyostelium discoideum
C;Date: 31-Jan-2000 #sequence_revision 31-Jan-2000 #text_change 09-Jul-2004
C;Accession: T45471
R;Boves, H.; Mintert, U.; Ditttrich, W.; Paix, J.; Gerisch, G.
submitted to the EMBL Data Library, September 1997
A;Reference number: Z22980
A;Accession: T45471
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-632 <BOV>
A;Cross-references: UNIPROT:O15766; EMBL:AF025951; PIDN:AAB81865.1
A;Experimental source: strain AX3
C;Genetics:
A;Gene: hsc70
A;Note: localized to filopodias and cortex
C;Superfamily: heat shock protein 70

Query Match 62.7%; Score 824; DB 2; Length 632;
Best Local Similarity 63.0%; Pred. No. 6.4e-46;
Matches 160; Conservative 40; Mismatches 46; Indels 8; Gaps 1;

QY 5 VQDILLDLVAPLSGLGTAGGVTALIKRNTIPTKTQTOIFTTYSNQPGLVQVY 64
DB 387 VADILLDLVAPLSGLGTAGGVTALIKRNTIPTKTQTOIFTTYSNQPGLVQVY 446
QY 65 AMTKNNLLGRFELSGIPAPRGVPQIEVTFDIDANGILNVATDKSTGKANKITI 124
DB 447 AMTKNNLLGRFELSGIPAPRGVPQIEVTFDIDANGILNVATDKSTGKANKITI 506
QY 125 GRLSKEIERMVQAEKYKAEDVQRRVSAKNALSYAFNMKSAVEDGLKQKIS 184
DB 507 GRLSKEIERMVQAEKYKAEDVQRRVSAKNALSYAFNMKSAVEDGLKQKIS 566
QY 185 KKVLDKQEVISWLDANTLAEKDFEHRKKELEQVNCNPIISGLYQAGGPGGFGAG 244
DB 567 KTVKESDEAINWLNHANDSATKEEYKAMKDLAVCSPIISKVYGOQGGNGPNF----- 621
QY 245 KGGSGSGPTIEVD 258
DB 622 ---SGAKTIEEDLD 632

RESULT 95

S14875
dnaK-type molecular chaperone hsp70 - Trypanosoma cruzi (fragment)
N;Alternate names: heat shock protein 70
C;Species: Trypanosoma cruzi
C;Date: 07-Apr-1994 #sequence_revision 07-Apr-1994 #text_change 09-Jul-2004
C;Accession: S14875
R;Levy Yevati, P.; Lafon, S.; Bonnefoy, S.; Levi, M.
submitted to the EMBL Data Library, April 1991
A;Description: Nucleotide sequence of a Trypanosoma cruzi HSP-70 c-DNA.
A;Reference number: S14875
A;Accession: S14875
A;Molecule type: mRNA
A;Residues: 1-261 <LEV>
A;Cross-references: UNIPROT:Q03929; EMBL:X58715; NID:g10623; PIDN:CAA41551.1; PID:g10624
C;Genetics:
A;Gene: hsp70
C;Function:
A;Description: involved in protein folding and assembling/disassembling of protein comp
C;Superfamily: heat shock protein 70
C;Keywords: ATP; molecular chaperone

Query Match 62.7%; Score 823.5; DB 2; Length 261;
Best Local Similarity 61.3%; Pred. No. 2.3e-46;
Matches 160; Conservative 38; Mismatches 46; Indels 17; Gaps 2;

```

Qy      15  PLSLGLETAGGVMTALIKRNSTIPTKQTQIETTTSDNQGVLIQVVEGERAMTKNNLLG  74 .
Db      1  PLTIGIETAGGVMTSLIKRNTTIPTKSQIFSTVPDNPQGVHIIQVVEGERAMTKDCHLLG  60
Qy      75  RFELSGIPPAPRGVPQIEVTFDIDANGILNVATATDKSTGKANKITITNDKGRLSKEEIER  134
Db      61  TFDLSGIPPAPRGVPQIEVTFDLDANGILNVASAEKGTGKRNQIVITNDKGRLSKADIER  120
Qy     135  MVQBAEKYKAEDVQORVRSNAKNALESYAFNMKSAVEDEGLKKGKISEADKKVKLDKQORV  194
Db     121  MVSEAAKYEAQDKQDRIDAKNGLENYAFNMKNTVNEPNVAGKTEADKNTITSAVEEA  180
Qy     195  ISWLDANTLAEKDFEHRKKELEOVCPNIIISGLYO--GAGGPGPGCGFCAQGPKG-----  246
Db     181  LQWLNNQBAKSEVEYHRQKELENICTPIMTKYQGMGAGGGMFGMFGMFGMFGMFGMFG  240
Qy     247  -----GSGSGPTTIEVD  258
Db     241  GMPGGANPSSSSGPKVEVD  261

RESULT 96
T45468
dnak-type molecular chaperone Hsp70 [imported] - bloodfluke planorb
N;Alternate names: heat shock protein 70
C;Species: Biomphalaria glabrata (bloodfluke planorb)
C;Date: 31-Jan-2000 #sequence_revision 31-Jan-2000 #text_change 09-Jul-2004
C;Accession: T45468
R;Yoshino, T.P.; Wu, X.J.; Liu, H.D.
submitted to the EMBL Data Library, November 1997
A;Description: Transfection and heat-inducible expression of a molluscan promoter
A;Reference number: 222978
A;Accession: T45468
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-636 <YOS>
A;Cross-references: UNIPROT:O44343; EMBL:AF025477; PIDN:AAE99911.1
A;Experimental source: strain PR albino
C;Genetics:
C;Gene: HSP70
C;Superfamily: heat shock protein 70

```

C;Date: 01-Dec-1993 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
C;Accession: A48439
C;R;Ortner, S.; Plaimauer, B.; Binder, M.; Wiedermann, G.; Scheiner, O.; Duchene, M.
Mol. Biochem. Parasitol. 54, 175-183, 1992
A;Title: Humoral immune response against a 70-kilodalton heat shock protein of Entamoeba
A;Reference number: A48439; MUID:93063033; PMID:1435858
A;Accession: A48439
A;Status: preliminary
A;Molecule type: nucleic acid
A;Residues: 1-656 <ORT>
A;Cross-references: UNIPROT:Q24842; GB:M84652; NID:gi58955; PIDN:AAA29102.1; PID:gi58956
A;Experimental source: SPL-3 trophozoites
A;Note: sequence extracted from NCBI backbone (NCBIN:117218, NCBIPI:117219)
C;Function:
A;Description: involved in protein folding and assembling/disassembling of protein compl
C;Superfamily: heat shock protein 70
C;Keywords: ATP; molecular chaperone

RESULT 97
A48439
dnaK-type molecular chaperone Hsp70 - Entamoeba histolytica
N;Alternate names: heat shock protein Hsp70
C:Species: Entamoeba histolytica

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OM protein - protein search, using sw model

Run on: April 6, 2005, 16:52:37 ; Search time 174 Seconds
(without alignments)

573.472 Million cell updates/sec

Title: US-09-646-835-1_COPY_384_641

Perfect score: 1314

Sequence: 1 KSNVQDLLLLLDVAPLSLGL.....FGAQKPGKGGSGFTIEEVD 258

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database : A Geneseq_16Dec04:*

1: Geneseqp1908s:*

2: Geneseqp1908s:*

3: Geneseqp2000s:*

4: Geneseqp2001s:*

5: Geneseqp2002s:*

6: Geneseqp2003as:*

7: Geneseqp2003bs:*

8: Geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1314	100.0	641	2	Aaw54349 Human hea
2	1314	100.0	641	3	Aab23652 Human hea
3	1314	100.0	641	4	Aab82534 Human hea
4	1314	100.0	641	4	Aae12986 Human Hsp
5	1314	100.0	641	6	Ahu89711 Protein d
6	1314	100.0	641	7	Add47459 Human Pro
7	1314	100.0	641	7	Adj27279 Human HSP
8	1314	100.0	641	8	Adj76981 Human pro
9	1314	100.0	641	8	Adl82939 Human PRO
10	1314	100.0	641	8	Abm80760 Tumour-as
11	1312	99.8	641	7	Adi20102 Hsp70. 4/
12	1309	99.6	476	7	Adm04781 Human pro
13	1309	99.6	641	6	Abm80400 Human Hsp
14	1309	99.6	641	7	Adf76349 Novel hum
15	1309	99.6	641	8	Abm80759 Tumour-as
16	1298.5	98.8	554	3	Aay88410 Human hea
17	1298.5	98.8	554	3	Aay88409 Human hea
18	1298.5	98.8	640	3	Aab23653 Human hea
19	1298.5	98.8	640	7	Add14137 Human src
20	1298.5	98.8	640	7	Adj68449 Human hea
21	1295	98.6	641	6	Abm80399 Bovine HS
22	1290.5	98.2	640	2	Aaw10065 Human hea
23	1290.5	98.2	640	3	Aay88408 Human hea
24	1282	97.6	640	2	Aar03929 Homo sapi
25	1278.5	97.3	640	3	Aay88411 Human hea

Abm80398 Rat Hsp70	641	6	ABR40398
Add46498 Rat Prote	641	7	ADD46498
Ades7092 Rat Prote	641	7	ADES7092
Add45046 Rat Prote	641	7	ADD45046
Add47457 Rat Prote	641	7	ADD47457
Adf30465 Rat angio	641	7	ADF30465
Adf30534 Rat angio	641	7	ADF30534
Abm09886 Hsp70 C-t	244	3	ABM09886
Aar43004 Mature mo	641	2	AAR43004
Abm40397 Mouse HSP	641	6	ABM40397
Adj27277 Mouse HSP	641	7	ADJ27277
Abm23650 Rat heat	641	7	ABM23650
Adf27275 Mouse HSP	641	7	ADF27275
Abm23252 Human Hsp	641	3	ABM23252
Aay88413 Human hea	554	3	AAY88413
Aay88412 Human hea	554	3	AAY88412
Adj69869 Human hea	641	7	ADJ69869
Aay17408 Mouse hea	641	2	AAY17408
Abm23649 Mouse hea	641	3	ABM23649
Abm04836 Rat heat	641	6	ABM04836
Adl18652 Human dis	641	7	ADL18652
Ada50750 Human hea	586	6	ADA50750
Adj69947 Human hea	586	7	ADJ69947
Aaw54364 Heat shoc	641	2	AAW54364
Aay17407 Human hea	641	2	AAY17407
Aab23651 Human hea	641	3	AAB23651
Aab82535 Human hea	641	4	AAB82535
Aae12987 Human Hsp	641	4	AAE12987
Aau75102 Heat shoc	641	5	AAU75102
Abu69612 Human NF-	641	6	ABU69612
Abu64224 Angiogene	641	6	ABU64224
Abu79083 Staphyloc	641	6	ABU79083
Adf22402 HLA-B46 T	641	7	ADF22402
Adf43323 Superanti	641	7	ADF43323
Adi20103 Hsc70. 4/	641	7	ADI20103
Adj68897 Human hea	641	7	ADJ68897
Ade76846 Human pro	641	8	ADE76846
Adn04484 Antipeori	641	8	ADN04484
Adq91627 Human hea	641	8	ADQ91627
Adq89812 Antagonis	641	8	ADQ89812
Adq89798 Antagonis	641	8	ADQ89798
Adp54908 Human PRO	641	8	ADP54908
Adp24120 PRO poly	641	8	ADP24120
Adt66611 Human cha	641	8	ADT66611
Aab22938 GFP-HSC70	890	3	AAB22938
Abg94501 Protease	890	5	ABG94501
Adm05456 Human pro	250	7	ADM05456
Adm85121 Mouse ato	641	8	ADM85121
Ade76908 Human pro	641	8	ADE76908
Add18948 Human dis	650	7	ADD18948
Add18946 Human dis	650	7	ADD18946
Adm04839 Human pro	621	7	ADM04839
Add48290 Rat Prote	641	7	ADD48290
Add48986 Rat Prote	641	7	ADD48986
Add48287 Rat Prote	641	7	ADD48287
Add45650 Rat Prote	641	7	ADD45650
Aar03927 Rat HSP (641	2	AAR03927
Adm05931 Human pro	641	7	ADM05931
Adf63493 Human pro	639	7	ADF63493
Adj69917 Human hea	639	7	ADJ69917
Adj69887 Human hea	639	7	ADJ69887
Adn04525 Antipeori	639	8	ADN04525
Aar43002 Mouse SLI	633	2	AAR43002
Ade63491 Rat Prote	633	7	ADE63491
Abm40401 Xenopus H	647	6	ABM40401
Aar03930 Gallus ga	634	2	AAR03930
Adn23580 Bacterial	640	8	ADN23580
Aar03928 Xenopus 1	647	2	AAR03928
Abb60514 Drosophil	651	4	ABB60514
Adq89618 Antagonis	651	8	ADQ89618
Aam48711 Human sch	643	5	AAM48711
Add18650 Human dis	643	7	ADD18650
Ade77039 Human pro	643	8	ADE77039

99 1012 77.0 643 8 ADP12947 Adp12947 Protein e
100 1012 77.0 643 8 ADRI4395 Adri4395 Human NF-

ALIGNMENTS

RESULT 1

AAW54349
ID AAW54349 standard; protein; 641 AA.

XX AAW54349;
XX
DT 14-AUG-1998 (first entry)
XX
DE Human heat shock 70 kD protein 1.
XX
KW Endometrium; hyperplasia; adenocarcinoma; proliferative phase;
KW 2D gel electrophoresis; detection.

XX Homo sapiens.
OS
XX
PN WO9810291-A1.

XX
PD 12-MAR-1998.

XX 05-SEP-1997; 97WO-GB002394.
XX
XX 06-SEP-1996; 96GB-00018600.
PR
PR 08-APR-1997; 97GB-00007132.

XX (CLIN-) CENT CLINICAL & BASIC RES.
PA
XX
XX Byrjaleen I, Larsen P, Fey SJ;

XX WPI; 1998-207057/18.
XX
XX Biochemical markers of human endometrium - useful for, e.g. diagnosis of
PT hyperplasia and adenocarcinoma.

XX Disclosure; Page 19; 77pp; English.
XX
XX Proteins AAW54349-W54364 are examples of proteins produced in the
CC endometrium during the hyperplasia, adenocarcinoma or proliferative phase
CC of the endometrium. The presence and quantities of these proteins can be
CC detected using 2D gel electrophoresis comparison of cell lysates. The
CC proteins can be used as biochemical markers to detect the phase of the
CC endometrium and can be measured in body fluids, obviating the need for
XX endometrial biopsies
XX
SQ Sequence 641 AA;

Query Match 100.0%; Score 1314; DB 2; Length 641;
Best Local Similarity 100.0%; Pred. No. 8.8e-101;
Matches 258; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KSENVQDILLDDVAPLSGLGTAGGVTALIKRNSTIPTKTQITFTYSDNQPGVLIQVY 60
DB 384 KSENVQDILLDDVAPLSGLGTAGGVTALIKRNSTIPTKTQITFTYSDNQPGVLIQVY 443

QY 61 EGERAMTKDNNLLGRFELSGIPPPAPRGVPQIEVTFDIDANGILNVTATDKSTGKANKITI 120
DB 444 EGERAMTKDNNLLGRFELSGIPPPAPRGVPQIEVTFDIDANGILNVTATDKSTGKANKITI 503

QY 121 TNDKRLSKBEIERMVQAEKYKAEDVQERVSAKNALESYAFNMKSAVEDGLGKGIS 180
DB 504 TNDKRLSKBEIERMVQAEKYKAEDVQERVSAKNALESYAFNMKSAVEDGLGKGIS 563

QY 181 EADKKKVLDDKQEVISWLDANTLAEKDFEHRKELEQVCNPIISGLYQGAGGPGPGFG 240
DB 564 EADKKKVLDDKQEVISWLDANTLAEKDFEHRKELEQVCNPIISGLYQGAGGPGPGFG 623

QY 241 AOGPKGGSGSGPTIEVD 258

DB 624 AOGPKGGSGSGPTIEVD 641

RESULT 2

AAAB23652
ID AAB23652 standard; protein; 641 AA.

XX AAB23652;
AC
XX

DT 05-JAN-2001 (first entry)
XX
XX Human heat shock protein Hsp70.1 protein sequence SEQ ID NO:4.

XX ATPase; Hsp70; heat shock protein; cytotoxic T lymphocyte; CTL;
KW immune response; infectious disease; malaria; cytotoxic T cell;
KW cytosolic; immunostimulant; cellular immune response inducer;
KW protozoaside; leukaemia; cancer.
XX
XX Homo sapiens.

XX
PN WO200049041-A1.

XX
PD 24-AUG-2000.

XX 18-FEB-2000; 2000WO-JP000941.
XX
XX 19-FEB-1999; 99JP-00041535.

XX (SUME) SUMITOMO ELECTRIC IND CO.
PA
XX
XX Shinbara N, Udono H, Yui K;

XX WPI; 2000-543748/49.
XX
XX Fused protein capable of inducing cellular immune response, useful as
PT active ingredient for drug compositions in preventing and/or treating
PT infectious diseases such as malaria or cancer.

XX Claim 3; Page 46-48; 72pp; Japanese.
XX
XX The present invention describes a fused protein (I) prepared from a
CC peptide containing a CTL (cytotoxic T lymphocyte) epitope recognised by
CC cytotoxic T cells and a protein containing the ATPase domain of a heat
CC shock protein. Also described are: (1) a drug composition containing (I)
CC as active ingredient; (2) a DNA encoding (I); (3) an expression vector
CC containing the DNA of (2); and (4) a transformant which can retain the
CC expression vector of (3). (I) has cytostatic, immunostimulant and
CC protozoaside activities, and can be used as a cellular immune response
CC inducer. The protein is useful as an active ingredient for drug
CC compositions in preventing and/or treating infectious diseases such as
CC malaria or cancer e.g. to provide systemic immunity against leukaemia.

CC The present sequence represents a specifically claimed heat shock protein
CC for use in a fused protein of the present invention
XX
SQ Sequence 641 AA;

Query Match 100.0%; Score 1314; DB 3; Length 641;
Best Local Similarity 100.0%; Pred. No. 8.8e-101;
Matches 258; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KSENVQDILLDDVAPLSGLGTAGGVTALIKRNSTIPTKTQITFTYSDNQPGVLIQVY 60
DB 384 KSENVQDILLDDVAPLSGLGTAGGVTALIKRNSTIPTKTQITFTYSDNQPGVLIQVY 443

QY 61 EGERAMTKDNNLLGRFELSGIPPPAPRGVPQIEVTFDIDANGILNVTATDKSTGKANKITI 120
DB 444 EGERAMTKDNNLLGRFELSGIPPPAPRGVPQIEVTFDIDANGILNVTATDKSTGKANKITI 503

QY 121 TNDKRLSKBEIERMVQAEKYKAEDVQERVSAKNALESYAFNMKSAVEDGLGKGIS 180
DB 504 TNDKRLSKBEIERMVQAEKYKAEDVQERVSAKNALESYAFNMKSAVEDGLGKGIS 563

QY 181 EADKKVLDKQCVISWLDANTLAEDFEHKKKELEQVNCNPIISGLYQAGGPGGPG 240
 DB 564 EADKKVLDKQCVISWLDANTLAEDFEHKKKELEQVNCNPIISGLYQAGGPGGPG 623

QY 241 AQPCKGSGSGPTIEVD 258
 DB 624 AQPCKGSGSGPTIEVD 641

RESULT 3
 AAB82534
 ID AAB82534 standard; protein; 641 AA.
 XX
 AC AAB82534;
 XX
 DT 17-SEP-2001 (first entry)
 XX
 DE Human heat shock protein Hsp71.
 XX
 KW Hsp71; human; heat shock protein; immunotherapy; therapy; cancer;
 KW infection; vaccine.
 KW
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT Binding-site 391..615
 FT /note= "peptide-binding domain"
 FT Region 395..502
 FT /note= "beta-helix motif"
 FT Binding-site 400..440
 FT /note= "peptide-binding core"
 XX
 XX WO200152791-A2.
 PN
 XX
 PD 26-JUL-2001.
 XX
 PF 18-JAN-2001; 2001WO-US0001781.
 XX
 PR 20-JAN-2000; 2000US-00488393.
 XX
 PA (UYCO-) UNIV CONNECTICUT HEALTH CENT.
 XX
 PI Srivastava PK;
 XX
 XX WPI; 2001-457506/49.
 DR
 XX
 PT Pharmaceutical composition, used to treat or prevent infection or cancer,
 PT comprises a complex comprising a heat shock protein-binding fragment
 PT associated with a molecule displaying antigenicity of an infectious agent
 PT or cancer cell.
 XX
 PS Claim 46; Fig 1C; 106pp; English.
 XX
 CC The present sequence is that of human heat shock protein (HSP) Hsp71, an
 CC inducible form of a Hsp70 family protein. The invention relates to
 CC complexes of peptide-binding fragments of HSPs with antigenic molecules
 CC and their use in immunotherapy for the treatment of infectious diseases
 CC and cancer. Claimed methods of treating or preventing cancer/infectious
 CC disease involve culturing a cancer cell/infected cell transformed with a
 CC nucleic acid encoding a HSP peptide-binding domain, recovering complexes
 CC of the HSP fragments noncovalently associated with peptides from the
 CC cancer cell/infected cell, and administering the recovered complexes.
 CC These methods can use Hsp71 peptide-binding fragments comprising amino
 CC acids 391-615 and 400-440 of the present sequence, i.e. the peptide-
 CC binding domain and peptide-binding core
 XX
 SQ Sequence 641 AA;
 Query Match 100.0%; Score 1314; DB 4; Length 641;
 Best Local Similarity 100.0%; Pred. No. 8.8e-101;
 Matches 258; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KSENVQDLLLDDVAPLSLGLTAGVMTALIKRNSTIPTKQTQIFTTSDNQFGLIQVY 60

DB 384 KSENVQDLLLDDVAPLSLGLTAGVMTALIKRNSTIPTKQTQIFTTSDNQFGLIQVY 443
 QY 61 EGERAMTKDNLLGRFELSGIPAPRGVQIEVTFDIDANGILNVTATDKSTGKANKITI 120
 DB 444 EGERAMTKDNLLGRFELSGIPAPRGVQIEVTFDIDANGILNVTATDKSTGKANKITI 503
 QY 121 TNDKGRLSKEEIERMVQEAKEYKAEDVQERVSAAKNALESYAFNMKSAVEDSGLGKIS 180
 DB 504 TNDKGRLSKEEIERMVQEAKEYKAEDVQERVSAAKNALESYAFNMKSAVEDSGLGKIS 563
 QY 181 EADKKVLDKQCVISWLDANTLAEDFEHKKKELEQVNCNPIISGLYQAGGPGGPG 240
 DB 564 EADKKVLDKQCVISWLDANTLAEDFEHKKKELEQVNCNPIISGLYQAGGPGGPG 623

QY 241 AQPCKGSGSGPTIEVD 258
 DB 624 AQPCKGSGSGPTIEVD 641

RESULT 4
 AAE12986
 ID AAE12986 standard; protein; 641 AA.
 XX
 AC AAE12986;
 XX
 DT 28-JAN-2002 (first entry)
 XX
 DE Human Hsp70 family homologue, Hsp71.
 XX
 KW Heat shock protein; HSP; HSP peptide-binding fragment; HSPB; vaccine;
 KW cytotoxic T cell response; hepatitis virus; herpes simplex virus;
 KW human immunodeficiency virus; bacteria; Mycobacteria; Rickettsia;
 KW protozoa; Leishmani; Trypanosoma; intracellular parasite; Chlamydia;
 KW sarcoma; carcinoma; cancer; human; Hsp70 homologue; Hsp71.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT Binding-site 391..615
 FT /note= "peptide binding domain"
 FT Binding-site 396..502
 FT /note= "p-helix motif"
 FT Domain 402..442
 FT /note= "Central core of peptide binding domain"
 XX
 XX US2001034042-A1.
 PN
 XX
 PD 25-OCT-2001.
 XX
 PF 12-JAN-2001; 2001US-00759010.
 XX
 PR 20-JAN-2000; 2000US-00488393.
 XX
 XX (SRIV/) SRIVASTAVA P K.
 XX
 XX Srivastava PK;
 XX
 XX WPI; 2001-656559/75.
 XX
 XX Vaccine compositions for vaccinating against cancers and infections,
 XX comprises peptide-binding fragments (PBPs) of heat shock proteins (HSPs)
 XX PT and non-covalent complexes of PBPs of HSPs and antigenic molecules.
 XX
 XX Disclosure; Fig 1C; 39pp; English.
 XX
 CC The invention relates to pharmaceutical compositions comprising peptide
 CC binding fragments of heat shock proteins (HSPs) and non-covalent
 CC complexes of HSP peptide-binding fragments (HSPB) in non-covalent
 CC association with antigenic molecules. Vaccines comprising peptide
 CC fragments of the invention may be used to stimulate an immune response,
 CC in particular cytotoxic T cell responses against cells infected with
 CC viruses (including hepatitis type A, B and C, influenza, varicella,

CC adenovirus, herpes simplex (HSV) type I and type II, rinderpest
CC rhinovirus, echovirus, rotavirus, respiratory syncytial virus, mumps
CC virus, papova virus, papilloma virus, arbovirus, cytomegalovirus,
CC echinovirus, hantavirus, coxsackie virus, measles virus, rubella virus,
CC polio virus, HIV-I, and HIV-II; bacteria including (including
CC Mycobacteria, Rickettsia, Mycoplasma, Neisseria and Legionella); protozoa
CC (including Leishmania, Kokzidioa and Trypanosoma) and intracellular
CC parasites (including Chlamydia and Rickettsia). The vaccines may be used
CC to treat cancers such as human sarcomas and carcinomas, pancreatic
CC cancer, breast cancer, ovarian cancer, prostate cancer, squamous cell
CC carcinoma, basal cell carcinoma, adenocarcinoma, sweat gland carcinoma,
CC sebaceous gland carcinoma, papillary carcinoma, papillary
CC adenocarcinomas, medullary carcinoma, cystadenocarcinoma, bronchogenic
CC carcinoma, renal cell carcinoma, hepatoma, bile duct carcinoma,
CC choriocarcinoma, seminoma and embryonal carcinoma. The present sequence
CC is human Hsp70 family homologue, Hsp71
XX
SQ Sequence 641 AA;

Query Match 100.0%; Score 1314; DB 4; Length 641;
Best Local Similarity 100.0%; Pred. No. 8.8e-101;
Matches 258; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 KSENVODLLLDVAPLSGLGLETAGGVMTALIKRNSTIPTKQTQIFTTYSNDQPGVLIQVY 60
DB 384 KSENVODLLLDVAPLSGLGLETAGGVMTALIKRNSTIPTKQTQIFTTYSNDQPGVLIQVY 443
QY 61 EGERAMTKONNLLGRFELSGIPAPRGVQPIEVTFDIDANGILNVTTATDKSTGKANKITI 120
DB 444 EGERAMTKONNLLGRFELSGIPAPRGVQPIEVTFDIDANGILNVTTATDKSTGKANKITI 503
QY 121 TNDKGRLSKEEIERMWQEAKEYKAEDVQERVSNAKNALESYAFNMKSAVEDGLGKGIS 180
DB 504 TNDKGRLSKEEIERMWQEAKEYKAEDVQERVSNAKNALESYAFNMKSAVEDGLGKGIS 563
QY 181 EADKKVLDKQCEVISWLDANTLAEKDEFEHKKRKELEQVCNPIISGLYQAGGPGGFG 240
DB 564 EADKKVLDKQCEVISWLDANTLAEKDEFEHKKRKELEQVCNPIISGLYQAGGPGGFG 623
QY 241 AQPKGGSGSGPTIEVD 258
DB 624 AQPKGGSGSGPTIEVD 641

RESULT 5
ABU89711
ID ABU89711 standard; protein; 641 AA.
XX
AC ABU89711;
XX
DT 10-JUL-2003 (first entry)
XX
DE Protein differentially expressed in cardiovascular disease #5.
XX
KW Cardiovascular disease; arteriosclerosis; ischaemia; angina pectoris;
KW myocardial infarction; cardiast; antiarteriosclerotic; antianginal;
KW gene therapy; differential gene expression.
XX
OS Homo sapiens.
XX
PN WO2003031650-A2.
XX
PD 17-APR-2003.
XX
PF 02-OCT-2002; 2002WO-EP011034.
XX
PR 08-OCT-2001; 2001GB-00024145.
XX
PA (FARB) BAYER AG.
XX
PI Munnes M, Gehrmann M, Wick M, Schmitz G;
XX WPI; 2003-403108/38.
DR

DR N-PSDB; ACA89884.
XX
PT Predicting, diagnosing or prognosing a cardiovascular disease, e.g.
PT angina, ischemia, myocardial infarction or arteriosclerosis by detection
PT of a polynucleotide in a biological sample comprises detecting a
PT hybridization complex.
XX
PS Claim 3; Page 260-263; 454pp; English.
XX
CC The invention describes a method of predicting, diagnosing or prognosing
CC a cardiovascular disease by detection of a polynucleotide in a biological
CC sample comprises hybridising at least one of the polynucleotide to a
CC nucleic acid material of a biological sample, thus forming a
CC hybridisation complex, and detecting the hybridisation complex. The
CC polynucleotides, polypeptides, antisense molecule, antibody and reagent
CC are useful for preparing compositions for preventing, predicting or
CC diagnosing, or a medicament for treating a cardiovascular disease, e.g.
CC arteriosclerosis, ischaemia, angina pectoris, or myocardial infarction.
CC This sequence represents a protein identified in the invention a being
CC differentially expressed in individuals with cardiovascular disease
XX
SQ Sequence 641 AA;

Query Match 100.0%; Score 1314; DB 6; Length 641;
Best Local Similarity 100.0%; Pred. No. 8.8e-101;
Matches 258; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 KSENVODLLLDVAPLSGLGLETAGGVMTALIKRNSTIPTKQTQIFTTYSNDQPGVLIQVY 60
DB 384 KSENVODLLLDVAPLSGLGLETAGGVMTALIKRNSTIPTKQTQIFTTYSNDQPGVLIQVY 443
QY 61 EGERAMTKONNLLGRFELSGIPAPRGVQPIEVTFDIDANGILNVTTATDKSTGKANKITI 120
DB 444 EGERAMTKONNLLGRFELSGIPAPRGVQPIEVTFDIDANGILNVTTATDKSTGKANKITI 503
QY 121 TNDKGRLSKEEIERMWQEAKEYKAEDVQERVSNAKNALESYAFNMKSAVEDGLGKGIS 180
DB 504 TNDKGRLSKEEIERMWQEAKEYKAEDVQERVSNAKNALESYAFNMKSAVEDGLGKGIS 563
QY 181 EADKKVLDKQCEVISWLDANTLAEKDEFEHKKRKELEQVCNPIISGLYQAGGPGGFG 240
DB 564 EADKKVLDKQCEVISWLDANTLAEKDEFEHKKRKELEQVCNPIISGLYQAGGPGGFG 623
QY 241 AQPKGGSGSGPTIEVD 258
DB 624 AQPKGGSGSGPTIEVD 641

RESULT 6
ADD47459
ID ADD47459 standard; protein; 641 AA.
XX
AC ADD47459;
XX
DT 02-DEC-2004 (revised)
DT 29-JAN-2004 (first entry)
XX
DE Human Protein AAA52697, SEQ ID NO 13154.
XX
KW Human; pain; neuronal tissue; gene therapy;
KW spinal segmental nerve injury; chronic constriction injury; CCI;
KW spared nerve injury; SNI; Chung.
XX
OS Homo sapiens.
OS Unidentified.
XX
PN WO2003016475-A2.
XX
PD 27-FEB-2003.
XX
PF 14-AUG-2002; 2002WO-US025765.
XX
PR 14-AUG-2001; 2001US-0312147P.

PR 01-NOV-2001; 2001US-0346382P.
 XX 26-NOV-2001; 2001US-0333347P.
 PA (GEOH) GEN HOSPITAL CORP.
 PA (FARB) BAYER AG.
 XX
 PI Woolf C, D'urso D, Befort K, Costigan M;
 XX
 XX WPI; 2003-268312/26.
 DR GENBANK; AAA52697.
 XX
 XX
 PT New composition comprising two or more isolated polypeptides, useful for
 PT preparing a medicament for treating pain in an animal.
 XX
 XX
 PS Example 1; Page: 1017pp; English.

XX The invention discloses a composition comprising two or more isolated rat
 CC or human polynucleotides or a polynucleotide which represents a fragment,
 CC derivative or allelic variation of the nucleic acid sequence. Also
 CC claimed are a vector comprising the novel polynucleotide, a host cell
 CC comprising the vector, a method for identifying a nucleotide sequence
 CC which is differentially regulated in an animal subjected to pain and a
 CC kit to perform the method, an array, a method for identifying an agent
 CC that increases or decreases the expression of the polynucleotide sequence
 CC that is differentially expressed in neuronal tissue of a first animal
 CC subjected to pain, a method for identifying a compound which regulates
 CC the expression of a polynucleotide sequence which is differentially
 CC expressed in an animal subjected to pain, a method for identifying a
 CC compound that regulates the activity of one or more of the
 CC polynucleotides, a method for producing a pharmaceutical composition, a
 CC method for identifying a compound or small molecule that regulates the
 CC activity in an animal of one or more of the polypeptides given in the
 CC specification, a method for identifying a compound useful in treating
 CC pain and a pharmaceutical composition comprising the one or more
 CC polypeptides or their antibodies. The polynucleotide or the compound that
 CC modulates its activity is useful for preparing a medicament for treating
 CC pain (e.g. spinal segmental nerve injury (Chung), chronic constriction
 CC injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene
 CC therapy). The sequence presented is a human protein (described in Table 3
 CC of the specification) which is differentially expressed during pain.
 CC Note: The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic form directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences.

ID ADJ27279 standard; protein; 641 AA.

XX ADJ27279;

DT 20-MAY-2004 (first entry)

XX Human HSP70.1.

XX heat shock protein-70; HSP70; HSP70.1; HSP70.3; inducible; induction;
 KW heat; tumour necrosis factor; TNF; interferon-gamma; tumour.

OS Homo sapiens.

XX WO2003061684-A2.

PN 31-JUL-2003.

XX 24-JAN-2003; 2003WO-EP000786.

XX 24-JAN-2002; 2002EP-00075297.

XX (VLA-) VLAAMS INTERUNIVERSITAIR INST BIOTECHNOG.

XX Libert C, Wielockx B, Van Molle W, Mahieu T;

XX WPI; 2003-608168/57.

DR N-PSDB; ADJ27278.

XX New pharmaceutical composition comprising HSP70 that is endogenously
 PT induced by heat and TNF, useful for the manufacture of a medicament for
 PT treating systemic tumor.

PS Disclosure; SEQ ID NO 6; 53pp; English.

XX This sequence represents human heat shock protein-70.1 (HSP70.1). HSP70.1
 CC and HSP70.3 are inducible members of the HSP70 family of proteins. The
 CC heat shock proteins of the invention are endogenously induced by heat and
 CC tumour necrosis factor (TNF). This heat shock protein may be used in a
 CC composition which further comprises interferon-gamma, and/or a
 CC chemotherapeutic compound. The pharmaceutical composition is useful for
 CC the manufacture of a medicament for treating systemic tumour.

XX Sequence 641 AA;

Query Match 100.0%; Score 1314; DB 7; Length 641;

Best Local Similarity 100.0%; Pred. No. 8.8e-101;

Matches 258; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KSENVODLLLDVAPLSLGLTAGGVTALIKENSTIPTKQTQIFFTYSDNQPGVLIQVY 60

DB 384 KSENVODLLLDVAPLSLGLTAGGVTALIKENSTIPTKQTQIFFTYSDNQPGVLIQVY 443

QY 61 EGERAMTKONNLLGRFELSGIPAPRGVPOIEVTFDIDANGILNVTATDKSTGKANKITI 120

DB 444 EGERAMTKONNLLGRFELSGIPAPRGVPOIEVTFDIDANGILNVTATDKSTGKANKITI 503

QY 121 TNDKGRLSKEEIERMWQAEKYAEDEVQERVSNAKNALESYAFNMKSAVEDEGLGKIS 180

DB 504 TNDKGRLSKEEIERMWQAEKYAEDEVQERVSNAKNALESYAFNMKSAVEDEGLGKIS 563

QY 181 EADKKVKLDKQCEVISWLDANTLAEKDFEHEKKELEQVCNPIISGLYQAGGPGGFG 240

DB 564 EADKKVKLDKQCEVISWLDANTLAEKDFEHEKKELEQVCNPIISGLYQAGGPGGFG 623

QY 241 AOGPKGGSGGPTIEVD 258

DB 624 AOGPKGGSGGPTIEVD 641

RESULT 8

ADE76981

ID ADE76981 standard; protein; 641 AA.

XX

Query Match 100.0%; Score 1314; DB 7; Length 641;

Best Local Similarity 100.0%; Pred. No. 8.8e-101;

Matches 258; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KSENVODLLLDVAPLSLGLTAGGVTALIKENSTIPTKQTQIFFTYSDNQPGVLIQVY 60

DB 384 KSENVODLLLDVAPLSLGLTAGGVTALIKENSTIPTKQTQIFFTYSDNQPGVLIQVY 443

QY 61 EGERAMTKONNLLGRFELSGIPAPRGVPOIEVTFDIDANGILNVTATDKSTGKANKITI 120

DB 444 EGERAMTKONNLLGRFELSGIPAPRGVPOIEVTFDIDANGILNVTATDKSTGKANKITI 503

QY 121 TNDKGRLSKEEIERMWQAEKYAEDEVQERVSNAKNALESYAFNMKSAVEDEGLGKIS 180

DB 504 TNDKGRLSKEEIERMWQAEKYAEDEVQERVSNAKNALESYAFNMKSAVEDEGLGKIS 563

QY 181 EADKKVKLDKQCEVISWLDANTLAEKDFEHEKKELEQVCNPIISGLYQAGGPGGFG 240

DB 564 EADKKVKLDKQCEVISWLDANTLAEKDFEHEKKELEQVCNPIISGLYQAGGPGGFG 623

QY 241 AOGPKGGSGGPTIEVD 258

DB 624 AOGPKGGSGGPTIEVD 641

RESULT 7

ADJ27279

AC	ADE76981;
XX	
DT	29-JAN-2004 (first entry)
XX	
DE	Human protein expressed in a liver disorder #42.
XX	
KW	human; liver disorder; hyperlipidaemia; hypertension; type II diabetes;
KW	tumour; liver; inflammatory disorder; immune response disorder;
KW	high-throughput screening; differential gene expression; gene therapy.
OS	Homo sapiens.
PN	US2003108871-A1.
PD	12-JUN-2003.
PF	30-JUL-2001; 2001US-00919039.
PR	28-JUL-2000; 2000US-0222113P.
PA	(KASE/) KASER M R.
PI	Kaser MR;
DR	WPI; 2004-031227/03.
XX	N-PSDB; ADE76980.
PT	Composition comprising several cDNAs that are differentially expressed in
PT	treated human C3A liver cell cultures, useful for treating liver
PT	disorders.
PS	Claim 1; SEQ ID NO 146; 4lpp; English.
XX	
CC	The invention relates to a composition comprising several cDNAs that are
CC	differentially expressed in a liver disorder. The composition is useful
CC	for treating liver disorder such as hyperlipidaemia, hypertension, type
CC	II diabetes, tumours of the liver and disorders of the inflammatory and
CC	immune response. The composition is useful for a high-throughput method
CC	of screening several molecules or compounds to identify a ligand which
CC	specifically binds a cDNA. A protein encoded by the cDNA is useful for a
CC	high-throughput method for using a protein to screen several molecules or
CC	compounds to identify at least one ligand which specifically binds the
CC	protein which involves combining the protein encoded by the cDNA with
CC	several of molecules or compounds under conditions to allow specific
CC	binding, and detecting specific binding between the protein and a
CC	molecule or compound, therefore identifying a ligand which specifically
CC	binds the protein. The composition is useful for detecting and
CC	quantifying differential gene expression, can be used in gene therapy, to
CC	formulate prognosis and to design a treatment regimen and to monitor the
CC	efficacy of treatment. The present sequence represents the amino acid
CC	sequence of a protein encoded by a cDNA differentially expressed in a
CC	liver disorder.
XX	
SQ	Sequence 641 AA; Query Match 100.0%; Score 1314; DB 8; Length 641; Best Local Similarity 100.0%; Pred. No. 8.8e-101; Matches 259; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy	1 KSENVQDLLLDVAPLSGLTETAGGVTALIKRNSITPTKTQTFTTSDNPQGVLIQY 60
Db	384 KSENVQDLLLDVAPLSGLTETAGGVTALIKRNSITPTKTQTFTTSDNPQGVLIQY 443
Qy	61 EGERAMTKNNLGRFELSGIPAPRGVQIEVTFDIDANGILNTATDKSTGKANKITI 120
Db	444 EGERAMTKNNLGRFELSGIPAPRGVQIEVTFDIDANGILNTATDKSTGKANKITI 503
Qy	121 TNDKGRSLKEEIERMVOAEKYKAEDVQRVSAAKNALESYAFNMKSADVEGLKGKIS 180
Db	504 TNDKGRSLKEEIERMVOAEKYKAEDVQRVSAAKNALESYAFNMKSADVEGLKGKIS 563
Qy	181 EADKKVKLDRCQEVISWLDAANTLAEDFEHRRKKELEVCNPIISGLYQAGGPGGPG 240

QY 61 EGERAMTKONNLLGRFELSGIPAPRGVPOIEVTFDIDANGILNVTATDKSTGKANKITI 120
 DB 444 EGERAMTKONNLLGRFELSGIPAPRGVPOIEVTFDIDANGILNVTATDKSTGKANKITI 503
 QY 121 TNDKGRLSKEIEIRMQEAEKYAEDEVQERVSANNALESYAFNMKSAVEDSLGKGKIS 180
 DB 504 TNDKGRLSKEIEIRMQEAEKYAEDEVQERVSANNALESYAFNMKSAVEDSLGKGKIS 563
 QY 181 EADKKVLDKQEVISWLDANTLAEKDEFEHKKKELEQVCNPIISGLYQAGGPGGPGF 240
 DB 564 EADKKVLDKQEVISWLDANTLAEKDEFEHKKKELEQVCNPIISGLYQAGGPGGPGF 623
 QY 241 AQPCKGSGSGPTIEVD 258
 DB 624 AQPCKGSGSGPTIEVD 641

RESULT 10
 ABM80760
 ID ABM80760 standard; protein; 641 AA.
 XX
 AC ABM80760;
 XX
 DT 18-NOV-2004 (first entry)
 XX
 DE Tumour-associated antigenic target (TAT) polypeptide PRO71095, SEQ:1964.
 XX
 KW Tumour-associated antigenic target; TAT; human; overexpression; cancer;
 KW tumour; diagnosis; cell proliferative disorder; breast cancer;
 KW colorectal cancer; lung cancer; ovarian cancer; liver cancer;
 KW central nervous system cancer; bladder cancer; pancreatic cancer;
 KW cervical cancer; melanoma; leukaemia; hybridisation probe;
 KW chromosome identification; chromosome mapping; gene mapping;
 KW gene therapy; cytostatic.
 XX
 OS Homo sapiens..
 XX
 PN WO2004030615-A2.
 XX
 PD 15-APR-2004.
 XX
 PF 29-SEP-2003; 2003WO-US028547.
 XX
 PR 02-OCT-2002; 2002US-0414971P.
 XX
 PA (GETH) GENENTECH INC.
 XX
 PI Wu TD, Zhang Z, Zhou Y;
 XX
 DR WPI; 2004-347921/32.
 DR N-PSDB; ACN38447.
 XX
 PT New tumor-associated antigenic target polypeptides and nucleic acids,
 PT useful in preparing a medicament for treating or detecting a
 PT proliferative disorder, e.g. breast, lung, colorectal, ovarian or
 PT prostate cancer or tumor.
 XX
 PS Claim 12; SEQ ID NO 1964; 7273pp; English.
 XX
 CC The invention relates to human tumour-associated antigenic target (TAT)
 CC polypeptides, and their related nucleic acids. The TAT polypeptides are
 CC overexpressed in cancer tissues compared to normal tissues, and may thus
 CC serve as effective targets for the diagnosis and treatment of cancer in
 CC mammals. The invention also relates to nucleic acid and polypeptide
 CC sequences at least 80% identical to the TAT nucleic acids and
 CC polypeptides; expression vectors and host cells comprising a TAT nucleic
 CC acid; an antibody specific for a TAT polypeptide; a peptide or organic
 CC molecule which binds to a TAT polypeptide; fusion proteins comprising a
 CC TAT polypeptide; and methods and compositions for the treatment or
 CC diagnosis of cancer in mammals. TAT polypeptides, nucleic acids,
 CC antibodies, antagonists, binding molecules and compositions are useful
 CC for diagnosing or treating a cell proliferative disorder associated with
 CC increased TAT expression, particularly cancers such as breast cancer,

CC colorectal cancer, lung cancer, ovarian cancer, liver cancer, bladder
 CC cancer, pancreatic cancer, cervical cancer, cancers of the central
 CC nervous system, melanoma and leukaemia. TAT nucleic acids may further be
 CC used as hybridisation probes, in chromosome and gene mapping, in
 CC chromosome identification and in gene therapy. The present sequence
 CC represents a TAT polypeptide of the invention
 XX
 SQ Sequence 641 AA;
 Query Match 100.0%; Score 1314; DB 8; Length 641;
 Best Local Similarity 100.0%; Pred. No. 8.8e-101; Indels 0; Gaps 0;
 Matches 258; Conservative 0; Mismatches 0;
 QY 1 KSENVQDLLLLDVAPLSGLTAGGVTALIKENSTIPTKQTQIFTTYSNQPGVLQVY 60
 DB 384 KSENVQDLLLLDVAPLSGLTAGGVTALIKENSTIPTKQTQIFTTYSNQPGVLQVY 443
 QY 61 EGERAMTKONNLLGRFELSGIPAPRGVPOIEVTFDIDANGILNVTATDKSTGKANKITI 120
 DB 444 EGERAMTKONNLLGRFELSGIPAPRGVPOIEVTFDIDANGILNVTATDKSTGKANKITI 503
 QY 121 TNDKGRLSKEIEIRMQEAEKYAEDEVQERVSANNALESYAFNMKSAVEDSLGKGKIS 180
 DB 504 TNDKGRLSKEIEIRMQEAEKYAEDEVQERVSANNALESYAFNMKSAVEDSLGKGKIS 563
 QY 181 EADKKVLDKQEVISWLDANTLAEKDEFEHKKKELEQVCNPIISGLYQAGGPGGPGF 240
 DB 564 EADKKVLDKQEVISWLDANTLAEKDEFEHKKKELEQVCNPIISGLYQAGGPGGPGF 623
 QY 241 AQPCKGSGSGPTIEVD 258
 DB 624 AQPCKGSGSGPTIEVD 641

RESULT 11
 ADI20102
 ID ADI20102 standard; protein; 641 AA.
 XX
 AC ADI20102;
 XX
 DT 22-APR-2004 (first entry)
 XX
 DE Hsp70.
 XX
 KW Inducible heat shock protein; Hsp70; constitutive heat shock protein;
 KW Hsc70; human leukocyte antigen; HLA.
 XX
 OS Unidentified.
 XX
 PN WO2003029288-A2.
 XX
 PD 10-APR-2003.
 XX
 PF 26-SEP-2002; 2002WO-EP010821.
 XX
 PR 27-SEP-2001; 2001EP-00402496.
 XX
 PA (IDMI-) IDM IMMUNO-DESIGNED MOLECULES.
 PA (INSR) INST ROUSSY GUSTAVE.
 PA (INRM) INSERM.
 XX
 PI Faure O, Kosmatopoulos K;
 DR WPI; 2003-449139/42.
 XX
 PT Novel peptide derived from inducible heat shock protein Hsp70, useful for
 PT inducing cytotoxic T lymphocyte response that targets cells expressing
 PT inducible Hsp70, and for preparing drugs for treating cancer.
 XX
 PS Disclosure; SEQ ID NO 1; 49pp; English.
 XX
 CC The present invention relates to a peptide comprising a sequence of at
 CC least 8 contiguous amino acids, having at least 65 % identity to a

CC portion inducible heat shock protein (Hsp)-70 sequence, differing from a
 CC sequence of constitutive heat shock protein Hsc70 by at least one amino
 CC acid, and capable of inducing cytotoxic T lymphocytes that specifically
 CC recognize cells naturally producing inducible Hsp70, in vitro or in vivo.
 CC The peptides are stable, and has high affinity for human leukocyte
 CC antigen (HLA) class I molecules. The present sequence represents Hsp 70.
 CC
 XX
 SQ Sequence 641 AA;

Query Match 99.8%; Score 1312; DB 7; Length 641;
 Best Local Similarity 99.6%; Pred. No. 1.3e-100;
 Matches 257; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KSENVQDLLLLDVAPLSGLGTAGGVTALIKENSTPTKQTFPTTYSNQPGLVLIQVY 60
 DB 384 KSENVQDLLLLDVAPLSGLGTAGGVTALIKENSTPTKQTFPTTYSNQPGLVLIQVY 443
 QY 61 EGERAMTKNNLLGRFELSGIPAPRGVPOIEVTFDIDANGILNVTATDKSTGKANKITI 120
 DB 444 EGERAMTKNNLLGRFELSGIPAPRGVPOIEVTFDIDANGILNVTATDKSTGKANKITI 503
 QY 121 TNDKGRLSKEEIERMVQEAKEYKADEVORERSAKNALESYAFNMKSAVEDGLKGIKIS 180
 DB 504 TNDKGRLSKEEIERMVQEAKEYKADEVORERSAKNALESYAFNMKSAVEDGLKGIKIS 563
 QY 181 EADKKKVLDKCOEIVISWLDANTLAEDKDEFEHKKRKELEQVNCNPIISGLYQAGGPGGFG 240
 DB 564 EADKKKVLDKCOEIVISWLDANTLAEDKDEFEHKKRKELEQVNCNPIISGLYQAGGPGGFG 623
 QY 241 AQGPKGGSGSGPTIEEVD 258
 DB 624 AQGPKGGSGSGPTIEEVD 641

RESULT 12
 ADM04781
 ID ADM04781 standard; protein; 476 AA.
 AC ADM04781;
 XX
 XX 20-MAY-2004 (first entry)
 XX Human protein of the invention SEQ ID NO:3466.
 XX human; gene therapy; diagnostic marker; pharmaceutical.
 XX Homo sapiens.
 XX EPI347046-A1.
 XX
 XX 24-SEP-2003.
 XX
 XX 12-APR-2002; 2002EP-00008400.
 XX
 XX 22-MAR-2002; 2002JP-00137785.
 XX (REAS-) RES ASSOC BIOTECHNOLOGY.
 XX
 XX Isogai T, Sugiyama T, Otsuki T, Wakamatsu A, Sato H, Ishii S;
 XX Yamamoto J, Isono Y, Hio Y, Otsuka K, Nagai K, Irie R, Tamechika I;
 XX Seki N, Yoshikawa T, Otsuka M, Nagahara K, Masuho Y;
 XX WPI; 2003-723558/69.
 XX N-PSDB; ADM02338.
 XX
 XX New polynucleotides and polypeptides are useful in gene therapy, for
 XX developing a diagnostic marker or medicines for regulating their
 XX expression and activity, or as a target of gene therapy.
 XX
 XX Claim 1; SEQ ID NO 3466; 305pp; English.
 XX
 XX The invention relates to a novel human polynucleotide and the encoded
 XX polypeptide. A polynucleotide of the invention may have a use in gene

CC therapy. An oligonucleotide of the invention ADM06202-ADM06773 is useful
 CC as a primer for synthesizing the polynucleotide or as a probe for
 CC detecting the polynucleotide. The polynucleotides ADM01316-ADM03758 are
 CC useful in gene therapy, for developing a diagnostic marker or medicines
 CC for regulating their expression and activity, or as a target of gene
 CC therapy. The proteins ADM03759-ADM06201 encoded by the polynucleotides
 CC are useful as pharmaceutical agents. The present sequence represents a
 CC protein sequence of the invention.
 CC
 XX
 SQ Sequence 476 AA;

Query Match 99.6%; Score 1309; DB 7; Length 476;
 Best Local Similarity 99.6%; Pred. No. 1.6e-100;
 Matches 257; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KSENVQDLLLLDVAPLSGLGTAGGVTALIKENSTPTKQTFPTTYSNQPGLVLIQVY 60
 DB 219 KSENVQDLLLLDVAPLSGLGTAGGVTALIKENSTPTKQTFPTTYSNQPGLVLIQVY 278
 QY 61 EGERAMTKNNLLGRFELSGIPAPRGVPOIEVTFDIDANGILNVTATDKSTGKANKITI 120
 DB 279 EGERAMTKNNLLGRFELSGIPAPRGVPOIEVTFDIDANGILNVTATDKSAGKANKITI 338
 QY 121 TNDKGRLSKEEIERMVQEAKEYKADEVORERSAKNALESYAFNMKSAVEDGLKGIKIS 180
 DB 339 TNDKGRLSKEEIERMVQEAKEYKADEVORERSAKNALESYAFNMKSAVEDGLKGIKIS 398
 QY 181 EADKKKVLDKCOEIVISWLDANTLAEDKDEFEHKKRKELEQVNCNPIISGLYQAGGPGGFG 240
 DB 399 EADKKKVLDKCOEIVISWLDANTLAEDKDEFEHKKRKELEQVNCNPIISGLYQAGGPGGFG 458
 QY 241 AQGPKGGSGSGPTIEEVD 258
 DB 459 AQGPKGGSGSGPTIEEVD 476

RESULT 13
 ABR40400
 ID ABR40400 standard; protein; 641 AA.
 AC ABR40400;
 XX
 XX 08-AUG-2003 (first entry)
 XX Human Hsp70 protein.
 XX heat shock protein; Hsp; cytokine; CC chemokine; nitric oxide; cancer;
 XX antimicrobial; virucide; cytostatic; microbial infection; anti-HIV;
 XX viral infection; immune system disorder; vaccine; HSP70; human.
 XX Homo sapiens.
 XX WO2003029289-A2.
 XX
 XX 10-APR-2003.
 XX
 XX 03-OCT-2002; 2002WO-GB004475.
 XX
 XX 03-OCT-2001; 2001GB-00023756.
 XX (UNLO) KINGS COLLEGE LONDON.
 XX
 XX Lehner T, Kelly CG, Singh M, Wang Y;
 XX WPI; 2003-430189/40.
 XX
 XX Novel heat shock protein fragment useful for treating microbial
 XX infection, viral infection or cancer, that can increase the level of
 XX cytokines and/or CC chemokines and/or nitric oxide produced by a cell.
 XX
 XX Example 3; Page 17-20; 30pp; English.
 XX
 XX The invention relates to a novel heat shock protein fragment (HSP) that

CC can increase the level of one or more cytokines and/or one or more CC
CC chemokines and/or nitric oxide produced by a cell, above that caused by
CC the corresponding full length heat shock protein. The protein fragment of
CC the invention has antimicrobial, virucide, and cytostatic activity. The
CC protein fragment is useful in therapy, in treatment or prophylaxis of a
CC disease and in the manufacture of a medicament for treatment or
CC prophylaxis of a disease such as microbial infection, viral infection,
CC disease of the immune system or cancer. The fragment is also useful as an
CC adjuvant in vaccines, preferably, anti-HIV vaccines. The present sequence
CC represents the human HSP70 protein
XX
SQ Sequence 641 AA;

Query Match 99.6%; Score 1309; DB 6; Length 641;
Best Local Similarity 99.6%; Pred. No. 2.3e-100;
Matches 257; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 KSENVQDLLLDVAPLSGLGTAGGVMTALIKRNSITPTKQTQITFTTYSNQPGVLIQVY 60
DB 384 KSENVQDLLLDVAPLSGLGTAGGVMTALIKRNSITPTKQTQITFTTYSNQPGVLIQVY 443
QY 61 EGERAMTKONNLGRFELSGIPAPRGVPQIEVTFDIDANGILNVATDKSTGKANKITI 120
DB 444 EGERAMTKONNLGRFELSGIPAPRGVPQIEVTFDIDANGILNVATDKSTGKANKITI 503
QY 121 TNDKGRLSKEEIERMVQEAERYKAEDVQERVSNAKNALESYAFNMKSAVEDGLGKGIS 180
DB 504 TNDKGRLSKEEIERMVQEAERYKAEDVQERVSNAKNALESYAFNMKSAVEDGLGKGIS 563
QY 181 EADKKVLDKCOEIVSWLDANTLAEDFEHKKRKELEQVNCNPIISGLYQAGGPGGPGF 240
DB 564 EADKKVLDKCOEIVSWLDANTLAEDFEHKKRKELEQVNCNPIISGLYQAGGPGGPGF 623
QY 241 AQGPKGGSGSGPTIEVD 258
DB 624 AQGPKGGSGSGPTIEVD 641

RESULT 14
ID ADF76349
XX ADF76349 standard; protein; 641 AA.
AC ADF76349;
XX
DT 26-FEB-2004 (first entry)
XX
DE Novel human secreted and transmembrane protein SeqID 22.
XX human; PRO; membrane bound protein; membrane bound receptor;
KW cell proliferation; cell migration; cell differentiation;
KW mitogenic factor; survival factor; cytotoxic factor;
KW differentiation factor; neurotrophic factor; hormone; cell receptor;
KW receptor-ligand interaction; cytostatic; chondrocyte; tumour.
XX
OS Homo sapiens.
XX
XX WO2003072035-A2.
XX
XX 04-SEP-2003.
XX
XX 21-FEB-2003; 2003WO-US005241.
XX
XX 22-FEB-2002; 2002US-0359461P.
XX
XX (GETH) GENENTECH INC.
XX Bodary SC, Clark H, Hunte B, Jackman JK, Schoenfeld JR;
PI Williams PM, Wood WI, Wu TD;
XX WPI; 2003-721702/68.
DR N-PSDB; ADF76348.
XX
XX New PRO polypeptides, useful for diagnosing and treating an immune

PT related disorder, e.g. systemic lupus erythematosus, rheumatoid
PT arthritis, osteoarthritis, juvenile chronic arthritis, thyroiditis or
XX diabetes mellitus.
PS Claim 10; SEQ ID NO 22; 918pp; English.
XX
CC This invention relates to novel nucleic acids encoding human PRO secreted
CC and transmembrane proteins. Extracellular proteins play important roles
CC in the formation, differentiation and maintenance of multicellular
CC organisms. The fate of many individual cells (for example proliferation,
CC migration or differentiation) is typically governed by information
CC received from other cells and the immediate environment. The information
CC is often transmitted by secreted polypeptides (for example mitogenic
CC factors, survival factors, cytotoxic factors, differentiation factors,
CC neurotrophic factors and hormones) which are received and interpreted by diverse
CC cell receptors or membrane bound proteins. These membrane bound proteins
CC and receptors may be of use as pharmaceutical and diagnostic agents, such
CC as in the blocking of receptor-ligand interactions. The current invention
CC provides the amino acid sequences of novel human membrane bound receptors
CC and proteins, along with the cDNA sequences encoding them. The novel
CC proteins of the invention may have cytostatic activities through the
CC stimulation of chondrocytes. The nucleic acids of the invention may be
CC useful for the manufacture of a medicament for diagnosing or treating a
CC tumour in a mammal. In addition, they may be useful for measuring or
CC detecting the expression of a tumour associated gene. The present
CC sequence is the amino acid sequence of a human PRO protein of the
CC invention.
XX
SQ Sequence 641 AA;

Query Match 99.6%; Score 1309; DB 7; Length 641;
Best Local Similarity 99.6%; Pred. No. 2.3e-100;
Matches 257; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 KSENVQDLLLDVAPLSGLGTAGGVMTALIKRNSITPTKQTQITFTTYSNQPGVLIQVY 60
DB 384 KSENVQDLLLDVAPLSGLGTAGGVMTALIKRNSITPTKQTQITFTTYSNQPGVLIQVY 443
QY 61 EGERAMTKONNLGRFELSGIPAPRGVPQIEVTFDIDANGILNVATDKSTGKANKITI 120
DB 444 EGERAMTKONNLGRFELSGIPAPRGVPQIEVTFDIDANGILNVATDKSTGKANKITI 503
QY 121 TNDKGRLSKEEIERMVQEAERYKAEDVQERVSNAKNALESYAFNMKSAVEDGLGKGIS 180
DB 504 TNDKGRLSKEEIERMVQEAERYKAEDVQERVSNAKNALESYAFNMKSAVEDGLGKGIS 563
QY 181 EADKKVLDKCOEIVSWLDANTLAEDFEHKKRKELEQVNCNPIISGLYQAGGPGGPGF 240
DB 564 EADKKVLDKCOEIVSWLDANTLAEDFEHKKRKELEQVNCNPIISGLYQAGGPGGPGF 623
QY 241 AQGPKGGSGSGPTIEVD 258
DB 624 AQGPKGGSGSGPTIEVD 641

RESULT 15
ID ADF76349
XX ADF76349 standard; protein; 641 AA.
AC ADF76349;
XX
DT 18-NOV-2004 (first entry)
XX
DE Tumour-associated antigenic target (TAT) polypeptide PRO38070, SEQ:1962.
XX Tumour-associated antigenic target; TAT; human; overexpression; cancer;
KW tumour; diagnosis; cell proliferative disorder; breast cancer;
KW colorectal cancer; lung cancer; ovarian cancer; liver cancer;
KW central nervous system cancer; bladder cancer; pancreatic cancer;
KW cervical cancer; melanoma; leukaemia; hybridisation probe;
KW chromosome identification; chromosome mapping; gene mapping;
KW gene therapy; cytostatic.
XX

OS	Homo sapiens.	AA88410	Standard; protein; 554 AA.
XX	W02004030615-A2.	XX	AA88410;
XX	15-APR-2004.	XX	31-JUL-2000 (first entry)
XX	29-SEP-2003; 2003WO-US028547.	XX	Human heat shock protein SHSP70 amino acid sequence.
XX	02-OCT-2002; 2002US-0414971P.	XX	Human; heat shock protein; HSP70; chromosome 6p21.3-22; stress;
XX	(GETH) GENENTECH INC.	XX	chromosome 14q22-24; transcription; rheumatism; schizophrenia;
XX	Wu TD, Zhang Z, Zhou Y;	XX	depression; nephrotic syndrome; SHSP70.
XX	WPI; 2004-347921/32.	XX	Homo sapiens.
XX	N-PSDB; ACN38446.	XX	JP2000069999-A.
XX	New tumor-associated antigenic target polypeptides and nucleic acids,	XX	07-MAR-2000.
XX	useful in preparing a medicament for treating or detecting a	XX	01-JUN-1995; 99JP-00257146.
XX	proliferative disorder, e.g. breast, lung, colorectal, ovarian or	XX	01-JUN-1995; 95JP-00158581.
XX	prostate cancer or tumor.	XX	(HOKE-) HOKEN KAGAKU KENKYUSHO KK.
XX	Claim 12; SEQ ID NO 1962; 7273pp; English.	XX	WPI; 2000-264458/23.
XX	The invention relates to human tumour-associated antigenic target (TAT)	XX	N-PSDB; AAA15622.
XX	polypeptides, and their related nucleic acids. The TAT polypeptides are	XX	Abnormal transcription of intracellular HSP70mRNA under acute and chronic
XX	overexpressed in cancer tissues compared to normal tissues, and may thus	XX	continuous load of stress in a human being and its application.
XX	serve as effective targets for the diagnosis and treatment of cancer in	XX	Disclosure; Fig 3; 11pp; Japanese.
XX	mammals. The invention also relates to nucleic acid and polypeptide	XX	This sequence represents the human heat shock protein SHSP70 amino acid
XX	sequences at least 80% identical to the TAT nucleic acids and	XX	sequence. Human heat shock proteins are located on chromosomes 6p21.3-22
XX	polypeptides; expression vectors and host cells comprising a TAT nucleic	XX	and 14q22-24. The invention relates to the abnormal transcription of
XX	acid; an antibody specific for a TAT polypeptide; a peptide or organic	XX	intracellular HSP70mRNA under acute and chronic stress lead in a human.
XX	molecule which binds to a TAT polypeptide; fusion proteins comprising a	XX	The abnormal transcription of HSP70 can be used in the improvement of
XX	TAT polypeptide; and methods and compositions for the treatment or	XX	stress and response and diagnosis of stress diseases including
XX	diagnosis of cancer in mammals. TAT polypeptides, nucleic acids,	XX	rheumatism, schizophrenia, depression and nephrotic syndrome
XX	antibodies, antagonists, binding molecules and compositions are useful	XX	Sequence 554 AA;
XX	for diagnosing or treating a cell proliferative disorder associated with	XX	Query Match 98.8%; Score 1298.5; DB 3; Length 554;
XX	increased TAT expression, particularly cancers such as breast cancer,	XX	Best Local Similarity 99.6%; Pred. No. 1.4e-99; Indels 1; Gaps 1;
XX	colorectal cancer, lung cancer, ovarian cancer, liver cancer, bladder	XX	Matches 257; Conservative 0; Mismatches 0;
XX	cancer, pancreatic cancer, cervical cancer, cancers of the central	XX	1 KSENVODLLLDVAPLSGLGTAGGVTALIKRNSITPTKQIIFTTYSNDQPGVLIQVY 60
XX	nervous system, melanoma and leukaemia. TAT nucleic acids may further be	XX	298 KSENVODLLLDVAPLSGLGTAGGVTALIKRNSITPTKQIIFTTYSNDQPGVLIQVY 357
XX	used as hybridisation probes, in chromosome and gene mapping, in	XX	61 EGERAMTKONNLLGRFELSGIIPAPRGVPOIEVTFDIDANGILNVTATDKSTGKANKITI 120
XX	chromosome identification and in gene therapy. The present sequence	XX	358 EGERAMTKONNLLGRFELSGIIPAPRGVPOIEVTFDIDANGILNVTATDKSTGKANKITI 416
XX	represents a TAT polypeptide of the invention	XX	121 TNDKGRLSKEEIERMVOEAKYKADEVQERVSNAKNALESYAFNMKSAVEDEGLGKIS 180
XX	Sequence 641 AA;	XX	417 TNDKGRLSKEEIERMVOEAKYKADEVQERVSNAKNALESYAFNMKSAVEDEGLGKIS 476
XX	Query Match 99.6%; Score 1309; DB 8; Length 641;	XX	181 EADKKVLDKQCEVISWLDANTLAEKDEFHKKRKELEQVCNPIISGLYQAGGPGGFG 240
XX	Best Local Similarity 99.6%; Pred. No. 2.3e-100;	XX	477 EADKKVLDKQCEVISWLDANTLAEKDEFHKKRKELEQVCNPIISGLYQAGGPGGFG 536
XX	Matches 257; Conservative 1; Mismatches 0; Indels 0; Gaps 0;	XX	241 AQGPKGGSGGPTIEVD 258
XX	1 KSENVODLLLDVAPLSGLGTAGGVTALIKRNSITPTKQIIFTTYSNDQPGVLIQVY 60	XX	537 AQGPKGGSGGPTIEVD 554
XX	384 KSENVODLLLDVAPLSGLGTAGGVTALIKRNSITPTKQIIFTTYSNDQPGVLIQVY 443	XX	RESULT 17
XX	61 EGERAMTKONNLLGRFELSGIIPAPRGVPOIEVTFDIDANGILNVTATDKSTGKANKITI 120	XX	AA88409
XX	444 EGERAMTKONNLLGRFELSGIIPAPRGVPOIEVTFDIDANGILNVTATDKSTGKANKITI 503	XX	ID AA88409 standard; protein; 554 AA.
XX	121 TNDKGRLSKEEIERMVOEAKYKADEVQERVSNAKNALESYAFNMKSAVEDEGLGKIS 180	XX	XX
XX	504 TNDKGRLSKEEIERMVOEAKYKADEVQERVSNAKNALESYAFNMKSAVEDEGLGKIS 563	XX	AC
XX	181 EADKKVLDKQCEVISWLDANTLAEKDEFHKKRKELEQVCNPIISGLYQAGGPGGFG 240		
XX	564 EADKKVLDKQCEVISWLDANTLAEKDEFHKKRKELEQVCNPIISGLYQAGGPGGFG 623		
XX	241 AQGPKGGSGGPTIEVD 258		
XX	624 AQGPKGGSGGPTIEVD 641		
XX	RESULT 16		

XX DT 31-JUL-2000 (first entry)
XX DE Human heat shock protein SHSP70 amino acid sequence.
XX DE
XX KW Human; heat shock protein; HSP70; chromosome 6p21.3-22; stress;
XX KW chromosome 14q22-24; transcription; rheumatism; schizophrenia;
XX KW depression; nephrotic syndrome; SHSP70.
XX OS
XX OS Homo sapiens.
XX PN JP2000069999-A.
XX PD 07-MAR-2000.
XX PF
XX PF 01-JUN-1995; 99JP-00257146.
XX PR 01-JUN-1995; 95JP-00158581.
XX PA (HOKI-) HOKEN KAGAKU KENKYUSHO KK.
XX WPI; 2000-264458/23.
XX DR N-PSDB; AAA15621.
XX DR
XX PT Abnormal transcription of intracellular HSP70mRNA under acute and chronic
XX PT continuous load of stress in a human being and its application.
XX PS Example; Fig 2; 11pp; Japanese.
XX CC This sequence represents the human heat shock protein SHSP70 amino acid
XX CC sequence. Human heat shock proteins are located on chromosomes 6p21.3-22
XX CC and 14q22-24. The invention relates to the abnormal transcription of
XX CC intracellular HSP70mRNA under acute and chronic stress load in a human.
XX CC The abnormal transcription of HSP70 can be used in the improvement of
XX CC stress and response and diagnosis of stress diseases including
XX CC rheumatism, schizophrenia, depression and nephrotic syndrome
XX CC
SQ Sequence 554 AA;
Query Match 98.8%; Score 1298.5; DB 3; Length 554;
Best Local Similarity 99.6%; Pred. No. 1.4e-99;
Matches 257; Conservative 0; Mismatches 0; Indels 1; Gaps 1;
QY 1 KSENVQDLLLDVAPLSLGLGTAGGVTALIKRNSTPTKQTQIFTTYSNQPGLVLIQVY 60
DB 298 KSENVQDLLLDVAPLSLGLGTAGGVTALIKRNSTPTKQTQIFTTYSNQPGLVLIQVY 357
QY 61 EGERAMTKDNNLLGRFELSGIPAPRGVPOIEVTFDIDANGILNVTATDKSTGKANKITI 120
DB 358 EGERAMTKDNNLLGRFELSGIPAPRGVPOIEVTFDIDANGILNVTATDKSTGKANKITI 416
QY 121 TNDKGRLSKEEIERMWQEAKEYKAEDVQERVSNAKNALESYAFNMKSAVEDSGLGKGIS 180
DB 417 TNDKGRLSKEEIERMWQEAKEYKAEDVQERVSNAKNALESYAFNMKSAVEDSGLGKGIS 476
QY 181 EADKKVLDKCQEVISWLDANTLAEKDEFEHKKRKELEQVCNPIISGLYQAGGPGGPGF 240
DB 477 EADKKVLDKCQEVISWLDANTLAEKDEFEHKKRKELEQVCNPIISGLYQAGGPGGPGF 536
QY 241 AQPCKGSGSGPTIEVD 258
DB 537 AQPCKGSGSGPTIEVD 554
RESULT 18
AAB23653
ID AAB23653 standard; protein; 640 AA.
XX AC AAB23653;
XX AC
XX DT 05-JAN-2001 (first entry)
XX DE Human heat shock protein Hsp70 protein sequence SEQ ID NO:5.

XX KW ATPase; Hsp70; heat shock protein; cytotoxic T lymphocyte; CTL;
XX KW immune response; infectious disease; malaria; cytotoxic T cell;
XX KW cytostatic; immunostimulant; cellular immune response inducer;
XX KW protozoacide; leukaemia; cancer.
XX OS
XX OS Homo sapiens.
XX PN WO200049041-A1.
XX PD 24-AUG-2000.
XX PF 18-FEB-2000; 2000WO-JP000941.
XX PR 19-FEB-1999; 99JP-00041535.
XX PA (SUME) SUMITOMO ELECTRIC IND CO.
XX PI Shinbara N, Udono H, Yui K;
XX WPI; 2000-543748/49.
XX DR
XX PT Fused protein capable of inducing cellular immune response, useful as
XX PT active ingredient for drug compositions in preventing and/or treating
XX PT infectious diseases such as malaria or cancer.
XX PS Claim 3; Page 49-52; 72pp; Japanese.
XX CC The present invention describes a fused protein (I) prepared from a
XX CC peptide containing a CTL (cytotoxic T lymphocyte) epitope recognised by
XX CC cytotoxic T cells and a protein containing the ATPase domain of a heat
XX CC shock protein. Also described are: (1) a drug composition containing (I)
XX CC as active ingredient; (2) a DNA encoding (I); (3) an expression vector
XX CC containing the DNA of (2); and (4) a transformant which can retain the
XX CC expression vector of (3). (1) has cytostatic, immunostimulant and
XX CC protozoacide activities, and can be used as a cellular immune response
XX CC inducer. The protein is useful as an active ingredient for drug
XX CC compositions in preventing and/or treating infectious diseases such as
XX CC malaria or cancer e.g. to provide systemic immunity against leukaemia.
XX CC The present sequence represents a specifically claimed heat shock protein
XX CC for use in a fused protein of the present invention
XX CC
SQ Sequence 640 AA;
Query Match 98.8%; Score 1298.5; DB 3; Length 640;
Best Local Similarity 99.6%; Pred. No. 1.7e-99;
Matches 257; Conservative 0; Mismatches 0; Indels 1; Gaps 1;
QY 1 KSENVQDLLLDVAPLSLGLGTAGGVTALIKRNSTPTKQTQIFTTYSNQPGLVLIQVY 60
DB 384 KSENVQDLLLDVAPLSLGLGTAGGVTALIKRNSTPTKQTQIFTTYSNQPGLVLIQVY 443
QY 61 EGERAMTKDNNLLGRFELSGIPAPRGVPOIEVTFDIDANGILNVTATDKSTGKANKITI 120
DB 444 EGERAMTKDNNLLGRFELSGIPAPRGVPOIEVTFDIDANGILNVTATDKSTGKANKITI 502
QY 121 TNDKGRLSKEEIERMWQEAKEYKAEDVQERVSNAKNALESYAFNMKSAVEDSGLGKGIS 180
DB 503 TNDKGRLSKEEIERMWQEAKEYKAEDVQERVSNAKNALESYAFNMKSAVEDSGLGKGIS 562
QY 181 EADKKVLDKCQEVISWLDANTLAEKDEFEHKKRKELEQVCNPIISGLYQAGGPGGPGF 240
DB 563 EADKKVLDKCQEVISWLDANTLAEKDEFEHKKRKELEQVCNPIISGLYQAGGPGGPGF 622
QY 241 AQPCKGSGSGPTIEVD 258
DB 623 AQPCKGSGSGPTIEVD 640
RESULT 19
ADD14137
ID ADD14137 standard; protein; 640 AA.
XX

ADD14137;
01-JAN-2004 (first entry)
Human src biomarker polypeptide SEQ ID NO:326.
predictor set; protein tyrosine kinase activity modulator;
protein tyrosine kinase pathway; protein tyrosine kinase; cytosolic;
gene therapy; drug sensitivity; genetic profile; cancer; human.
Homo sapiens.
WO2003062395-A2.
31-JUL-2003.
17-JAN-2003; 2003WO-US001981.
18-JAN-2002; 2002US-0350061P.
(BRIM) BRISTOL-MYERS SQUIBB CO.
Huang F, Fairchild CR, Lee FY, Shaw P;
WPI; 2003-636735/60.
N-PSDB; ADD14739.
New polynucleotides and polypeptides for predicting the activity of
compounds that interact with protein tyrosine kinases and/or protein
tyrosine kinase pathways.
Claim 10; SEQ ID NO 326; 139pp; English.
The present invention describes a predictor set comprising a plurality of
polynucleotides or polypeptides whose expression pattern is predictive of
the response of cells to treatment with a compound that modulates protein
tyrosine kinase activity or members of the protein tyrosine kinase
pathway. Also described: (1) predicting whether a compound is capable of
modulating the activity of cells, comprising obtaining a sample of cells,
determining whether the cells express a plurality of markers, and
correlating the expression of the markers to the compound's ability to
modulate the activity of the cells; (2) a plurality of cell lines for
identifying polynucleotides and polypeptides whose expression levels
correlate with compound sensitivity or resistance of cells associated
with a disease state; and (3) identifying polynucleotides and
polypeptides that predict compound sensitivity or resistance of cells
associated with a disease state, comprising subjecting the plurality of
cell lines to one or more compounds, analysing the expression pattern of
a microarray of polynucleotides or polypeptides, and selecting
polynucleotides or polypeptides that predict the sensitivity or
resistance of cells associated with a disease state by using the
expression pattern of the microarray. The polynucleotides and
polypeptides have cytostatic activities, and can be used in gene therapy.
The polynucleotides and polypeptides are useful in predicting the
activity of compounds that interact with protein tyrosine kinases and/or
protein tyrosine kinase pathways. These may be used in determining drug
sensitivity in patients to allow the development of individualized
genetic profiles which aid in treating diseases and disorders (e.g.
cancer) based on patient response at a molecular level. The present
sequence is used in the exemplification of the present invention.
Sequence 640 AA;
Query Match 98.8%; Score 1298.5; DB 7; Length 640;
Best Local Similarity 99.6%; Pred No. 1.7e-99;
Matches 257; Conservative 0; Mismatches 0; Indels 1; Gaps 1;
1 KSENVQDLLLLLVAPLSLGLTAGVMTALIKRNSTIPTKTQTFTTYSNDQPGVLQVY 60
384 KSENVQDLLLLLVAPLSLGLTAGVMTALIKRNSTIPTKTQTFTTYSNDQPGVLQVY 443.
61 EGERAMTKDNNLLGRFELSGIPAPRGVQPIEVTFDIDANGILNVATDKSTGKANKITI 120

444 EGERAMTKDNNLLGRFELSGIPAPRGVQPIEVTFDIDANGILNVATDKSTGKANKITI 502
121 TNDKGRLSKEETRMVQAEKYKAEDEVQRBRVSNALESYAFNMKSAVEDGLKKGKIS 180
503 TNDKGRLSKEETRMVQAEKYKAEDEVQRBRVSNALESYAFNMKSAVEDGLKKGKIS 562
181 EADKKKVLDDKQEVISWLDANTLAERKDEFEHKKRKELEQVCNPIISGLYQGAGGPGGFG 240
563 EADKKKVLDDKQEVISWLDANTLAERKDEFEHKKRKELEQVCNPIISGLYQGAGGPGGFG 622
241 AQPFGGSGSGPTIEVD 258
623 AQPFGGSGSGPTIEVD 640
RESULT 20
ADJ68449
ID ADJ68449 standard; protein; 640 AA.
XX
AC ADJ68449;
XX
DT 06-MAY-2004 (first entry)
XX
DE Human heat mitochondrial protein as a therapeutic target SeqID255.
XX
KW mitochondrial; human; screening assay; diabetes mellitus;
KW Huntington's disease; osteoarthritis;
KW Leber's hereditary optic neuropathy; LHON;
KW mitochondrial encephalopathy lactic acidosis and stroke; MELAS;
KW myoclonic epilepsy ragged red fibre syndrome; MERRF; cancer;
KW neuroprotective; nootropic; antidiabetic; anticonvulsant; antiarthritic;
KW osteopathic; ophthalmological; cytostatic.
XX
OS Homo sapiens.
XX
PN WO2003087768-A2.
XX
PD 23-OCT-2003.
XX
PF 04-APR-2003; 2003WO-US010870.
XX
PR 12-APR-2002; 2002US-0372843P.
PR 17-JUN-2002; 2002US-0389887P.
PR 20-SEP-2002; 2002US-0412418P.
XX
PA (MITO-) MITOKOR.
PA (BUCK-) BUCK INST AGE RES.
XX
PI Ghosh SS, Fahy ED, Zhang B, Gibson BW, Taylor SW, Glenn GM;
PI Warnock DE;
XX
DR WPI; 2003-845369/78.
XX
PT Identifying a mitochondrial target for drug screening assays and for
PT treating diseases associated with altered mitochondrial function,
PT comprises detecting a modified polypeptide in a sample and correlating
PT with the disease.
XX
PS Claim 1; SEQ ID NO 255; 180pp; English.
XX
CC This invention relates to novel mitochondrial targets that can be used
CC for therapeutic intervention in treating a disease associated with
CC altered mitochondrial function. Specifically, it refers to a method for
CC identifying proteins of the human heart mitochondrial proteome that are
CC useful for drug screening assays, as well as therapeutic targets. The
CC present invention describes a method for identifying such proteins that
CC can be used in the treatment of various diseases associated with altered
CC mitochondrial function including diabetes mellitus, Huntington's disease,
CC osteoarthritis, Leber's hereditary optic neuropathy (LHON), mitochondrial
CC encephalopathy lactic acidosis and stroke (MELAS), myoclonic epilepsy
CC ragged red fibre syndrome (MERRF) or cancer. Accordingly, these
CC compositions have neuroprotective, nootropic, antidiabetic,
CC anticonvulsant, antiarthritic, osteopathic, ophthalmological and

CC cytotostatic activities. This polypeptide sequence is a human heat
 XX mitochondrial protein of the invention.
 SQ Sequence 640 AA;

Query Match 98.8%; Score 1298.5; DB 7; Length 640;
 Best Local Similarity 99.6%; Pred. No. 1.7e-99;
 Matches 257; Conservative 0; Mismatches 0; Indels 1; Gaps 1;
 1 KSENVQDLLLDVAPLSGLGLETAGGVMTALIKRNSITPTKQTQIFTTYSNQPGVLIQVY 60
 384 KSENVQDLLLDVAPLSGLGLETAGGVMTALIKRNSITPTKQTQIFTTYSNQPGVLIQVY 443
 61 EGERAMTKNNLLGRFELSGIPAPRGVQPIEVTFDIDANGILNVATDSTGKANKITI 120
 444 EGERAMTKNNLLGRFELSGIPAPRGVQPIEVTFDIDANGILNVATDSTGKANKITI 502
 121 TNDKGRLSKEEIERMWQEAESKYAEDEVQERVSANNALESYAFNMKSAVEDSGLGKIS 180
 503 TNDKGRLSKEEIERMWQEAESKYAEDEVQERVSANNALESYAFNMKSAVEDSGLGKIS 562
 181 EADKKVLDKQCEVISWLDANTLAEKDFEHEKKELEQVCNPIISGLYQAGGPGGFG 240
 563 EADKKVLDKQCEVISWLDANTLAEKDFEHEKKELEQVCNPIISGLYQAGGPGGFG 622
 241 AQPCKGSGSGPTIEVD 258
 623 AQPCKGSGSGPTIEVD 640

RESULT 21

ABR40399
 ID ABR40399 standard; protein; 641 AA.

AC ABR40399;

DT 08-AUG-2003 (first entry)

XX Bovine Hsp70 protein.

XX heat shock protein; HSP; cytokine; CC chemokine; nitric oxide; cancer;
 XX antimicrobial; virucide; cytostatic; microbial infection; anti-HIV;
 XX viral infection; immune system disorder; vaccine; HSP70; bovine.

XX Bos taurus.

XX WO2003029289-A2.

XX 10-APR-2003.

XX 03-OCT-2002; 2002WO-GB004475.

XX 03-OCT-2001; 2001GB-00023756.

XX (UNLO) KINGS COLLEGE LONDON.

XX Lehner T, Kelly CG, Singh M, Wang Y;

XX WPI; 2003-430189/40.

XX Novel heat shock protein fragment useful for treating microbial
 PT infection, viral infection or cancer, that can increase the level of
 PT cytokines and/or CC chemokines and/or nitric oxide produced by a cell.

XX Example 3; Page 17-20; 30pp; English.

XX The invention relates to a novel heat shock protein fragment (HSP) that
 CC can increase the level of one or more cytokines and/or one or more CC
 CC chemokines and/or nitric oxide produced by a cell, above that caused by
 CC the corresponding full length heat shock protein. The protein fragment of
 CC the invention has antimicrobial, virucide, and cytostatic activity. The
 CC protein fragment is useful in therapy, in treatment or prophylaxis of a
 CC disease and in the manufacture of a medicament for treatment or

CC prophylaxis of a disease such as microbial infection, viral infection,
 CC disease of the immune system or cancer. The fragment is also useful as an
 CC adjuvant in vaccines, preferably, anti-HIV vaccines. The present sequence
 CC represents the bovine HSP70 protein
 XX
 SQ Sequence 641 AA;

Query Match 98.6%; Score 1295; DB 6; Length 641;
 Best Local Similarity 98.8%; Pred. No. 3.4e-99;
 Matches 255; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
 1 KSENVQDLLLDVAPLSGLGLETAGGVMTALIKRNSITPTKQTQIFTTYSNQPGVLIQVY 60
 384 KSENVQDLLLDVAPLSGLGLETAGGVMTALIKRNSITPTKQTQIFTTYSNQPGVLIQVY 443
 61 EGERAMTKNNLLGRFELSGIPAPRGVQPIEVTFDIDANGILNVATDSTGKANKITI 120
 444 EGERAMTKNNLLGRFELSGIPAPRGVQPIEVTFDIDANGILNVATDSTGKANKITI 503
 121 TNDKGRLSKEEIERMWQEAESKYAEDEVQERVSANNALESYAFNMKSAVEDSGLGKIS 180
 504 TNDKGRLSKEEIERMWQEAESKYAEDEVQERVSANNALESYAFNMKSAVEDSGLGKIS 563
 181 EADKKVLDKQCEVISWLDANTLAEKDFEHEKKELEQVCNPIISGLYQAGGPGGFG 240
 564 EADKKVLDKQCEVISWLDANTLAEKDFEHEKKELEQVCNPIISGLYQAGGPGGFG 623
 241 AQPCKGSGSGPTIEVD 258
 624 AQPCKGSGSGPTIEVD 641

RESULT 22

AAW10065
 ID AAW10065 standard; protein; 640 AA.

AC AAW10065;

DT 24-OCT-1997 (first entry)

XX Human heat shock protein 70.

XX Human; heat shock protein 70; HSP70; primer; probe; detection;
 XX intracellular; abnormal transcription; acute; chronic; sustained; stress.

XX Homo sapiens.

XX JP08322577-A.

XX 10-DEC-1996.

XX 01-JUN-1995; 95JP-00158581.

XX 01-JUN-1995; 95JP-00158581.

XX (HOKE-) HOKEN KAGAKU KENKYUSHO KK.

XX WPI; 1997-081088/08.

XX N-PSDB; AAT58086.

XX Detection of abnormal transcription of HSP70 mRNA - using HSP70 specific
 PT primer or probe, used in detection of human acute and chronic sustained
 PT stress load.

XX Claim 1; Fig 1; 13pp; Japanese.

XX The cDNA encoding the present sequence, human heat shock protein 70
 CC (HSP70), is located on human chromosome 6p 21.3-22 and 14q 22-24 and 21.
 CC Primers and probes based on the HSP70 cDNA coding sequence can be used to
 CC detect the abnormal transcription of intracellular HSP70 mRNA in human
 CC acute and chronic sustained stress load

XX Sequence 640 AA;

Query Match 98.2%; Score 1290.5; DB 2; Length 640;
 Best Local Similarity 99.2%; Pred. No. 8e-99; 1; Indels 1; Gaps 1;
 Matches 256; Conservative 0; Mismatches 1;

QY 1 KSENVQDLLLDVAPLSLGLTAGGVTALIKRNSTIPTKQTQIFFTYSDNQPGVLIQVY 60
 DB 384 KSENVQDLLLDVAPLSLGLTAGGVTALIKRNSTIPTKQTQIFFTYSDNQPGVLIQVY 443

QY 61 EGERAMTKONLLGRFELSGIPAPRGVPOIETVTFDIDANGILNVTATDKSTGKANKITI 120
 DB 444 EGERAMTKONLLGRFELSGIPAPRGVPOIETVTFDIDANGILNVTATDKSTGKANKITI 502

QY 121 TNDKGRLSKEEIERMWQEAKEYKAEDVQREVSANNALESYAFNMKSAVEDGLGKIS 180
 DB 503 TNDKGRLSKEEIERMWQEAKEYKAEDVQREVSANNALESYAFNMKSAVEDGLGKIS 562

QY 181 EADKKVLDKQCEVISWLDANTLAEKDFEHRKELEQVCNPIISGLYQAGGPGPGFG 240
 DB 563 EADKKVLDKQCEVISWLDANTLAEKDFEHRKELEQVCNPIISGLYQAGGPGPGFG 622

QY 241 AQPCKGSGSGPTIEVD 258
 DB 623 AQPCKGSGSGPTIEVD 640

RESULT 23
 AAY88408
 ID AAY88408 standard; protein; 640 AA.
 AC AAY88408;
 XX
 DT 31-JUL-2000 (first entry)
 DE Human heat shock protein HSP70 amino acid sequence.
 KW Human; heat shock protein; HSP70; chromosome 6p21.3-22; stress;
 KW chromosome 14q22-24; transcription; rheumatism; schizophrenia;
 KW depression; nephrotic syndrome.
 XX
 OS Homo sapiens.
 XX
 FN JP2000069999-A.
 XX
 PD 07-MAR-2000.
 XX
 PF 01-JUN-1995; 99JP-00257146.
 XX
 PR 01-JUN-1995; 95JP-00158581.
 XX
 PA (HOKE-) HOKEN KAGAKU KENKYUSHO KK.
 XX
 XX WPI; 2000-264458/23.
 DR N-PSDB; AAA15620.
 XX
 PT Abnormal transcription of intracellular HSP70mRNA under acute and chronic
 XX continuous load of stress in a human being and its application.
 PS Claim 2; Fig 1; 11pp; Japanese.
 XX
 CC This sequence represents the human heat shock protein HSP70 amino acid
 CC sequence. Human heat shock proteins are located on chromosomes 6p21.3-22
 CC and 14q22-24. The invention relates to the abnormal transcription of
 CC intracellular HSP70mRNA under acute and chronic stress load in a human.
 CC The abnormal transcription of HSP70 can be used in the improvement of
 CC stress and response and diagnosis of stress diseases including
 CC rheumatism, schizophrenia, depression and nephrotic syndrome
 XX
 SQ Sequence 640 AA;

Query Match 98.2%; Score 1290.5; DB 3; Length 640;
 Best Local Similarity 99.2%; Pred. No. 8e-99; 1; Indels 1; Gaps 1;
 Matches 256; Conservative 0; Mismatches 1;

QY 1 KSENVQDLLLDVAPLSLGLTAGGVTALIKRNSTIPTKQTQIFFTYSDNQPGVLIQVY 60
 DB 384 KSENVQDLLLDVAPLSLGLTAGGVTALIKRNSTIPTKQTQIFFTYSDNQPGVLIQVY 443

QY 61 EGERAMTKONLLGRFELSGIPAPRGVPOIETVTFDIDANGILNVTATDKSTGKANKITI 120
 DB 444 EGERAMTKONLLGRFELSGIPAPRGVPOIETVTFDIDANGILNVTATDKSTGKANKITI 502

QY 121 TNDKGRLSKEEIERMWQEAKEYKAEDVQREVSANNALESYAFNMKSAVEDGLGKIS 180
 DB 503 TNDKGRLSKEEIERMWQEAKEYKAEDVQREVSANNALESYAFNMKSAVEDGLGKIS 562

QY 181 EADKKVLDKQCEVISWLDANTLAEKDFEHRKELEQVCNPIISGLYQAGGPGPGFG 240
 DB 563 EADKKVLDKQCEVISWLDANTLAEKDFEHRKELEQVCNPIISGLYQAGGPGPGFG 622

QY 241 AQPCKGSGSGPTIEVD 258
 DB 623 AQPCKGSGSGPTIEVD 640

RESULT 24
 AAR03929
 ID AAR03929 standard; protein; 640 AA.
 AC AAR03929;
 XX
 DT 30-AUG-1990 (first entry)
 DE Homo sapiens HSP (humhsp70).
 KW Hsp70; heat shock protein; Trypanosoma cruzi; vaccines; HSP.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT Misc-difference 640
 FT /note= "residue given as "O" in specification"
 XX
 PN WO9002564-A.
 XX
 PD 22-MAR-1990.
 XX
 PF 12-SEP-1988; 88US-00243474.
 XX
 PR 12-SEP-1988; 88US-00243474.
 XX
 PA (CODO-) CODON.
 XX
 PI Dragon E, Paulds D, Sias S;
 XX
 XX WPI; 1990-115820/15.
 DR
 XX Proteins homologous to heat shock proteins of Trypanosoma cruzi - used in
 PT vaccines and diagnosis for species of e.g. muco-plasma or mycobacteria.
 XX
 PS Disclosure; Fig 2.1-2.14; 86pp; English.
 XX
 CC According to the legend of Fig 2, the H. sapiens HSP sequence has 641
 CC amino acid residues, the sequence itself has only 640, including "O" (?)
 CC at position 640. Fig. 2 provides an alignment of heat shock proteins from
 CC a variety of organisms: 1. M. hyopneumoniae (Mhysp70 - AAR03922); 2.
 CC Bacillus megaterium (BmeHsp70 - AAR03923); 3. E. coli (dhak - AAR03924);
 CC 4. T. cruzi (tc70kd - AAR03925); 5. T. cruzi (AAR03926); 6. Rat rattus
 CC (rathsp70 - AAR03927); 7. Xenopus laevis (xl170 - AAR03928); 8. Homo
 CC sapiens (humhsp70 - AAR03929); 9. Gallus gallus (chkhsp70 - AAR03930);
 CC 10. Zea mays (mzeHsp70 - AAR03931); 11. Serratia marcescens (smahsp70 -
 CC AAR03932). The proteins having homology to hsp's of T. cruzi can be used
 CC in vaccines and diagnosis involving e.g. Trypanosoma, Mycoplasma and
 CC Mycobacteria species
 XX
 SQ Sequence 640 AA;

Query Match		97.6%; Score 1282; DB 2; Length 640;
Best Local Similarity		99.2%; Pred. No. 4.1e-98;
Matches 256; 'Conservative		0; Mismatches 0; Indels 2; Gaps 2;
QY	1 KSENVODLLLDVAPLSGLGLETAGGVTALIKRNSIPTKQTOIFTTYSNQPGLIQVY	60
DB	384 KSENVODLLLDVAPLSGLGLETAGGVTALIKRNSIPTKQTOIFTTYSNQPGLIQVY	443
QY	61 EGERAMTKDNLLGRFELSGIPAPRGVPOIEVTFDIDANGILNVTATDKSTGKANKITI	120
DB	444 EGERAMTKDNLLGRFELSGIPAPRGVPOIEVTFDIDANGILNVTATDKSTGKANKITI	502
QY	121 TNDKGRLSKEEIERMVEAEKYKAEDVQERVSNAKNALESYAFNMKSAYEDELKLGKIS	180
DB	503 TNDKGRLSKEEIERMVEAEKYKAEDVQERVSNAKNALESYAFNMKSAYEDELKLGKIS	562
QY	181 EADKKKVLKQCVISWLDANTLAEKDFEHRKELEQVCNPIISGLYQAGGPGGPGG	240
DB	563 EADKKKVLKQCVISWLDANTLAEKDFEHRKELEQVCNPIISGLYQAGGPGGPGG	622
QY	241 AQPCKGGSGSGPTIEVD 258	
DB	623 AQPCKGGSGSGPTIEVD 640	
RESULT 26		
ID	ABR40398	
XX	ABR40398 standard; protein; 641 AA.	
AC	ABR40398;	
XX		
DT	08-AUG-2003 (first entry)	
XX		
DE	Rat HSP70 protein.	
XX		
KW	heat shock protein; HSP; cytokine; CC chemokine; nitric oxide; cancer;	
KW	antimicrobial; virucide; cytostatic; microbial infection; anti-HIV;	
KW	viral infection; immune system disorder; vaccine; HSP70; rat.	
XX		
OS	Rattus sp.	
XX		
PN	WO2003029289-A2.	
XX		
PD	10-APR-2003.	
XX		
PF	03-OCT-2002; 2002WO-GB004475.	
XX		
PR	03-OCT-2001; 2001GB-00023756.	
XX		
PA	(UNLO) KINGS COLLEGE LONDON.	
XX		
PI	Lehner T, Kelly CG, Singh M, Wang Y;	
XX		
DR	WPI; 2003-430189/40.	
XX		
PT	Novel heat shock protein fragment useful for treating microbial	
PT	infection, viral infection or cancer, that can increase the level of	
PT	cytokines and/or CC chemokines and/or nitric oxide produced by a cell.	
XX		
PS	Example 3; Page 17-20; 30pp; English.	
XX		
CC	The invention relates to a novel heat shock protein fragment (HSP) that	
CC	can increase the level of one or more cytokines and/or one or more CC	
CC	chemokines and/or nitric oxide produced by a cell, above that caused by	
CC	the corresponding full length heat shock protein. The protein fragment of	
CC	the invention has antimicrobial, virucide, and cytostatic activity. The	
CC	protein fragment is useful in therapy, in treatment or prophylaxis of a	
CC	disease and in the manufacture of a medicament for treatment or	
CC	prophylaxis of a disease such as microbial infection, viral infection,	
CC	disease of the immune system or cancer. The fragment is also useful as an	
CC	adjuvant in vaccines, preferably, anti-HIV vaccines. The present sequence	
XX	represents the rat HSP70 protein	
SQ	Sequence 641 AA;	
Query Match		
Best Local Similarity		
Matches 253; 'Conservative		
95.7%; Score 1258; DB 6; Length 641;		
Best Local Similarity		
95.3%; Pred. No. 4.1e-96;		

Matches 246; Conservative 7; Mismatches 5; Indels 0; Gaps 0;

QY 1 KSENVODLLLDVAPLSGLGLETAGGVTALIKENSTIPTKQTOIFTTYSNQPGLIOVY 60
DB 384 KSENVODLLLDVAPLSGLGLETAGGVTALIKENSTIPTKQTOIFTTYSNQPGLIOVY 443
QY 61 EGERAMTKDNLLGRFELSGIPAPRGVPOIEVTFDIDANGILNVATDKSTGKANKITI 120
DB 444 EGERAMTRDNLLGRFELSGIPAPRGVPOIEVTFDIDANGILNVATDKSTGKANKITI 503
QY 121 TNDKGRLSKEEIERMVQEAERYKAEDVQERVAAKNALESYAFNMKSAVEDGLGKIS 180
DB 504 TNDKGRLSKEEIERMVQEAERYKAEDVQERVAAKNALESYAFNMKSAVEDGLGKIS 563
QY 181 EADKKVLDKCOEIVSWLDANTLAEKDEFHKKLEOVNCNPIISGLYQAGGPGGFG 240
DB 564 EADKKVLDKCOEIVSWLDNTLAKEEFVHKREELRVNCNPIISGLYQAGGPGGFG 623
QY 241 AQPKGGSGSGPTIEVD 258
DB 624 AQAPKGGSGSGPTIEVD 641

RESULT 27
ADD46498
ID ADD46498 standard; protein; 641 AA.
AC ADD46498;
XX
XX
XX 29-JAN-2004 (first entry)
XX
XX Rat Protein Q07439, SEQ ID NO 12179.
XX
XX Rat; pain; neuronal tissue; gene therapy; spinal segmental nerve injury;
XX chronic constriction injury; CCI; spared nerve injury; SNI; Chung.
XX
XX Rattus norvegicus.
XX
XX WO2003016475-A2.
XX
XX 27-FEB-2003.
XX
XX 14-AUG-2002; 2002WO-US025765.
XX
XX 14-AUG-2001; 2001US-0312147P.
XX PR 01-NOV-2001; 2001US-0346382P.
XX PR 26-NOV-2001; 2001US-0333347P.
XX
XX (GEHO) GEN HOSPITAL CORP.
XX (FARB) BAYER AG.
XX
XX Woolf C, D'urso D, Befort K, Costigan M;
XX
XX WPI; 2003-268312/26.
XX DR GENBANK; Q07439.
XX
XX New composition comprising two or more isolated polypeptides, useful for
XX preparing a medicament for treating pain in an animal.
XX
XX Claim 1; Page; 1017pp; English.
XX
XX The invention discloses a composition comprising two or more isolated rat
XX or human polynucleotides or a polynucleotide which represents a fragment,
XX derivative or allelic variation of the nucleic acid sequence. Also
XX claimed are a vector comprising the novel polynucleotide, a host cell
XX comprising the vector, a method for identifying a nucleotide sequence
XX which is differentially regulated in an animal subjected to pain and a
XX kit to perform the method, an array, a method for identifying an agent
XX that increases or decreases the expression of the polynucleotide sequence
XX that is differentially expressed in neuronal tissue of a first animal
XX subjected to pain, a method for identifying a compound which regulates
XX the expression of a polynucleotide sequence which is differentially
XX expressed in an animal subjected to pain, a method for identifying a

compound that regulates the activity of one or more of the
polynucleotides, a method for producing a pharmaceutical composition, a
method for identifying a compound or small molecule that regulates the
activity in an animal of one or more of the polypeptides given in the
specification, a method for identifying a compound useful in treating
pain and a pharmaceutical composition comprising the one or more
polypeptides or their antibodies. The polynucleotide or the compound that
modulates its activity is useful for preparing a medicament for treating
pain (e.g. spinal segmental nerve injury (Chung), chronic constriction
injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene
therapy). The sequence presented is a rat protein (shown in Table 2 of
the specification) which is differentially expressed during pain. Note:
The sequence data for this patent did not form part of the printed
specification, but was obtained in electronic form directly from WIPO at
ftp.wipo.int/pub/published_pct_sequences.

XX
XX Sequence 641 AA;

Query Match 95.7%; Score 1258; DB 7; Length 641;
Best Local Similarity 95.3%; Pred. No. 4.1e-96;
Matches 246; Conservative 7; Mismatches 5; Indels 0; Gaps 0;

QY 1 KSENVODLLLDVAPLSGLGLETAGGVTALIKENSTIPTKQTOIFTTYSNQPGLIOVY 60
DB 384 KSENVODLLLDVAPLSGLGLETAGGVTALIKENSTIPTKQTOIFTTYSNQPGLIOVY 443
QY 61 EGERAMTKDNLLGRFELSGIPAPRGVPOIEVTFDIDANGILNVATDKSTGKANKITI 120
DB 444 EGERAMTRDNLLGRFELSGIPAPRGVPOIEVTFDIDANGILNVATDKSTGKANKITI 503
QY 121 TNDKGRLSKEEIERMVQEAERYKAEDVQERVAAKNALESYAFNMKSAVEDGLGKIS 180
DB 504 TNDKGRLSKEEIERMVQEAERYKAEDVQERVAAKNALESYAFNMKSAVEDGLGKIS 563
QY 181 EADKKVLDKCOEIVSWLDANTLAEKDEFHKKLEOVNCNPIISGLYQAGGPGGFG 240
DB 564 EADKKVLDKCOEIVSWLDNTLAKEEFVHKREELRVNCNPIISGLYQAGGPGGFG 623
QY 241 AQPKGGSGSGPTIEVD 258
DB 624 AQAPKGGSGSGPTIEVD 641

RESULT 28
ADES7092
ID ADES7092 standard; protein; 641 AA.
XX
XX AC ADES7092;
XX
XX 29-JAN-2004 (first entry)
XX
XX Rat Protein Q07439, SEQ ID NO 2952.
XX
XX Rat; pain; neuronal tissue; gene therapy; spinal segmental nerve injury;
XX chronic constriction injury; CCI; spared nerve injury; SNI; Chung.
XX
XX Rattus norvegicus.
XX
XX WO2003016475-A2.
XX
XX 27-FEB-2003.
XX
XX 14-AUG-2002; 2002WO-US025765.
XX
XX 14-AUG-2001; 2001US-0312147P.
XX PR 01-NOV-2001; 2001US-0346382P.
XX PR 26-NOV-2001; 2001US-0333347P.
XX
XX (GEHO) GEN HOSPITAL CORP.
XX (FARB) BAYER AG.
XX
XX Woolf C, D'urso D, Befort K, Costigan M;

DR WPI; 2003-268312/26.
 XX GENBANK; Q07439.
 PT New composition comprising two or more isolated polypeptides, useful for
 XX preparing a medicament for treating pain in an animal.
 XX
 PS Claim 1; Page; 1017pp; English.
 XX
 CC The invention discloses a composition comprising two or more isolated rat
 CC or human polynucleotides or a polynucleotide which represents a fragment,
 CC derivative or allelic variation of the nucleic acid sequence. Also
 CC claimed are a vector comprising the novel polynucleotide, a host cell
 CC comprising the vector, a method for identifying a nucleotide sequence
 CC which is differentially regulated in an animal subjected to pain and a
 CC kit to perform the method, an array, a method for identifying an agent
 CC that increases or decreases the expression of the polynucleotide sequence
 CC that is differentially expressed in neuronal tissue of a first animal
 CC subjected to pain, a method for identifying a compound which regulates
 CC the expression of a polynucleotide sequence which is differentially
 CC expressed in an animal subjected to pain, a method for identifying a
 CC compound that regulates the activity of one or more of the
 CC polynucleotides, a method for producing a pharmaceutical composition, a
 CC method for identifying a compound or small molecule that regulates the
 CC activity in an animal of one or more of the polypeptides given in the
 CC specification, a method for identifying a compound useful in treating
 CC pain and a pharmaceutical composition comprising the one or more
 CC polypeptides or their antibodies. The polynucleotide or the compound that
 CC modulates its activity is useful for preparing a medicament for treating
 CC injury (e.g. spinal segmental nerve injury (SNI)) in an animal (e.g. gene
 CC therapy). The sequence presented is a rat protein (shown in Table 2 of
 CC the specification) which is differentially expressed during pain. Note:
 CC The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic form directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences.
 XX
 SQ Sequence 641 AA;
 Query Match 95.7%; Score 1258; DB 7; Length 641;
 Best Local Similarity 95.3%; Pred. No. 4.1e-96;
 Matches 246; Conservative 7; Mismatches 5; Indels 0; Gaps 0;
 QY 1 KSENVQDLLLLDVAPLSGLGTAGGVTALIKRNSTIPTKQTQFTTYSNQPGLVLIQVY 60
 DB 384 KSENVQDLLLLDVAPLSGLGTAGGVTALIKRNSTIPTKQTQFTTYSNQPGLVLIQVY 443
 QY 61 EGERAMTKDNLLGRFELSGIPAPRGVQPIEVTFDIDANGILNVTTATDKSTGKANKITI 120
 DB 444 EGERAMTRDNNLLGRFELSGIPAPRGVQPIEVTFDIDANGILNVTTATDKSTGKANKITI 503
 QY 121 TNDKGRLSKEEIERMVOEAEKYKAEDVQERVSAAKNALESYAFNMKSAVEDGLGKGIS 180
 DB 504 TNDKGRLSKEEIERMVOEAEKYKAEDVQERVSAAKNALESYAFNMKSAVEDGLGKGIS 563
 QY 181 EADKKVLDKCOEIVSWLDANTLAEXDFEHPKRELEQVCNPIISGLYQAGGPGGFG 240
 DB 564 EADKKVLDKCOEIVSWLDNTLAEXDFEHPKRELERVCNPIISGLYQAGGPGGFG 623
 QY 241 AQPKPGSGSGPTIEVD 258
 DB 624 AQAPKGGSGSGPTIEVD 641
 RESULT 29
 ID ADD45046
 XX ADD45046 standard; protein; 641 AA.
 AC ADD45046;
 XX
 DT 29-JAN-2004 (first entry)
 XX
 DE Rat Protein Q07439, SEQ ID NO 10478.
 XX

KW Rat; pain; neuronal tissue; gene therapy; spinal segmental nerve injury;
 KW chronic constriction injury; CCI; spared nerve injury; SNI; Chung.
 XX Rattus norvegicus.
 OS
 PN WO2003016475-A2.
 XX
 PD 27-FEB-2003.
 XX
 PF 14-AUG-2002; 2002WO-US025765.
 XX
 PR 14-AUG-2001; 2001US-0312147P.
 PR 01-NOV-2001; 2001US-0346382P.
 PR 26-NOV-2001; 2001US-0333347P.
 XX
 PA (GEO) GEN HOSPITAL CORP.
 PA (FARB) BAYER AG.
 XX
 PI Woolf C, D'urso D, Befort K, Costigan M;
 XX WPI; 2003-268312/26.
 DR GENBANK; Q07439.
 XX
 XX New composition comprising two or more isolated polypeptides, useful for
 PT preparing a medicament for treating pain in an animal.
 XX
 PS Claim 1; Page; 1017pp; English.
 XX
 CC The invention discloses a composition comprising two or more isolated rat
 CC or human polynucleotides or a polynucleotide which represents a fragment,
 CC derivative or allelic variation of the nucleic acid sequence. Also
 CC claimed are a vector comprising the novel polynucleotide, a host cell
 CC comprising the vector, a method for identifying a nucleotide sequence
 CC which is differentially regulated in an animal subjected to pain and a
 CC kit to perform the method, an array, a method for identifying an agent
 CC that increases or decreases the expression of the polynucleotide sequence
 CC that is differentially expressed in neuronal tissue of a first animal
 CC subjected to pain, a method for identifying a compound which regulates
 CC the expression of a polynucleotide sequence which is differentially
 CC expressed in an animal subjected to pain, a method for identifying a
 CC compound that regulates the activity of one or more of the
 CC polynucleotides, a method for producing a pharmaceutical composition, a
 CC method for identifying a compound or small molecule that regulates the
 CC activity in an animal of one or more of the polypeptides given in the
 CC specification, a method for identifying a compound useful in treating
 CC pain and a pharmaceutical composition comprising the one or more
 CC polypeptides or their antibodies. The polynucleotide or the compound that
 CC modulates its activity is useful for preparing a medicament for treating
 CC injury (e.g. spinal segmental nerve injury (SNI)) in an animal (e.g. gene
 CC therapy). The sequence presented is a rat protein (shown in Table 2 of
 CC the specification) which is differentially expressed during pain. Note:
 CC The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic form directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences.
 XX
 SQ Sequence 641 AA;
 Query Match 95.7%; Score 1258; DB 7; Length 641;
 Best Local Similarity 95.3%; Pred. No. 4.1e-96;
 Matches 246; Conservative 7; Mismatches 5; Indels 0; Gaps 0;
 QY 1 KSENVQDLLLLDVAPLSGLGTAGGVTALIKRNSTIPTKQTQFTTYSNQPGLVLIQVY 60
 DB 384 KSENVQDLLLLDVAPLSGLGTAGGVTALIKRNSTIPTKQTQFTTYSNQPGLVLIQVY 443
 QY 61 EGERAMTKDNLLGRFELSGIPAPRGVQPIEVTFDIDANGILNVTTATDKSTGKANKITI 120
 DB 444 EGERAMTRDNNLLGRFELSGIPAPRGVQPIEVTFDIDANGILNVTTATDKSTGKANKITI 503
 QY 121 TNDKGRLSKEEIERMVOEAEKYKAEDVQERVSAAKNALESYAFNMKSAVEDGLGKGIS 180
 DB 504 TNDKGRLSKEEIERMVOEAEKYKAEDVQERVSAAKNALESYAFNMKSAVEDGLGKGIS 563
 QY 181 EADKKVLDKCOEIVSWLDANTLAEXDFEHPKRELEQVCNPIISGLYQAGGPGGFG 240
 DB 564 EADKKVLDKCOEIVSWLDNTLAEXDFEHPKRELERVCNPIISGLYQAGGPGGFG 623
 QY 241 AQPKPGSGSGPTIEVD 258
 DB 624 AQAPKGGSGSGPTIEVD 641
 RESULT 29
 ID ADD45046
 XX ADD45046 standard; protein; 641 AA.
 AC ADD45046;
 XX
 DT 29-JAN-2004 (first entry)
 XX
 DE Rat Protein Q07439, SEQ ID NO 10478.
 XX

QY 181 EADKKVLDKQCVISWLDANTLAEDKDFEHRKKELEFQVNCNPIISGLYQAGGPGGFG 240
 Db 564 EADKKVLDKQCVISWLDNTLAEDKDFEHRKKELEFQVNCNPIISGLYQAGGPGGFG 623

QY 241 AQPKGGSGSGPTIEVD 258
 Db 624 AQPKGGSGSGPTIEVD 641

RESULT 30

ADD47457
 ID ADD47457 standard; protein; 641 AA.

XX AC ADD47457;

XX 02-DEC-2004 (revised)

DT 29-JAN-2004 (first entry)

XX Rat Protein NP_114177, SEQ ID NO 13152.

XX Rat; pain; neuronal tissue; gene therapy; spinal segmental nerve injury;
 KW chronic constriction injury; CCI; spared nerve injury; SNI; Chung.

XX Rattus norvegicus.

OS Unidentified.

XX W02003016475-A2.

XX 27-FEB-2003.

XX 14-AUG-2002; 2002WO-US025765.

XX 14-AUG-2001; 2001US-0312147P.

PR 01-NOV-2001; 2001US-0346382P.

PR 26-NOV-2001; 2001US-0333347P.

XX (GEHO) GEN HOSPITAL CORP.

PA (FARB) BAYER AG.

XX Woolf C, D'urbo D, Belfort K, Costigan M;

XX WPI; 2003-268312/26.

DR GENBANK; NP_114177.

XX New composition comprising two or more isolated polypeptides, useful for
 PT preparing a medicament for treating pain in an animal.

XX Example 1; Page; 1017pp; English.

XX The invention discloses a composition comprising two or more isolated rat
 CC or human polynucleotides or a polynucleotide which represents a fragment,
 CC derivative or allelic variation of the nucleic acid sequence. Also
 CC claimed are a vector comprising the novel polynucleotide, a host cell
 CC comprising the vector, a method for identifying a nucleotide sequence
 CC which is differentially regulated in an animal subjected to pain and a
 CC kit to perform the method, an array, a method for identifying an agent
 CC that increases or decreases the expression of the polynucleotide sequence
 CC that is differentially expressed in neuronal tissue of a first animal
 CC subjected to pain, a method for identifying a compound which regulates
 CC the expression of a polynucleotide sequence which is differentially
 CC expressed in an animal subjected to pain, a method for identifying a
 CC compound that regulates the activity of one or more of the
 CC polynucleotides, a method for producing a pharmaceutical composition, a
 CC method for identifying a compound or small molecule that regulates the
 CC activity in an animal of one or more of the polypeptides given in the
 CC specification, a method for identifying a compound useful in treating
 CC pain and a pharmaceutical composition comprising the one or more
 CC polypeptides or their antibodies. The polynucleotide or the compound that
 CC modulates its activity is useful for preparing a medicament for treating
 CC pain (e.g. spinal segmental nerve injury (Chung)), chronic constriction
 CC injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene
 CC therapy). The sequence presented is a rat protein (described in Table 3

CC of the specification) which is differentially expressed during pain.
 CC Note: The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic form directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences.

XX SQ Sequence 641 AA;

Query Match 95.7%; Score 1258; DB 7; Length 641;
 Best Local Similarity 95.3%; Pred. No. 4.1e-96;
 Matches 246; Conservative 7; Mismatches 5; Indels 0; Gaps 0;

QY 1 KSENVQDLLLLDVAPLSGLGLETAGGYMTALIKENSTIPTKQTQITFTTYSNQPGLVLIQVY 60
 Db 384 KSENVQDLLLLDVAPLSGLGLETAGGYMTALIKENSTIPTKQTQITFTTYSNQPGLVLIQVY 443

QY 61 EGERAMTKDNLLGRFELSGIPPPAPRGVQIEVTFDIDANGILNVTTATDKSTGKANKITI 120
 Db 444 EGERAMTRDNLGRFELSGIPPPAPRGVQIEVTFDIDANGILNVTTATDKSTGKANKITI 503

QY 121 TNDKGRLSKBEIERVMQEAERKARDEVORERVSAKNALESYAFNMKSAVEDGLGKGIS 180
 Db 504 TNDKGRLSKBEIERVMQEAERKARDEVORERVSAKNALESYAFNMKSAVEDGLGKGIS 563

QY 181 EADKKVLDKQCVISWLDANTLAEDKDFEHRKKELEFQVNCNPIISGLYQAGGPGGFG 240
 Db 564 EADKKVLDKQCVISWLDNTLAEDKDFEHRKKELEFQVNCNPIISGLYQAGGPGGFG 623

QY 241 AQPKGGSGSGPTIEVD 258

Db 624 AQPKGGSGSGPTIEVD 641

RESULT 31

ADP30465
 ID ADP30465 standard; protein; 641 AA.

XX AC ADP30465;

XX 12-FEB-2004 (first entry)

XX Rat angiogenesis modulating protein #9.

XX rat; angiogenesis; angiogenesis modulating protein;
 KW retinal neovascularisation; choroidal neovascularisation;
 KW chronic inflammation; myocardial ischaemia; stroke;
 KW coronary artery disease; peripheral vascular disease.

OS Rattus norvegicus.

XX US2003162706-A1.

XX 28-AUG-2003.

XX 10-DEC-2002; 2002US-00316253.

XX 08-FEB-2002; 2002US-0355295P.

XX 26-JUN-2002; 2002US-0391758P.

XX (PROC) PROCTER & GAMBLE CO.

XX Peters KG, Thompson LJ, Wang F, Greis KD;

XX WPI; 2003-711557/67.

XX N-PSDB; ADP30464.

XX Treating angiogenesis-mediated disorder, e.g., retinal or choroidal
 PT neovascularization or diseases associated with chronic inflammation,
 PT myocardial ischemia, stroke, coronary artery disease or peripheral
 PT vascular disease.

XX Claim 2; SEQ ID NO 28; 26pp; English.

XX The invention relates to a method of treating an angiogenesis-mediated

CC disorder in a subject. The method is useful for treating angiogenesis-mediated disorder, e.g., retinal or choroidal neovascularisation or mediated disorder, e.g., retinal or choroidal neovascularisation or diseases associated with chronic inflammation, myocardial ischaemia, CC stroke, coronary artery disease or peripheral vascular disease. The CC present sequence is used in the exemplification of the invention.

XX
SQ Sequence 641 AA;

Query Match 95.7%; Score 1258; DB 7; Length 641;
Best Local Similarity 95.3%; Pred. No. 4.1e-96;
Matches 246; Conservative 7; Mismatches 5; Indels 0; Gaps 0;

QY 1 KSENVQDLLLDVAPLSGLGLETAGGVTALIKENSTIPTKQTQIFTTYSNQPGLIQVY 60
DB 384 KSENVQDLLLDVAPLSGLGLETAGGVTALIKENSTIPTKQTQIFTTYSNQPGLIQVY 443

QY 61 EGERAMTKNNLLGRFELSGIPAPRGVPOIEVTFDIDANGILNVTTATDKSTGKANKITI 120
DB 444 EGERAMTRDNNLLGRFELSGIPAPRGVPOIEVTFDIDANGILNVTTATDKSTGKANKITI 503

QY 121 TNDKGRLSKEEIERMVOEAEKYKADEVQERVSAKNALESYAFNMKSAVEDGLGKIS 180
DB 504 TNDKGRLSKEEIERMVOEAEKYKADEVQERVSAKNALESYAFNMKSAVEDGLGKIS 563

QY 181 EADKKVLDKQCEVISWLDANTLAEDFEHKKKELEQVCNPIISGLYQAGGPGGFG 240
DB 564 EADKKVLDKQCEVISWLDANTLAEDFEHKKKELEQVCNPIISGLYQAGGPGGFG 623

QY 241 AQPKGGSGSGPTIEVD 258
DB 624 AQPKGGSGSGPTIEVD 641

RESULT 32
ADF30534
ID ADF30534 standard; protein; 641 AA.
AC ADF30534;
DT 12-FEB-2004 (first entry)
XX Rat angiogenesis modulating protein #56.
DE rat; angiogenesis; angiogenesis modulating protein;
KW retinal neovascularisation; choroidal neovascularisation;
KW chronic inflammation; myocardial ischaemia; stroke;
KW coronary artery disease; peripheral vascular disease.
XX Rattus norvegicus.
OS
XX
XX US2003162706-A1.
XX
XX PD 28-AUG-2003.
XX
XX PF 10-DEC-2002; 2002US-00316253.
XX
XX PR 08-FEB-2002; 2002US-0355295P.
XX PR 26-JUN-2002; 2002US-0391758P.
XX
XX PA (PROC) PROCTER & GAMBLE CO.
XX
XX PI Peters KG, Thompson LJ, Wang F, Greis KD;
XX
XX DR WPI; 2003-711557/67.
XX DR N-PSDB; ADF30533.
XX
XX PT Treating angiogenesis-mediated disorder, e.g., retinal or choroidal
PT neovascularization or diseases associated with chronic inflammation,
PT myocardial ischemia, stroke, coronary artery disease or peripheral
PT vascular disease.
XX
XX PS Claim 2; SEQ ID NO 97; 26pp; English.
XX

CC The invention relates to a method of treating an angiogenesis-mediated disorder in a subject. The method is useful for treating angiogenesis-mediated disorder, e.g., retinal or choroidal neovascularisation or diseases associated with chronic inflammation, myocardial ischaemia, CC stroke, coronary artery disease or peripheral vascular disease. The CC present sequence is used in the exemplification of the invention.

XX
SQ Sequence 641 AA;

Query Match 95.7%; Score 1258; DB 7; Length 641;
Best Local Similarity 95.3%; Pred. No. 4.1e-96;
Matches 246; Conservative 7; Mismatches 5; Indels 0; Gaps 0;

QY 1 KSENVQDLLLDVAPLSGLGLETAGGVTALIKENSTIPTKQTQIFTTYSNQPGLIQVY 60
DB 384 KSENVQDLLLDVAPLSGLGLETAGGVTALIKENSTIPTKQTQIFTTYSNQPGLIQVY 443

QY 61 EGERAMTKNNLLGRFELSGIPAPRGVPOIEVTFDIDANGILNVTTATDKSTGKANKITI 120
DB 444 EGERAMTRDNNLLGRFELSGIPAPRGVPOIEVTFDIDANGILNVTTATDKSTGKANKITI 503

QY 121 TNDKGRLSKEEIERMVOEAEKYKADEVQERVSAKNALESYAFNMKSAVEDGLGKIS 180
DB 504 TNDKGRLSKEEIERMVOEAEKYKADEVQERVSAKNALESYAFNMKSAVEDGLGKIS 563

QY 181 EADKKVLDKQCEVISWLDANTLAEDFEHKKKELEQVCNPIISGLYQAGGPGGFG 240
DB 564 EADKKVLDKQCEVISWLDANTLAEDFEHKKKELEQVCNPIISGLYQAGGPGGFG 623

QY 241 AQPKGGSGSGPTIEVD 258
DB 624 AQPKGGSGSGPTIEVD 641

RESULT 33
AAB09886
ID AAB09886 standard; protein; 244 AA.
AC AAB09886;
DT 06-NOV-2000 (first entry)
XX Hsp70 C-terminal 244 amino acid polypeptide sequence.
DE
XX DE Heat shock protein 70; Hsp70; NF-kappaB; transplant rejection;
KW Heat shock protein 70; Hsp70; NF-kappaB; transplant rejection;
KW autoimmune disease; inflammatory disease; cancer; vascular disease.
XX
OS Homo sapiens.
XX
XX PN W0200031113-A1.
XX
XX PD 02-JUN-2000.
XX
XX PF 17-NOV-1999; 99WO-US027244.
XX
XX PR 24-NOV-1998; 98US-0109872P.
XX
XX PA (BRIM) BRISTOL-MYERS SQUIBB CO.
XX
XX PI Fujihara SM, Nadler SG;
XX
XX DR WPI; 2000-400029/34.
XX
XX PT Intracellular targeted delivery of compounds using the 70 kilodalton heat
PT shock protein, useful in the treatment of transplant rejection,
PT autoimmune diseases and cancer.
XX
XX PS Claim 6; Page 17; 37pp; English.
XX
XX CC The present sequence is the C-terminal 244 amino acids of the 70kD heat
CC shock protein (Hsp70). This sequence was used in a fusion protein with
CC the p50 subunit of transcription factor NF-kappaB, the sequence of which
CC is indicated in the specification as being SEQ ID NO: 1, but which is not

CC given. This fusion protein was created in order to determine the ability
CC of the Hsp70 sequence to direct other proteins into the cell. It was
CC shown that Hsp70 fragments are able to direct other proteins into the
CC cell, a feature which can be used in the treatment of transplant
CC rejection, autoimmune diseases such as rheumatoid arthritis, multiple
CC sclerosis, diabetes, asthma, inflammatory bowel disease, psoriasis,
CC hepatitis, Graves' disease and viteligo, inflammatory diseases including
CC osteoarthritis, pancreatitis and adult respiratory distress syndrome,
CC cancer, vascular diseases (such as restenosis and atherosclerosis) and
CC DNA and RNA viral replication diseases (including herpes)
XX
SQ Sequence 244 AA;
Query Match 95.1%; Score 1249; DB 3; Length 244;
Best Local Similarity 100.0%; Pred. No. 6.7e-96;
Matches 244; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 15 PLSLGLETAGVMTALIKRNSTIPTKQTQFTTYSNQPGVLIQVYGERAMTKNNLLG 74
Db 1 PLSLGLETAGVMTALIKRNSTIPTKQTQFTTYSNQPGVLIQVYGERAMTKNNLLG 60
QY 75 RFELSGIPAPRGVPOIEVTFDANGILNVATDKSTGKANKITITNDKGRLSKEIER 134
Db 61 RFELSGIPAPRGVPOIEVTFDANGILNVATDKSTGKANKITITNDKGRLSKEIER 120
QY 135 MVQEAERYKAEDVQERVSNAKNALESYAFNMKSAVEDGLKGKISEADKKVLDKQEV 194
Db 121 MVQEAERYKAEDVQERVSNAKNALESYAFNMKSAVEDGLKGKISEADKKVLDKQEV 180
QY 195 ISWLDANTLAEKDFEHRKELQVNCNPIISGLYQAGGPGPGGQAQPGKGGSGGPTI 254
Db 181 ISWLDANTLAEKDFEHRKELQVNCNPIISGLYQAGGPGPGGQAQPGKGGSGGPTI 240
QY 255 EEVD 258
Db 241 EEVD 244
RESULT 34
AAR43004
ID AAR43004 standard; protein; 641 AA.
XX AAR43004;
AC
CC
DT 14-MAY-2003 (revised)
DT 25-MAR-2003 (revised)
DT 20-MAY-1994 (first entry)
XX Mature mouse sperm 70kD heat shock protein.
DE
XX Sulphoglycolipid immobilising protein 1; sperm plasma membrane; HSC70B;
KW mammalian; infertility; mycoplasma; HSP70.
XX
OS Mus musculus.
FH
FH Key Location/Qualifiers
FH Region 1..385
FT /label= 44kD ATPase fragment
FT /note= "peptides comprising an intact domain from the
FT ATPase fragment of hsp70 are claimed; the peptides are
FT homologous to sequences conserved between SLIP1 and
FT 74.5kD mycoplasma protein"
FT 1..39
FT Domain /label= IA
FT /note= "part"
FT 40..115
FT Domain /label= IB
FT 116..188
FT Domain /label= IA
FT /note= "part"
FT 189..228
FT Domain /label= IIA
FT /note= "part"

FT Domain 229..306
FT /label= IIB
FT Domain 307..385
FT /label= IIA
FT /note= "part"
XX
PN WO9321954-A1.
XX
PD 11-NOV-1993.
XX
XX 22-APR-1993; 93WO-US003816.
XX
XX 24-APR-1992; 92US-00873961.
PA (BERL-) BERLEX LAB INC.
PA (OTTA-) OTTAWA CIVIC HOSPITAL.
XX
PI Faulds DH, Lingwood CA, Tanphaichitr N;
XX WPI; 1993-368422/46.
XX
XX Mammalian fertilisation decrease for detecting and treating infertility -
PT using sulpho glyco lipid immobilising protein 1-sulphated-glyco moiety
PT interfering compsn., for mycoplasma infection treatment.
XX
PS Claim 2, 17; Page 60-62; 77pp; English.
XX
CC The likelihood of mammalian fertilisation is decreased by contacting a
CC gamete with a sulphoglycolipid immobilising protein 1 (SLIP1)/ sulphated
CC glyco-moiety interfering composition. The interfering compsn. is e.g. the
CC heat shock 70kD protein, SLIP1 (or analogues such as the mouse SLIP1
CC analogue "HSC70B" comprising the amino acid sequence AAR43002) or the
CC 74.5kD mycoplasma protein (AAR43003). (Updated on 25-MAR-2003 to correct
CC PN field.) (Updated on 14-MAY-2003 to correct PS field.)
XX
SQ Sequence 641 AA;
Query Match 94.3%; Score 1239; DB 2; Length 641;
Best Local Similarity 93.4%; Pred. No. 1.6e-94;
Matches 241; Conservative 11; Mismatches 6; Indels 0; Gaps 0;
QY 1 KSENVODLLLDVAPLSLGLETAGVMTALIKRNSTIPTKQTQFTTYSNQPGVLIQVY 60
Db 384 KSENVODLLLDVAPLSLGLETAGVMTALIKRNSTIPTKQTQFTTYSNQPGVLIQVY 443
QY 61 EGERAMTKDNNLLGRFELSGIPAPRGVPOIEVTFDANGILNVATDKSTGKANKITI 120
Db 444 EGERAMTKDNNLLGRFELSGIPAPRGVPOIEVTFDANGILNVATDKSTGKANKITI 503
QY 121 TNDKGRLSKEIERMVQEAERYKAEDVQERVSNAKNALESYAFNMKSAVEDGLKGKIS 180
Db 504 TNDKGRLSKEIERMVQEAERYKAEDVQERVSNAKNALESYAFNMKSAVEDGLKGKIS 563
QY 181 EADKKVLDKQEVISWLDANTLAEKDFEHRKELQVNCNPIISGLYQAGGPGGPG 240
Db 564 EADKKVLDKQEVISWLDANTLAEKDFEHRKELQVNCNPIISGLYQAGGPGGPG 623
QY 241 AQPKGSGSGGPTIEVD 258
Db 624 AQPKGSGSGGPTIEVD 641
RESULT 35
ABR40397
ID ABR40397 standard; protein; 641 AA.
XX
AC ABR40397;
XX
DT 08-AUG-2003 (first entry)
XX
DE Mouse Hsp70 protein.
XX heat shock protein; HSP; cytokine; CC chemokine; nitric oxide; cancer;

KW antimicrobial; virucide; cytostatic; microbial infection; anti-HIV;
 KW viral infection; immune system disorder; vaccine; HSP70; mouse.
 XX Mus sp.
 XX WO2003029289-A2.
 XX 10-APR-2003.
 XX 03-OCT-2002; 2002WO-GB004475.
 XX 03-OCT-2001; 2001GB-00023756.
 XX (UNLO) KINGS COLLEGE LONDON.
 XX Lehner T, Kelly CG, Singh M, Wang Y;
 XX WPI; 2003-430189/40.
 XX Novel heat shock protein fragment useful for treating microbial
 PT infection, viral infection or cancer, that can increase the level of
 PT cytokines and/or CC chemokines and/or nitric oxide produced by a cell.
 XX Example 3; Page 17-20; 30pp; English.
 XX The invention relates to a novel heat shock protein fragment (HSP) that
 CC can increase the level of one or more cytokines and/or one or more CC
 CC chemokines and/or nitric oxide produced by a cell, above that caused by
 CC the corresponding full length heat shock protein. The protein fragment of
 CC the invention has antimicrobial, virucide, and cytostatic activity. The
 CC protein fragment is useful in therapy, in treatment or prophylaxis of a
 CC disease and in the manufacture of a medicament for treatment or
 CC prophylaxis of a disease such as microbial infection, viral infection,
 CC disease of the immune system or cancer. The fragment is also useful as an
 CC adjuvant in vaccines, preferably, anti-HIV vaccines. The present sequence
 CC represents the mouse HSP70 protein
 XX
 SQ Sequence 641 AA;

Query Match 94.3%; Score 1239; DB 6; Length 641;
 Best Local Similarity 93.4%; Pred. No. 1.6e-94;
 Matches 241; Conservative 11; Mismatches 6; Indels 0; Gaps 0;
 QY 1 KSENVQDLLLDVAPLSLGLTAGGVTALIKENSTPTKQTQFTTYSNQPGLVLIQVY 60
 DB 384 KSENVQDLLLDVAPLSLGLTAGGVTALIKENSTPTKQTQFTTYSNQPGLVLIQVY 443
 QY 61 EGERAMTKNNLLGRFELSGIPAPRGVPOIEVTFDIDANGILNVTATDKSTGKANKITI 120
 DB 444 EGERAMTRDNNLLGRFELSGIPAPRGVPOIEVTFDIDANGILNVTATDKSTGKANKITI 503
 QY 121 TNDKGRLSKEEIERMWQEAERYKAEDVQREVSAKNALESYAFNMKSAVEDGLGKGLS 180
 DB 504 TNDKGRLSKEEIERMWQEAERYKAEDVQREVSAKNALESYAFNMKSAVEDGLGKGLS 563
 QY 181 EADKKVLDKQCEVISWLDANTLAEDFEHKKRKELEQVNCNPIISGLYQAGGPGGFG 240
 DB 564 EADKKVLDKQCEVISWLDNTLADKEEFVHKREELERVCSPIISGLYQAGGPGGFG 623
 QY 241 AQPKGSGSGPTIEVD 258
 DB 624 AQAPKGASGSGPTIEVD 641

RESULT 36
 ADJ27277
 ID ADJ27277 standard; protein; 641 AA.
 XX
 AC ADJ27277;
 XX
 DT 20-MAY-2004 (first entry)
 XX
 DE Mouse HSP70.3.

XX heat shock protein-70; HSP70; HSP70.1; HSP70.3; inducible; induction;
 KW heat; tumour necrosis factor; TNF; interferon-gamma; tumour.
 XX Mus sp.
 XX WO2003061684-A2.
 XX 31-JUL-2003.
 XX 24-JAN-2003; 2003WO-BP000786.
 XX 24-JAN-2002; 2002EP-00075297.
 XX (VLA-) VLAAMS INTERUNIVERSITAIR INST BIOTECHNOG.
 XX Libert C, Wielockx B, Van Molle W, Mahieu T;
 XX WPI; 2003-608168/57.
 DR N-PSDB; ADJ27276.
 XX New pharmaceutical composition comprising HSP70 that is endogenously
 PT induced by heat and TNF, useful for the manufacture of a medicament for
 PT treating systemic tumor.
 XX Disclosure; SEQ ID NO 4; 53pp; English.
 XX This sequence represents mouse heat shock protein-70.3 (HSP70.3). HSP70.1
 CC and HSP70.3 are inducible members of the HSP70 family of proteins. The
 CC heat shock proteins of the invention are endogenously induced by heat and
 CC tumour necrosis factor (TNF). This heat shock protein may be used in a
 CC composition which further comprises interferon-gamma, and/or a
 CC chemotherapeutic compound. The pharmaceutical composition is useful for
 CC the manufacture of a medicament for treating systemic tumour.
 XX
 SQ Sequence 641 AA;

Query Match 94.3%; Score 1239; DB 7; Length 641;
 Best Local Similarity 93.4%; Pred. No. 1.6e-94;
 Matches 241; Conservative 11; Mismatches 6; Indels 0; Gaps 0;
 QY 1 KSENVQDLLLDVAPLSLGLTAGGVTALIKENSTPTKQTQFTTYSNQPGLVLIQVY 60
 DB 384 KSENVQDLLLDVAPLSLGLTAGGVTALIKENSTPTKQTQFTTYSNQPGLVLIQVY 443
 QY 61 EGERAMTKNNLLGRFELSGIPAPRGVPOIEVTFDIDANGILNVTATDKSTGKANKITI 120
 DB 444 EGERAMTRDNNLLGRFELSGIPAPRGVPOIEVTFDIDANGILNVTATDKSTGKANKITI 503
 QY 121 TNDKGRLSKEEIERMWQEAERYKAEDVQREVSAKNALESYAFNMKSAVEDGLGKGLS 180
 DB 504 TNDKGRLSKEEIERMWQEAERYKAEDVQREVSAKNALESYAFNMKSAVEDGLGKGLS 563
 QY 181 EADKKVLDKQCEVISWLDANTLAEDFEHKKRKELEQVNCNPIISGLYQAGGPGGFG 240
 DB 564 EADKKVLDKQCEVISWLDNTLADKEEFVHKREELERVCSPIISGLYQAGGPGGFG 623
 QY 241 AQPKGSGSGPTIEVD 258
 DB 624 AQAPKGASGSGPTIEVD 641

RESULT 37
 AAB23650
 ID AAB23650 standard; protein; 642 AA.
 XX
 AC AAB23650;
 XX
 DT 05-JAN-2001 (first entry)
 XX
 DE Rat heat shock protein Hsp70.1 protein sequence SEQ ID NO:2.
 XX
 KW ATPase; Hsp70; heat shock protein; cytotoxic T lymphocyte; CTL;

immune response; infectious disease; malaria; cytotoxic T cell;
 cytostatic; immunostimulant; cellular immune response inducer;
 protozoacide; leukaemia; cancer.

Rattus sp.
 WO200049041-A1.
 24-AUG-2000.

18-FEB-2000; 2000WO-JP000941.
 19-FEB-1999; 99JP-00041535.

(SUME) SUMITOMO ELECTRIC IND CO.
 Shinbara N, Udono H, Yui K;
 WPI; 2000-543748/49.

Fused protein capable of inducing cellular immune response, useful as
 active ingredient for drug compositions in preventing and/or treating
 infectious diseases such as malaria or cancer.

Claim 3; Page 39-42; 72pp; Japanese.

The present invention describes a fused protein (I) prepared from a
 peptide containing a CTL (cytotoxic T lymphocyte) epitope recognised by
 cytotoxic T cells and a protein containing the Afpase domain of a heat
 shock protein. Also described are: (1) a drug composition containing (I)
 as active ingredient; (2) a DNA encoding (I); (3) an expression vector
 containing the DNA of (2); and (4) a transformant which can retain the
 expression vector of (3). (I) has cytostatic, immunostimulant and
 protozoacide activities, and can be used as a cellular immune response
 inducer. The protein is useful as an active ingredient for drug
 compositions in preventing and/or treating infectious diseases such as
 malaria or cancer e.g. to provide systemic immunity against leukaemia.
 The present sequence represents a specifically claimed heat shock protein
 for use in a fused protein of the present invention

XX SQ Sequence 642 AA;
 Query Match 93.5%; Score 1228.5; DB 3; Length 642;
 Best Local Similarity 93.1%; Pred. No. 1.2e-93;
 Matches 241; Conservative 11; Mismatches 6; Indels 1; Gaps 1;
 QY 1 KSENVQDLLLLDVAPLSLGLETAGGVTALIKRNSTIPTKQTQFTTYSNQPGVLIQVY 60
 DB 384 KSENVQDLLLLDVAPLSLGLETAGGVTALIKRNSTIPTKQTQFTTYSNQPGVLIQVY 443
 QY 61 EGERAMTKDNNLLGRPELSGIPPPAPRGVPOIEVTFDIDANGILNVATDKSTGKANKITI 120
 DB 444 EGERAMTRDNNLLGRPELSGIPPPAPRGVPOIEVTFDIDANGILNVATDKSTGKANKITI 503
 QY 121 TNDKGRLSKEEIERMVOEAEKYKAEDVQVRERSAKNALESYAFNMKSAVEDEGLKGKIS 180
 DB 504 TNDKGRLSKEEIERMVOEAEKYKAEDVQVRERSAKNALESYAFNMKSAVEDEGLKGKIS 563
 QY 181 EADKKVKLDKQCEVISWLDANTLAERDEFEHKKRKELEQVNCNPIISGLYQAGAGPGGFG 240
 DB 564 EADKKVKLDKQCEVISWLDNSNTLADKEEFVHKREELERVCSPIISGLYQAGAGPGGFG 623
 QY 241 AQG-PKGGSGSGPTIEVD 258
 DB 624 AQAPPKGASGSGPTIEVD 642

RESULT 38
 ADJ27275
 ID ADJ27275 standard; protein; 642 AA.
 XX AC
 AC ADJ27275;
 XX

20-MAY-2004 (first entry)
 Mouse HSP70.1.
 heat shock protein-70; HSP70; HSP70.1; HSP70.3; inducible; induction;
 heat; tumour necrosis factor; TNF; interferon-gamma; tumour.

Mus sp.
 WO2003061684-A2.
 31-JUL-2003.

24-JAN-2003; 2003WO-BP000786.
 24-JAN-2002; 2002EP-00075297.

(VLA-) VLAAMS INTERUNIVERSITAIR INST BIOTECHNOG.
 Libert C, Wielockx B, Van Molle W, Mahieu T;
 WPI; 2003-608168/57.
 N-PSDB; ADJ27274.

New pharmaceutical composition comprising HSP70 that is endogenously
 induced by heat and TNF, useful for the manufacture of a medicament for
 treating systemic tumor.

Disclosure; SEQ ID NO 2; 53pp; English.

This sequence represents mouse heat shock protein-70.1 (HSP70.1). HSP70.1
 and HSP70.3 are inducible members of the HSP70 family of proteins. The
 heat shock proteins of the invention are endogenously induced by heat and
 tumour necrosis factor (TNF). This heat shock protein may be used in a
 composition which further comprises interferon-gamma, and/or a
 chemotherapeutic compound. The pharmaceutical composition is useful for
 the manufacture of a medicament for treating systemic tumour.

XX SQ Sequence 642 AA;
 Query Match 93.5%; Score 1228.5; DB 7; Length 642;
 Best Local Similarity 93.1%; Pred. No. 1.2e-93;
 Matches 241; Conservative 11; Mismatches 6; Indels 1; Gaps 1;
 QY 1 KSENVQDLLLLDVAPLSLGLETAGGVTALIKRNSTIPTKQTQFTTYSNQPGVLIQVY 60
 DB 384 KSENVQDLLLLDVAPLSLGLETAGGVTALIKRNSTIPTKQTQFTTYSNQPGVLIQVY 443
 QY 61 EGERAMTKDNNLLGRPELSGIPPPAPRGVPOIEVTFDIDANGILNVATDKSTGKANKITI 120
 DB 444 EGERAMTRDNNLLGRPELSGIPPPAPRGVPOIEVTFDIDANGILNVATDKSTGKANKITI 503
 QY 121 TNDKGRLSKEEIERMVOEAEKYKAEDVQVRERSAKNALESYAFNMKSAVEDEGLKGKIS 180
 DB 504 TNDKGRLSKEEIERMVOEAEKYKAEDVQVRERSAKNALESYAFNMKSAVEDEGLKGKIS 563
 QY 181 EADKKVKLDKQCEVISWLDANTLAERDEFEHKKRKELEQVNCNPIISGLYQAGAGPGGFG 240
 DB 564 EADKKVKLDKQCEVISWLDNSNTLADKEEFVHKREELERVCSPIISGLYQAGAGPGGFG 623
 QY 241 AQG-PKGGSGSGPTIEVD 258
 DB 624 AQAPPKGASGSGPTIEVD 642

RESULT 39
 AAB23252
 ID AAB23252 standard; protein; 624 AA.
 XX AC
 AC AAB23252;
 XX DT
 DT 29-JAN-2001 (first entry)
 XX

DE Human Hsp72 (heat shock protein 72).

XX Human Hsp72; heat shock protein 72; chromosome 6p21.3; Hsp72 inhibitor;
 XX expression modulator; JNK phosphatase inhibitor; antiproliferative;
 KW drug screening; cancer; leukaemia; lymphoma; solid tumour; sarcoma;
 KW carcinoma; breast cancer; prostate cancer; premalignant condition.
 XX Homo sapiens.

OS WO200054814-A1.
 XX 21-SEP-2000.
 XX 17-MAR-2000; 2000WO-US007350.
 XX 18-MAR-1999; 99US-0125046P.
 XX (PHYL-) PHYLOGENY INC.
 XX Volloch VZ, Sherman M;
 XX WPI: 2000-647056/62.
 XX N-PSDB; AAA97541.

XX Identifying compounds that inhibit proliferation of cells and capable of
 PT modulating the expression of heat shock protein 72 gene and/or activity
 PT of Hsp72 useful for treating cancers such as leukemia, lymphoma.
 XX Example; Fig 16B; 77pp; English.

XX The invention relates to a novel method of identifying compounds that
 CC inhibit proliferation of cells comprising contacting a test compound with
 CC a cell which overexpresses Hsp72 (heat shock protein 72), and determining
 CC if the test compound inhibits activity or expression of Hsp72.
 CC Optionally, Hsp72 is contacted with the test compound under optimum
 CC conditions to allow the two components to interact and bind, forming a
 CC complex which is detected. The invention also relates to a method of
 CC identifying compounds that inhibit Hsp72-mediated JNK phosphatase
 CC activation, comprising contacting a test compound with a cell which
 CC expresses Hsp72, exposing the cell to a heat induced stress and
 CC determining if the compound inhibits JNK phosphatase activity. The
 CC invention additionally encompasses compositions comprising an inhibitor
 CC of Hsp72 or JNK phosphatase activity. The compounds identified as
 CC inhibitors of Hsp72 or JNK phosphatase activity are useful for inhibiting
 CC the proliferation of cells. Modulation of the activity of the JNK
 CC phosphatase or Hsp72 is used to treat a proliferative disorder such as
 CC cancers (e.g., leukaemia, lymphoma, solid tumours such as sarcomas and
 CC carcinomas, breast cancer, prostate cancer). The compounds that inhibit
 CC Hsp72 activity can also be administered to treat premalignant conditions
 CC and to prevent progression to a neoplastic or malignant state. The
 CC compounds that inhibit Hsp72 function are administered to a patient
 CC having a disease or disorder mediated by an increase of Hsp72 expression
 CC or activity relative to normal levels. The present sequence represents
 CC human Hsp72 used in the exemplifications of the invention

XX
 SQ Sequence 624 AA;

Query Match 93.1%; Score 1223; DB 3; Length 624;
 Best Local Similarity 100.0%; Pred. No. 3.3e-93;
 Matches 241; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KSENVQDLLLDVAPLSGLTAGGVTALIKENSTIPTKQTQIFTTSDNQGVLIQVY 60
 DB 384 KSENVQDLLLDVAPLSGLTAGGVTALIKENSTIPTKQTQIFTTSDNQGVLIQVY 443

QY 61 EGERAMTKNNLLGRFELSIPAPRGVPOIEVTFDIDANGILNVTATDKSTGKANKITI 120
 DB 444 EGERAMTKNNLLGRFELSIPAPRGVPOIEVTFDIDANGILNVTATDKSTGKANKITI 503

QY 121 TNDKGRLSKEEIERMWQEAKEYKADEVQERVSANNALESYAFNMKSAVEDSGLGKIS 180
 DB 504 TNDKGRLSKEEIERMWQEAKEYKADEVQERVSANNALESYAFNMKSAVEDSGLGKIS 563

QY 181 EADKKVKLDKQCVISWLDANTLAEDFEHKKRKELEQVCNPIISGLYQAGGPGGFG 240
 DB 564 EADKKVKLDKQCVISWLDANTLAEDFEHKKRKELEQVCNPIISGLYQAGGPGGFG 623

QY 241 A 241
 DB 624 A 624

RESULT 40
 AAY88413
 ID AAY88413 standard; protein; 554 AA.
 XX
 AC AAY88413;
 XX
 DT 31-JUL-2000 (first entry)
 XX
 DE Human heat shock protein SHSP70 amino acid sequence.

XX Human; heat shock protein; HSP70; chromosome 6p21.3-22; stress;
 KW chromosome 14q22-24; transcription; rheumatism; schizophrenia;
 KW depression; nephrotic syndrome; SHSP70.
 XX
 OS Homo sapiens.
 XX JP2000069999-A.
 PN 07-MAR-2000.
 PD
 XX 01-JUN-1995; 99JP-00257146.
 PF
 XX 01-JUN-1995; 95JP-00158581.
 PR
 XX (HOKE-) HOKEN KAGAKU KENKYUSHO KK.
 PA
 XX WPI: 2000-264458/23.
 DR
 XX Abnormal transcription of intracellular HSP70mRNA under acute and chronic
 PT continuous load of stress in a human being and its application.
 PT
 XX Disclosure; Fig 6; 11pp; Japanese.

XX This sequence represents the human heat shock protein SHSP70 amino acid
 CC sequence. Human heat shock proteins are located on chromosomes 6p21.3-22
 CC and 14q22-24. The invention relates to the abnormal transcription of
 CC intracellular HSP70mRNA under acute and chronic stress load in a human.
 CC The abnormal transcription of HSP70 can be used in the improvement of
 CC stress and response and diagnosis of stress diseases including
 CC rheumatism, schizophrenia, depression and nephrotic syndrome

XX Sequence 554 AA;

Query Match 92.7%; Score 1217.5; DB 3; Length 554;
 Best Local Similarity 95.3%; Pred. No. 8.2e-93;
 Matches 246; Conservative 3; Mismatches 8; Indels 1; Gaps 1;

QY 1 KSENVQDLLLDVAPLSGLTAGGVTALIKENSTIPTKQTQIFTTSDNQGVLIQVY 60
 DB 298 KSENVQDLLLDVAPLSGLTAGGVTALIKENSTIPTKQTQIFTTSDNQGVLIQVY 357

QY 61 EGERAMTKNNLLGRFELSIPAPRGVPOIEVTFDIDANGILNVTATDKSTGKANKITI 120
 DB 358 EGERAMTKNNLLGRFELSIPAPRGVPOIEVTFDIDANGILNVTATDKSTGKANKITI 416

QY 121 TNDKGRLSKEEIERMWQEAKEYKADEVQERVSANNALESYAFNMKSAVEDSGLGKIS 180
 DB 417 TNDKGRLSKEEIERMWQEAKEYKADEVQERVSANNALESYAFNMKSAVEDSGLGKIS 476

QY 181 EADKKVKLDKQCVISWLDANTLAEDFEHKKRKELEQVCNPIISGLYQAGGPGGFG 240
 DB 477 EADKKVKLDKQCVISWLDANTLAEDFEHKKRKELEQVCNPIISGLYQAGGPGGFG 536

QY 241 AQGPKGGSGSGPTIEVD 258

Db 537 AQPCKGGSGGPTIEYD 554
|||||
RESULT 41
AA98412
ID AAY88412 standard; protein; 554 AA.
XX AC AAY88412;
XX DT 31-JUL-2000 (first entry)
XX DE Human heat shock protein SHSP70 amino acid sequence.
XX KW Human; heat shock protein; HSP70; chromosome 6p21.3-22; stress;
XX KW chromosome 14q22-24; transcription; rheumatism; schizophrenia;
XX KW depression; nephrotic syndrome; SHSP70.
XX OS Homo sapiens.
XX PN JP2000069999-A.
XX PD 07-MAR-2000.
XX PF 01-JUN-1995; 99JP-00257146.
XX PR 01-JUN-1995; 95JP-00158581.
XX PA (HOKE-) HOKEN KAGAKU KENKUSHO KK.
XX DR WPI; 2000-264458/23.
XX PT Abnormal transcription of intracellular HSP70mRNA under acute and chronic
XX continuous load of stress in a human being and its application.
XX PS Disclosure; Fig 5; 11pp; Japanese.
XX SS This sequence represents the human heat shock protein SHSP70 amino acid
CC sequence. Human heat shock proteins are located on chromosomes 6p21.3-22
CC and 14q22-24. The invention relates to the abnormal transcription of
CC intracellular HSP70mRNA under acute and chronic stress load in a human.
CC The abnormal transcription of HSP70 can be used in the improvement of
CC stress and response and diagnosis of stress diseases including
CC rheumatism, schizophrenia, depression and nephrotic syndrome
XX Sequence 554 AA;
Query Match 91.1%; Score 1196.5; DB 3; Length 554;
Best Local Similarity 94.6%; Pred. No. 4.6e-91;
Matches 244; Conservative 3; Mismatches 10; Indels 1; Gaps 1;
QY 1 KSENVODLLLDVAPLSGLTAGGVTALIKRNSTPTKQTQIFFTYSDNQPGVLIQVY 60
Db 298 KSENVODLLLDVAPLSGLTAGGVTALIKRNSTPTKQTQIFFTYSDNQPGVLIQVY 357
QY 61 EGERAMTKNNLLGRFELSGLTAPRGVQIETVFDIDANGILNVTATDKSTGKANKITI 120
Db 358 EGERAMTKNNLLGKPFELSGIFFAP-CVPIETVFDIDANGILNVTATDKSTGKANKITI 416
QY 121 TNDKGRLSKEIEIRMQEAKYAEDEVQERVSNAKNALESYAFNMKSAVEDGLGKGIS 180
Db 417 TNDHGRLSKEIEIRMQEAKYAEDEVQERVSNAKNALESYAFNMKSAVEDGLGKGIS 476
QY 181 EADKKVLDKQCVISWLDANTLAEKDFEPEHKEKELEOVNCPNIIISGLYQAGGPGGFG 240
Db 477 EADKKVLDKQCVISWLDANTLAEKDFEPEHKEKELEOVNCPNIIISGLYQAGGPGGFG 536
QY 241 AQPCKGGSGGPTIEYD 258
Db 537 AQPCKGGSGGPTIEYD 554
RESULT 42

ADJ69869
ID ADJ69869 standard; protein; 641 AA.
XX AC ADJ69869;
XX DT 06-MAY-2004 (first entry)
XX DE Human heat mitochondrial protein as a therapeutic target SeqID1675.
XX KW mitochondrial; human; screening assay; diabetes mellitus;
XX KW Huntington's disease; osteoarthritis;
XX KW Leber's hereditary optic neuropathy; LHON;
XX KW mitochondrial encephalopathy lactic acidosis and stroke; MELAS;
XX KW myoclonic epilepsy ragged red fibre syndrome; MERRF; cancer;
XX KW neuroprotective; neurotropic; antidiabetic; anticonvulsant; antiarthritic;
XX KW osteopathic; ophthalmological; cytostatic.
XX OS Homo sapiens.
XX PN WO2003087768-A2.
XX PD 23-OCT-2003.
XX PF 04-APR-2003; 2003WO-US010870.
XX PR 12-APR-2002; 2002US-0372843P.
XX PR 17-JUN-2002; 2002US-0389987P.
XX PR 20-SEP-2002; 2002US-0412418P.
XX PA (MITO-) MITOKOR.
XX PA (BUCK-) BUCK INST AGE RES.
XX PI Ghosh SS, Fahy ED, Zhang B, Gibson BW, Taylor SW, Glenn GM;
PI Warnock DE;
XX WPI; 2003-845369/78.
XX PT Identifying a mitochondrial target for drug screening assays and for
CC treating diseases associated with altered mitochondrial function,
CC comprises detecting a modified polypeptide in a sample and correlating
CC with the disease.
XX Claim 1; SEQ ID NO 1675; 180pp; English.
XX SS This invention relates to novel mitochondrial targets that can be used
CC for therapeutic intervention in treating a disease associated with
CC altered mitochondrial function. Specifically, it refers to a method for
CC identifying proteins of the human heart mitochondrial proteome that are
CC useful for drug screening assays, as well as therapeutic targets. The
CC present invention describes a method for identifying such proteins that
CC can be used in the treatment of various diseases associated with altered
CC mitochondrial function including diabetes mellitus, Huntington's disease,
CC osteoarthritis, Leber's hereditary optic neuropathy (LHON), mitochondrial
CC encephalopathy lactic acidosis and stroke (MELAS), myoclonic epilepsy
CC ragged red fibre syndrome (MERRF) or cancer. Accordingly, these
CC compositions have neuroprotective, neurotropic, antidiabetic,
CC anticonvulsant, antiarthritic, osteopathic, ophthalmological and
CC cytostatic activities. This polypeptide sequence is a human heart
CC mitochondrial protein of the invention.
XX Sequence 641 AA;
Query Match 83.9%; Score 1103; DB 7; Length 641;
Best Local Similarity 82.3%; Pred. No. 3.5e-83;
Matches 218; Conservative 16; Mismatches 15; Indels 16; Gaps 2;
QY 1 KSENVODLLLDVAPLSGLTAGGVTALIKRNSTPTKQTQIFFTYSDNQPGVLIQVY 60
Db 386 KSENVODLLLDVAPLSGLTAGGVTALIKRNSTPTKQTQIFFTYSDNQPGVLIQV 445
QY 61 EGERAMTKNNLLGRFELSGLTAPRGVQIETVFDIDANGILNVTATDKSTGKANKITI 120
Db 446 EGERAMTKNNLLGRFELDTGIPAPRGVQIETVFDIDANGILNVTAMDKSTGKANKITI 505

QY 121 TNDKRLSKKEIERMVOEAKYKAEDVQERVSANNALESYAFNMKSAVEDGLGKIS 180
DB 506 TNDKRLSKKEIERMVOEAKYKAEDVQERVSANNALESYAFNMKSAVEDGLGKIS 565
QY 181 EADKKVLDKCOEIVSWLDANTLAEDFEHKEKELEQVNCNPIISGLYQAGGPGGFC 240
DB 566 ESKNKILDKCNELLSWLVNQLAEKDFDHRKKELEQVNCNPIITKLQYQ-----G 616
QY 241 AQCPKGGSG-----SGPTIEVD 258
DB 617 CTGPACGTGVVGRPATGPTIEVD 641

RESULT 43

AAV17408
ID AAV17408 standard; protein; 646 AA.

AC AAV17408;

DT 26-JUL-1999 (first entry)

DE Mouse heat shock cognate 73.

KW Heat shock cognate 73; HSC73; cancer gene; diagnosis; neoplasia;

KW detection; carcinoma; breast; tumour.

OS Mus musculus.

PN WO9923252-A1.

PD 14-MAY-1999.

PF 05-NOV-1998; 98WO-GB003375.

PR 05-NOV-1997; 97GB-00023412.

PR 19-AUG-1998; 98GB-00018118.

XX (ISIS-) ISIS INNOVATION LTD.

XX Bakkenist CJ, Koreth J, Mcgee JO;

XX WPI; 1999-337489/28.

DR N-PSDB; AAX56459.

XX Method for diagnosis of cancer by detecting aberrant expression of gene.

XX Disclosure; Fig 6; 49pp; English.

XX A method of diagnosis performed on a biological sample has been developed comprising detecting the aberrant expression of a gene at the heat shock cognate 73 (HSC73) locus, or detecting a mutation at the HSC73 locus. The method is used for diagnosing neoplasia or a susceptibility to neoplasia especially malignant neoplasia, and carcinomas of the breast. Gene or protein therapy of mutated HSC73 is performed by administration of native HSC73, and the transgenic mammal is useful as an experimental model for technical development of gene therapy. The HSC73 gene was transfected into cell lines, which were introduced into test animals. These animals were injected with untransfected cells of a breast cancer line. Expression of wild type HSC73 prevented breast cancer cells forming tumours in the mice. The present sequence represents mouse HSC73 from the present invention

XX Sequence 646 AA;

Query Match 83.8%; Score 1100.5; DB 2; Length 646;

Best Local Similarity 81.7%; Pred. No. 5.8e-83;

Matches 215; Conservative 23; Mismatches 20; Indels 5; Gaps 3;

QY 1 KSENVODLLLDVAPLSLGTAGVMTALIKENSTIPTKTQTFTTYSNQPGVLIQVY 60

DB 384 KSENVODLLLDVTPUSLGTAGVMTALIKRNTTPTKTQTFTTYSNQPGVLIQVY 443

QY 61 EGERAMTKNNLLGRFELSGIPPAKGVQIEVTFDIDANGILNVTTATDKSTGKANKITI 120
DB 444 EGERAMTKNNLLGKFEFGTIPPAKGVQIEVTFDIDANGILNVSAVDKSTGKANKITI 503
QY 121 TNDKRLSKKEIERMVOEAKYKAEDVQERVSANNALESYAFNMKSAVEDGLGKIS 180
DB 504 TNDKRLSKKEIERMVOEAKYKAEDVQERVSANNALESYAFNMKSAVEDGLGKIS 563
QY 181 EADKKVLDKCOEIVSWLDANTLAEDFEHKEKELEQVNCNPIISGLYQAGG-PG--PG 237
DB 564 DEDKQKILDKCNEIISWLDKNOTAEKEFEHQKKELEKVCNPIITKLQYSGAGGMPGMPG 623
QY 238 GP--GAQPKGGSGSGPTIEVD 258
DB 624 GPPGGGAPPSPGSGSGPTIEVD 646

RESULT 44

AAB23649

ID AAB23649 standard; protein; 646 AA.

XX AAB23649;

DT 05-JAN-2001 (first entry)

DE Mouse heat shock protein Hsc70 protein sequence SEQ ID NO:1.

KW ATPase; Hsp70; heat shock protein; cytotoxic T lymphocyte; CTL;

KW immune response; infectious disease; malaria; cytotoxic T cell;

KW cytototoxic; immunostimulant; cellular immune response inducer;

KW protozoacide; leukaemia; cancer.

XX Mus sp.

PN WO200049041-A1.

PD 24-AUG-2000.

PF 18-FEB-2000; 2000WO-JP000941.

PR 19-FEB-1999; 99JP-00041535.

XX (SUME) SUMITOMO ELECTRIC IND CO.

XX Shinbara N, Udono H, Yui K;

XX WPI; 2000-543748/49.

XX Fused protein capable of inducing cellular immune response, useful as active ingredient for drug compositions in preventing and/or treating infectious diseases such as malaria or cancer.

XX Claim 3; Page 36-39; 72pp; Japanese.

XX The present invention describes a fused protein (I) prepared from a peptide containing a CTL (cytotoxic T lymphocyte) epitope recognised by cytotoxic T cells and a protein containing the ATPase domain of a heat shock protein. Also described are: (1) a drug composition containing (I) as active ingredient; (2) a DNA encoding (I); (3) an expression vector containing the DNA of (2); and (4) a transformant which can retain the expression vector of (3). (I) has cytostatic, immunostimulant and protozoacide activities, and can be used as a cellular immune response inducer. The protein is useful as an active ingredient for drug compositions in preventing and/or treating infectious diseases such as malaria or cancer e.g. to provide systemic immunity against leukaemia. The present sequence represents a specifically claimed heat shock protein for use in a fused protein of the present invention

XX Sequence 646 AA;

Query Match 83.8%; Score 1100.5; DB 3; Length 646;

Best Local Similarity 81.7%; Pred. No. 5.8e-83;

Matches 215; Conservative 23; Mismatches 20; Indels 5; Gaps 3;

QY 1 KSENVQDLLLLLDVAPLSGLTAGGVTALIKRNSIPTKQTOIFTTYSNQPGLIOVY 60
 DB 384 KSENVQDLLLLLDVAPLSGLTAGGVTALIKRNTTPTKQTOFTTYSNQPGLIOVY 443
 QY 61 EGERAMTKDNLLGRFELSGIPAPRGVPOIEVTFDIDANGILNVATDKSTGKANKITI 120
 DB 444 EGERAMTKDNLLGRFELSGIPAPRGVPOIEVTFDIDANGILNVSAVDKSTGKANKITI 503
 QY 121 TNDKRLSKKEEIERMVQEAKEYKAEDVQREVRSKNALESYAFNMKSAVEDGLKKGKIS 180
 DB 504 TNDKRLSKKEEIERMVQEAKEYKAEDKQDKVSKNSLESYAFNMKATVEDEKLQKGIN 563
 QY 181 EADKKVLDKQCEVSWLDANTLAEKDFEHRKELEOVCPNPIISGLYQAGG-PG--PG 237
 DB 564 DEDKQKILDKCNELIISWLDKNTAKESFEHQKLEKVCNPIITIKLYQAGGPGMPG 623
 QY 238 GF--GAQGPKGSGSGPTIEEVD 258
 DB 624 GPPGGGAPPSGGASSGPTIEEVD 646

RESULT 45
 ADD18652
 ID ADD18652 standard; protein; 646 AA.
 XX AC ADD18652;
 XX DT 22-SEP-2003 (first entry)
 XX DE Rat heat shock cognate protein 70.
 XX KW spinal cord; neuropathic pain; central sensitisation pain; pain;
 XX KW analgesic; gene therapy.
 XX OS Rattus norvegicus.
 XX PN EP1284298-A2.
 XX PD 19-FEB-2003.
 XX PF 26-JUL-2002; 2002EP-00255229.
 XX PR 27-JUL-2001; 2001GB-00018354.
 XX PR 07-FEB-2002; 2002GB-00002883.
 XX FA (WARN) WARNER LAMBERT CO.
 XX PI Brooksbank RA, Dixon AK, Lee K, Pinnock RD;
 XX DR WPI; 2003-543489/52.
 XX DR N-PSDB; ACF25380.
 XX PT Use of an isolated gene sequence in the screening of compounds for
 XX PT diagnosing or treating pain.
 XX PS Claim 1; Page 170-172; 189pp; English.
 XX CC The invention relates to a novel isolated gene sequence that is
 XX CC downregulated in the spinal cord of a mammal in response to mechanically
 XX CC distinct first and second models of neuropathic or central sensitisation
 XX CC pain, useful in the screening of compounds for diagnosing or treating
 XX CC pain. A protein encoded by a gene of the invention has analgesic
 XX CC activity. A polynucleotide of the invention may have a use in gene
 XX CC therapy. The gene sequence is useful for preparing a composition for
 XX CC diagnosing or treating pain. The present sequence represents a protein
 XX CC encoded by a gene of the invention
 XX SQ Sequence 646 AA;

Query Match 83.8%; Score 1100.5; DB 6; Length 646;
 Best Local Similarity 81.7%; Pred. No. 5.8e-83;
 Matches 215; Conservative 23; Mismatches 20; Indels 5; Gaps 3;

QY 1 KSENVQDLLLLLDVAPLSGLTAGGVTALIKRNSIPTKQTOIFTTYSNQPGLIOVY 60
 DB 384 KSENVQDLLLLLDVAPLSGLTAGGVTALIKRNTTPTKQTOFTTYSNQPGLIOVY 443
 QY 61 EGERAMTKDNLLGRFELSGIPAPRGVPOIEVTFDIDANGILNVATDKSTGKANKITI 120
 DB 444 EGERAMTKDNLLGRFELSGIPAPRGVPOIEVTFDIDANGILNVSAVDKSTGKANKITI 503
 QY 121 TNDKRLSKKEEIERMVQEAKEYKAEDVQREVRSKNALESYAFNMKSAVEDGLKKGKIS 180
 DB 504 TNDKRLSKKEEIERMVQEAKEYKAEDKQDKVSKNSLESYAFNMKATVEDEKLQKGIN 563
 QY 181 EADKKVLDKQCEVSWLDANTLAEKDFEHRKELEOVCPNPIISGLYQAGG-PG--PG 237
 DB 564 DEDKQKILDKCNELIISWLDKNTAKESFEHQKLEKVCNPIITIKLYQAGGPGMPG 623
 QY 238 GF--GAQGPKGSGSGPTIEEVD 258
 DB 624 GPPGGGAPPSGGASSGPTIEEVD 646

RESULT 46
 ADD18652
 ID ADD18652 standard; protein; 641 AA.
 XX AC ADD18652;
 XX DT 15-JAN-2004 (first entry)
 XX DE Human disease related protein SeqID83.
 XX KW human; disease state; cytostatic; antiinflammatory; ophthalmological;
 XX KW antiarteriosclerotic; vulnary; gene therapy;
 XX KW hypoxia-regulated condition; tumorigenesis; angiogenesis; apoptosis;
 XX KW inflammation; erythropoiesis; glycolysis; gluconeogenesis;
 XX KW glucose transport; catecholamine synthesis; iron transport;
 XX KW nitric oxide synthesis; cancer; ischaemic condition; reperfusion injury;
 XX KW retinopathy; neonatal stress; pre-eclampsia; atherosclerosis;
 XX KW inflammatory condition; wound healing.
 XX OS Homo sapiens.
 XX PN WO2003018621-A2.
 XX PD 06-MAR-2003.
 XX PF 23-AUG-2002; 2002WO-GB003892.
 XX PR 23-AUG-2001; 2001GB-00020558.
 XX PR 05-OCT-2001; 2001GB-00024037.
 XX PA (OXFO-) OXFORD BIOMEDICA UK LTD.
 XX PI Kingman SM, White J, Ward NR, Harris RA, Naylor S, Mundy CR;
 XX DR WPI; 2003-290046/28.
 XX DR N-PSDB; ADD18653.
 XX PT New substantially purified polypeptide, useful for diagnosing or treating
 XX PT a hypoxia-regulated condition, such as cancer, ischemia, reperfusion
 XX PT injury, retinopathy, pre-eclampsia, atherosclerosis, inflammation, or
 XX PT wound healing.
 XX PS Claim 25; SEQ ID NO 83; 424pp; English.
 XX CC This invention relates to novel human genes and gene product which are
 XX CC implicated in certain disease states. Compounds which modulate the
 XX CC proteins of the invention may have cytostatic, antiinflammatory, or
 XX CC ophthalmological, antiarteriosclerotic or vulnary activities. The
 XX CC sequences of the invention may be useful for gene therapy. The invention
 XX CC may be useful for diagnosing or treating a hypoxia-regulated condition,
 XX CC such as tumorigenesis, angiogenesis, apoptosis, inflammation,

CC erythropoiesis, or the biological response to hypoxia conditions
 CC including processes such as glycolysis, gluconeogenesis, glucose
 CC transportation, catecholamine synthesis, iron transport or nitric oxide
 CC synthesis. The disease includes cancer, ischemic conditions, reperfusion
 CC injury, retinopathy, neonatal stress, pre-eclampsia, atherosclerosis,
 CC inflammatory conditions or wound healing. The present sequence is that of
 CC a disease related protein of the invention.

XX
 SQ Sequence 641 AA;

Query Match 83.6%; Score 1099; DB 7; Length 641;
 Best Local Similarity 81.9%; Pred. No. 7.6e-83;
 Matches 217; Conservative 16; Mismatches 16; Indels 16; Gaps 2;

QY 1 KSENVQDLLLLDVAPLSGLGLETAGGVTALIKENSTIPKQTQIPTYSDNQGVLIQVY 60
 DB 386 KSEKVDLLLLDVAPLSGLGLETAGGVTALIKENSTIPKQTQIPTYSDNQGVLIQVY 445
 QY 61 EGERAMTKDNLLGRPELSGIPAPRGVPOIEVTFDIDANGILNVATDKSTGKANKITI 120
 DB 446 EGERAMTKDNLLGRPELSGIPAPRGVPOIEVTFDIDANGILNVATDKSTGKANKITI 505
 QY 121 TNDKGLSKSEIEERVMQVQAEKAEDEVQREVSNAKNALESYAFNMKSAVEDGLGKGIS 180
 DB 506 TNDKGLSKSEIEERVMQVQAEKAEDEVQREVSNAKNALESYAFNMKSAVEDGLGKGIS 565
 QY 181 EADKKKVLQKQEVISWLDANTLAEDFEHKKRKELEQVNCNPIISGLYQAGGPGGFG 240
 DB 566 ESDNKILDKCNELLSWLVNQAEKAEDEVQREVSNAKNALESYAFNMKSAVEDGLGKGIS 616
 QY 241 AQGPKGGSG-----SGPTIEEVD 258
 DB 617 CTGPGAGTGYVGRPATGTIEEVD 641

RESULT 47
 ADA50750
 ID ADA50750 standard; protein; 586 AA.
 XX
 AC ADA50750;
 XX
 DT 20-NOV-2003 (first entry)
 XX
 DE Human heat shock cognate protein-71 (FOXc2-interacting) protein (HSC71).
 XX
 KW protein kinase stimulator; protein kinase inhibitor; human; FOXc2;
 KW FOXc2-interacting protein; FOXc2 protein complex; obesity;
 KW hypertriglyceridemia; diet-induced insulin resistance; type 2 diabetes;
 KW anorexia; HSC71; heat shock cognate protein-71.
 XX
 OS Homo sapiens.
 XX
 PN WO2003064467-A1.
 XX
 PD 07-AUG-2003.
 XX
 PF 28-JAN-2003; 2003WO-SR000139.
 XX
 PR 29-JAN-2002; 2002SE-00000265.
 PR 30-APR-2002; 2002US-0377349P.
 XX
 PA (BIOV-) BIOVITRUM AB.
 XX
 PI Climent-Johansson I, Enerbaeck S;
 XX
 DR WPI; 2003-663466/62.
 XX
 PT New substantially pure FOXc2 protein complex, useful for treating or
 PT preventing a medical condition treatable by modulated FOXc2 activity,
 PT e.g. obesity, hypertriglyceridemia, diet-induced insulin resistance or
 PT anorexia.
 XX
 PS Claim 1; Page 27-29; 46pp; English.

XX
 CC The invention comprises a protein complex of human FOXc2 protein and a
 CC FOXc2-interacting protein. The FOXc2 protein complex is useful for
 CC treating or preventing a medical condition treatable by modulated FOXc2
 CC activity, such as: obesity, hypertriglyceridemia, diet-induced insulin
 CC resistance, type 2 diabetes, and anorexia. The present amino acid
 CC sequence represents a human FOXc2-interacting protein of the invention.

XX
 SQ Sequence 586 AA;

Query Match 83.5%; Score 1097.5; DB 6; Length 586;
 Best Local Similarity 81.4%; Pred. No. 9.1e-83;
 Matches 214; Conservative 24; Mismatches 20; Indels 5; Gaps 3;

QY 1 KSENVQDLLLLDVAPLSGLGLETAGGVTALIKENSTIPKQTQIPTYSDNQGVLIQVY 60
 DB 324 KSENVQDLLLLDVAPLSGLGLETAGGVTALIKENSTIPKQTQIPTYSDNQGVLIQVY 383
 QY 61 EGERAMTKDNLLGRPELSGIPAPRGVPOIEVTFDIDANGILNVATDKSTGKANKITI 120
 DB 384 EGERAMTKDNLLGRPELSGIPAPRGVPOIEVTFDIDANGILNVATDKSTGKANKITI 443
 QY 121 TNDKGLSKSEIEERVMQVQAEKAEDEVQREVSNAKNALESYAFNMKSAVEDGLGKGIS 180
 DB 444 TNDKGLSKSEIEERVMQVQAEKAEDEVQREVSNAKNALESYAFNMKSAVEDGLGKGIS 503
 QY 181 EADKKKVLQKQEVISWLDANTLAEDFEHKKRKELEQVNCNPIISGLYQAGG-PG--PG 237
 DB 504 DEDKQKILDKCNELINWLDKNQTAKEEHEHQKLEKVCNPIITKLYQSAGGMPGMPG 563
 QY 238 GF--GAQGPKGGSGSGPTIEEVD 258
 DB 564 GPGGAGGAPPGGAGSGPTIEEVD 586

RESULT 48
 ADJ69947
 ID ADJ69947 standard; protein; 586 AA.
 XX
 AC ADJ69947;
 XX
 DT 06-MAY-2004 (first entry)
 XX
 DE Human heat mitochondrial protein as a therapeutic target SeqID1753.
 XX
 KW mitochondrial; human; screening assay; diabetes mellitus;
 KW Huntington's disease; osteoarthritis;
 KW Leber's hereditary optic neuropathy; LHON;
 KW mitochondrial encephalopathy lactic acidosis and stroke; MELAS;
 KW myoclonic epilepsy ragged red fibre syndrome; MERRF; cancer;
 KW neuroprotective; neurotropic; antidiabetic; anticonvulsant; antiarthritic;
 KW osteopathic; ophthalmological; cytostatic.
 XX
 OS Homo sapiens.
 XX
 PN WO2003087768-A2.
 XX
 PD 23-OCT-2003.
 XX
 PF 04-APR-2003; 2003WO-US010870.
 XX
 PR 12-APR-2002; 2002US-0372843P.
 PR 17-JUN-2002; 2002US-0389987P.
 PR 20-SEP-2002; 2002US-0412418P.
 XX
 PA (MITO-) MITOKOR.
 PA (BUCK-) BUCK INST AGE RES.
 XX
 PI Ghosh SS, Fahy ED, Zhang B, Gibson BW, Taylor SW, Glenn GM;
 PI Warnock DE;
 XX
 DR WPI; 2003-845369/78.
 XX

PT Identifying a mitochondrial target for drug screening assays and for
PT treating diseases associated with altered mitochondrial function,
PT comprises detecting a modified polypeptide in a sample and correlating
PT with the disease.

XX Claim 1; SEQ ID NO 1753; 180pp; English.

XX This invention relates to novel mitochondrial targets that can be used
CC for therapeutic intervention in treating a disease associated with
CC altered mitochondrial function. Specifically, it refers to a method for
CC identifying proteins of the human heart mitochondrial proteome that are
CC useful for drug screening assays, as well as therapeutic targets. The
CC present invention describes a method for identifying such proteins that
CC can be used in the treatment of various diseases associated with altered
CC mitochondrial function including diabetes mellitus, Huntington's disease,
CC osteoarthritis, Leber's hereditary optic neuropathy (LHON), mitochondrial
CC encephalopathy lactic acidosis and stroke (MELAS), myoclonic epilepsy
CC ragged red fibre syndrome (MERRF) or cancer. Accordingly, these
CC compositions have neuroprotective, neurotropic, antidiabetic,
CC anticonvulsant, antiarthritic, osteopathic, ophthalmological and
CC cytoskeletal activities. This polypeptide sequence is a human heart
CC mitochondrial protein of the invention.

XX Sequence 586 AA;

Query Match 83.5%; Score 1097.5; DB 7; Length 586;
Best Local Similarity 81.4%; Pred. No. 9.1e-83;
Matches 214; Conservative 24; Mismatches 20; Indels 5; Gaps 3;
QY 1 KSENVQDLLLDVAPLSLGLTAGGVTALIKRNTIPTKTQITFTTYSNQPGLVIQY 60
DB 324 KSENVQDLLLDVTPLSLGIETAGGVTMLIKRNTIPTKTQITFTTYSNQPGLVIQY 383
QY 61 EGERAMTKDNLLGRFELSGIPAPRGVPOIEVTFDIDANGILNVATDKSTGKANKITI 120
DB 384 EGERAMTKDNLLGRFELSGIPAPRGVPOIEVTFDIDANGILNVSAVDKSTGKANKITI 443
QY 121 TNDKGRLSKEEIERMVOEAEKYKAEDVQREVRSNAKNALESYAFNMKSAVEDGLKGLIS 180
DB 444 TNDKGRLSKEDIERMVOEAEKYKAEDKQDKVSSKNLSLEYAFNMKATVEDEKLQKIN 503
QY 181 EADKKVLDKQEVISWLDANTLAEKDEPEHKKRKELEQVNCNPIISGLYQAGG-PG--PG 237
DB 504 DEDKQILDKCNEIINWLDKNQTAKEEPEHQQKELEKVCNPIITTKLYQAGGMPGMPG 563
QY 238 GF--GAQGPKGSGSGPTIEVD 258
DB 564 GFPGGAPPSSGGSGSGPTIEVD 586

RESULT 49
AAW54364
ID AAW54364 standard; protein; 646 AA.

XX AAW54364;
AC AAW54364;
DT 14-AUG-1998 (first entry)
DE Heat shock cognate 71 kD protein.
XX Endometrium; hyperplasia; adenocarcinoma; proliferative phase;
KW 2D gel electrophoresis; detection.
XX Homo sapiens.

OS WO9810291-A1.
FN 12-MAR-1998.
PD 05-SEP-1997; 97WO-GB002394.
XX 06-SEP-1996; 96GB-00018600.
PR 08-APR-1997; 97GB-00007132.

XX (CLIN-) CENT CLINICAL & BASIC RES.
XX Byrjalsen I, Larsen P, Fey SJ;
PI WPI; 1998-207057/18.
XX Biochemical markers of human endometrium - useful for, e.g. diagnosis of
XX hyperplasia and adenocarcinoma.
XX Disclosure; Page 23; 77pp; English.

XX Proteins AAW54349-W54364 are examples of proteins produced in the
CC endometrium during the hyperplasia, adenocarcinoma or proliferative phase
CC of the endometrium. The presence and quantities of these proteins can be
CC detected using 2D gel electrophoresis comparison of cell lysates. The
CC proteins can be used as biochemical markers to detect the phase of the
CC endometrium and can be measured in body fluids, obviating the need for
CC endometrial biopsies
XX Sequence 646 AA;

Query Match 83.5%; Score 1097.5; DB 2; Length 646;
Best Local Similarity 81.4%; Pred. No. 1e-82;
Matches 214; Conservative 24; Mismatches 20; Indels 5; Gaps 3;
QY 1 KSENVQDLLLDVAPLSLGLTAGGVTALIKRNTIPTKTQITFTTYSNQPGLVIQY 60
DB 384 KSENVQDLLLDVTPLSLGIETAGGVTMLIKRNTIPTKTQITFTTYSNQPGLVIQY 443
QY 61 EGERAMTKDNLLGRFELSGIPAPRGVPOIEVTFDIDANGILNVATDKSTGKANKITI 120
DB 444 EGERAMTKDNLLGRFELSGIPAPRGVPOIEVTFDIDANGILNVSAVDKSTGKANKITI 503
QY 121 TNDKGRLSKEEIERMVOEAEKYKAEDVQREVRSNAKNALESYAFNMKSAVEDGLKGLIS 180
DB 504 TNDKGRLSKEDIERMVOEAEKYKAEDKQDKVSSKNLSLEYAFNMKATVEDEKLQKIN 563
QY 181 EADKKVLDKQEVISWLDANTLAEKDEPEHKKRKELEQVNCNPIISGLYQAGG-PG--PG 237
DB 564 DEDKQILDKCNEIINWLDKNQTAKEEPEHQQKELEKVCNPIITTKLYQAGGMPGMPG 623
QY 238 GF--GAQGPKGSGSGSGPTIEVD 258
DB 624 GFPGGAPPSSGGSGSGPTIEVD 646

RESULT 50
AAW17407
ID AAW17407 standard; protein; 646 AA.

XX AAW17407;
AC AAW17407;
DT 26-JUL-1999 (first entry)
DE Human heat shock cognate 73.
XX Heat shock cognate 73; HSC73; cancer gene; diagnosis; neoplasia;
KW detection; carcinoma; breast; tumour.

OS Homo sapiens.
XX WO9923252-A1.
FN 14-MAY-1999.
PD 05-NOV-1998; 98WO-GB003375.
XX 05-NOV-1997; 97GB-00023412.
PR 19-AUG-1998; 98GB-00018118.
XX (ISIS-) ISIS INNOVATION LTD.

PI Bakkenist CJ, Koreth J, Mcgee JO;
 XX WPI; 1999-337489/28.
 XX DR N-PSDB; AAX56457.
 XX Method for diagnosis of cancer by detecting aberrant expression of gene.
 XX PT Disclosure; Fig 5; 49pp; English.
 XX PS
 CC A method of diagnosis performed on a biological sample has been developed
 CC comprising detecting the aberrant expression of a gene at the heat shock
 CC cognate 73 (HSC73) locus, or detecting a mutation at the HSC73 locus. The
 CC method is used for diagnosing neoplasia or a susceptibility to neoplasia
 CC especially malignant neoplasia, and carcinomas of the breast. Gene or
 CC protein therapy of mutated HSC73 is performed by administration of native
 CC HSC73, and the transgenic mammal is useful as an experimental model for
 CC technical development of gene therapy. The HSC73 gene was transfected
 CC into cell lines, which were introduced into test animals. These animals
 CC were injected with untransfected cells of a breast cancer line.
 CC Expression of wild type HSC73 prevented breast cancer cells forming
 CC tumors in the mice. The present sequence represents human HSC73 from the
 CC present invention
 XX SQ
 SQ Sequence 646 AA;
 Query Match 83.5%; Score 1097.5; DB 2; Length 646;
 Best Local Similarity 81.4%; Pred. No. 1e-82;
 Matches 214; Conservative 24; Mismatches 20; Indels 5; Gaps 3;
 QY 1 KSENVODLLDVLAPISLGLTAGGVTALIKENSTIPTKQTOIFTTYSNQGVLIOVY 60
 DB 384 KSENVODLLDVLAPISLGLTAGGVTALIKENSTIPTKQTOIFTTYSNQGVLIOVY 443
 QY 61 EGERAMTKNNLLGRFELSGIPAPRGVPOIEVTFDIDANGILNVATDKSTGKANKITI 120
 DB 444 EGERAMTKNNLLGRFELSGIPAPRGVPOIEVTFDIDANGILNVATDKSTGKANKITI 503
 QY 121 TNDKGRLSKEIERMVOEAKYKAEDVQVRVSAKNALESYAFNMKSAVEDGLKQKIS 180
 DB 504 TNDKGRLSKEDIERMVOEAKYKAEDKQKRDVSKNSLESYAFNMKATVEDEKLQKIN 563
 QY 181 EADKKVLDKCOEIVSWLDANTLAEKDEFEHKKKELEOVNPIISGLYQAGG-PG--PG 237
 DB 564 DEDKQKILDKCNEIINWLDKNTAEKEEFHQKELEKVCNPIITTKLYSAGGMPGMPG 623
 QY 238 GF--GAQGPKGSGSGPTIEVD 258
 DB 624 GPPGGAPPSSGASSGPTIEVD 646
 RESULT 51
 AAB23651
 ID AAB23651 standard; protein; 646 AA.
 XX AAB23651;
 XX
 XX 05-JAN-2001 (first entry)
 XX Human heat shock protein Hsc70 protein sequence SEQ ID NO:3.
 XX
 XX ATPase; Hsp70; heat shock protein; cytotoxic T lymphocyte; CTL;
 KW immune response; infectious disease; malaria; cytotoxic T cell;
 KW cytostatic; immunostimulant; cellular immune response inducer;
 KW protozoicide; leukaemia; cancer.
 XX
 OS Homo sapiens.
 XX WO200049041-A1.
 XX
 XX 24-AUG-2000.
 XX
 XX 18-FEB-2000; 2000WO-JP000941.
 XX

PR 19-FEB-1999; 99JP-00041535.
 XX (SUME) SUMITOMO ELECTRIC IND CO.
 XX Shinbara N, Udono H, Yui K;
 XX WPI; 2000-543748/49.
 XX
 PT Fused protein capable of inducing cellular immune response, useful as
 PT active ingredient for drug compositions in preventing and/or treating
 PT infectious diseases such as malaria or cancer.
 XX
 PS Claim 3; Page 42-45; 72pp; Japanese.
 XX
 CC The present invention describes a fused protein (I) prepared from a
 CC peptide containing a CTL (cytotoxic T lymphocyte) epitope recognised by
 CC cytotoxic T cells and a protein containing the ATPase domain of a heat
 CC shock protein. Also described are: (1) a drug composition containing (I)
 CC as active ingredient; (2) a DNA encoding (I); (3) an expression vector
 CC containing the DNA of (2); and (4) a transformant which can retain the
 CC expression vector of (3). (I) has cytostatic, immunostimulant and
 CC protozoicide activities, and can be used as a cellular immune response
 CC inducer. The protein is useful as an active ingredient for drug
 CC compositions in preventing and/or treating infectious diseases such as
 CC malaria or cancer e.g. to provide systemic immunity against leukaemia.
 CC The present sequence represents a specifically claimed heat shock protein
 CC for use in a fused protein of the present invention
 XX SQ
 SQ Sequence 646 AA;
 Query Match 83.5%; Score 1097.5; DB 3; Length 646;
 Best Local Similarity 81.4%; Pred. No. 1e-82;
 Matches 214; Conservative 24; Mismatches 20; Indels 5; Gaps 3;
 QY 1 KSENVODLLDVLAPISLGLTAGGVTALIKENSTIPTKQTOIFTTYSNQGVLIOVY 60
 DB 384 KSENVODLLDVLAPISLGLTAGGVTALIKENSTIPTKQTOIFTTYSNQGVLIOVY 443
 QY 61 EGERAMTKNNLLGRFELSGIPAPRGVPOIEVTFDIDANGILNVATDKSTGKANKITI 120
 DB 444 EGERAMTKNNLLGRFELSGIPAPRGVPOIEVTFDIDANGILNVATDKSTGKANKITI 503
 QY 121 TNDKGRLSKEIERMVOEAKYKAEDVQVRVSAKNALESYAFNMKSAVEDGLKQKIS 180
 DB 504 TNDKGRLSKEDIERMVOEAKYKAEDKQKRDVSKNSLESYAFNMKATVEDEKLQKIN 563
 QY 181 EADKKVLDKCOEIVSWLDANTLAEKDEFEHKKKELEOVNPIISGLYQAGG-PG--PG 237
 DB 564 DEDKQKILDKCNEIINWLDKNTAEKEEFHQKELEKVCNPIITTKLYSAGGMPGMPG 623
 QY 238 GF--GAQGPKGSGSGPTIEVD 258
 DB 624 GPPGGAPPSSGASSGPTIEVD 646
 RESULT 52
 AAB82535
 ID AAB82535 standard; protein; 646 AA.
 XX AAB82535;
 XX
 XX 17-SEP-2001 (first entry)
 XX Human heat shock protein Hsc70.
 XX
 XX Hsc70; human; heat shock protein; immunotherapy; therapy; cancer;
 KW infection; vaccine.
 XX
 OS Homo sapiens.
 XX
 XX Key Location/Qualifiers
 PH Binding-site 391..615
 FT /note= "peptide-binding domain"
 FT

QY 61 EGERAMTKNNLLGRFELSGIPAPRGVPOIEVTFDIDANGILNVATDKSTGKANKITI 120
 Db 444 EGERAMTKNNLLGKFLTGIPAPRGVPOIEVTFDIDANGILNVSAVDKSTGKANKITI 503
 QY 121 TNDKGRLSKEEIERMWQAEKYKAEDVQERYSAKNALESYAFNMKSAVEDGLGKIS 180
 Db 504 TNDKGRLSKEDIERMWQAEKYKAEDKQDKVSSKNSLESYAFNMKATVEDEKLQKIN 563
 QY 181 EADKKVLDKQEVISWLDANTLAEDFEHFKRKELEBOVCNPIISGLYQAGG-PG--PG 237
 Db 564 DEDKQKILDKCNELIINWLDKNQTAKEEFHQKELEKVCNPIITKLYQAGGMPGMPG 623
 QY 238 GF--GAQPGKGGSGPTIEVD 258
 Db 624 GFPGGGAPPSSGSGPTIEVD 646

RESULT 54
 AAU75102
 ID AAU75102 standard; protein; 646 AA.
 AC AAU75102;
 XX
 DT
 DT 09-APR-2002 (first entry)
 XX
 DE Heat shock protein 8 (Hsp8).
 XX
 DE MAPKAP-K3; AP-3 delta; APP-695; amyloid A4; Hsp8; heat shock protein 8;
 KW L130; NY-REN-58; P38 Beta; ERK3; KIAA0934; CDK9;
 KW cell cycle dependent kinase 9; CLK; C-NAP-1; clathrin heavy chain;
 KW amphiphysin; PN9109; KIAA1106; neurodegenerative disorder;
 KW non-insulin dependent diabetes mellitus; NIDDM; Alzheimer's disease;
 KW inflammatory disease; cardiac hypertrophy; hypoxic brain injury;
 KW atherosclerosis; rheumatoid arthritis; inflammatory bowel disorder;
 KW yeast two-hybrid; signal transduction pathway; human;
 KW mitogen activated protein kinase.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT 260..533
 FT Region
 FT /note= "This region binds the mitogen activated protein
 FT kinase (MAPK) AP-K3 (see ABK1301), the bait protein in a
 FT yeast two-hybrid assay, producing a complex claimed in
 FT claim 1"
 FT
 XX
 PN WO200198524-A2.
 XX
 XX 27-DEC-2001.
 XX
 XX 21-JUN-2001; 2001WO-US019762.
 XX
 XX 22-JUN-2000; 2000US-0213245P.
 XX
 XX (MYRI-) MYRIAD GENETICS INC.
 XX
 XX Heichman K, Bartel PL;
 XX
 XX WPI; 2002-122287/16.
 XX
 XX New protein complexes comprising protein-protein interactions (e.g.
 FT MAPKAP-K3/AP-3 delta or C-NAP-1/clathrin HC), useful for diagnosing
 FT physiological generative disorders or screening drugs for these diseases.
 XX
 XX Example 4; Page; 60pp; English.
 XX
 CC The invention describes an isolated protein complex, comprising two
 CC proteins. The protein complex comprises: protein kinase MAPKAP-K3 and AP-
 CC 3 adaptor complex delta sub-unit; MAPKAP-K3 and amyloid A4 precursor
 CC protein, APP-695; MAPKAP-K3 and heat shock protein (Hsp) 8; leucine rich
 CC L130 and NY-REN-58; P38 Alpha and P38 Beta; protein kinase ERK3 and
 CC KIAA0934 (unknown function); ERK3 and cell cycle dependent kinase (CDK) 9
 CC ; ERK3 and protein kinase CLK; C-NAP-1 and Clathrin heavy chain; C-NAP-1

CC and Amphiphysin; C-NAP-1 and novel protein PN9109 or C-NAP-1 and KIAA1106
 CC (unknown function) interactions. The protein complexes are useful for
 CC diagnosing physiological generative disorders, drug screening for agents
 CC that modulate the interaction of the proteins (thus identify drug
 CC targets), and identifying additional proteins in the pathway common to
 CC the proteins. These physiological disorders include non-insulin dependent
 CC diabetes mellitus (NIDDM), neurodegenerative disorders (e.g. Alzheimer's
 CC disease), inflammatory diseases (e.g. rheumatoid arthritis and
 CC inflammatory bowel disorder) and other human disease such as
 CC atherosclerosis, cardiac hypertrophy and hypoxic brain injury. This
 CC sequence represents heat shock protein 8 (Hsp8) residues 260-533 of which
 CC binds to the bait protein MAPKAP-K3 (see ABK13301 for nucleotide
 CC sequence) in a yeast two-hybrid assay for determining components of
 CC signal transduction pathways and forms an interaction claimed in claim 1
 CC of the invention. Note: This sequence does not appear in the
 CC specification but has been obtained from a reference given in the
 XX invention
 XX
 SQ Sequence 646 AA;
 Query Match 83.5%; Score 1097.5; DB 5; Length 646;
 Best Local Similarity 81.4%; Pred. No. 1e-82;
 Matches 214; Conservative 24; Mismatches 20; Indels 5; Gaps 3;
 QY 1 KSENVQDLLLLDVAPLSGLTAGGTAGGVTALIKKNSIPIKQTOIFTTYSNQPGVLIQVY 60
 Db 384 KSENVQDLLLLDVTPLSGLTAGGTAGGVTMLIKRNTTPTKQTFTTYSNQPGVLIQVY 443
 QY 61 EGERAMTKNNLLGRFELSGIPAPRGVPOIEVTFDIDANGILNVATDKSTGKANKITI 120
 Db 444 EGERAMTKNNLLGKFLTGIPAPRGVPOIEVTFDIDANGILNVSAVDKSTGKANKITI 503
 QY 121 TNDKGRLSKEEIERMWQAEKYKAEDVQERYSAKNALESYAFNMKSAVEDGLGKIS 180
 Db 504 TNDKGRLSKEDIERMWQAEKYKAEDKQDKVSSKNSLESYAFNMKATVEDEKLQKIN 563
 QY 181 EADKKVLDKQEVISWLDANTLAEDFEHFKRKELEBOVCNPIISGLYQAGG-PG--PG 237
 Db 564 DEDKQKILDKCNELIINWLDKNQTAKEEFHQKELEKVCNPIITKLYQAGGMPGMPG 623
 QY 238 GF--GAQPGKGGSGPTIEVD 258
 Db 624 GFPGGGAPPSSGSGPTIEVD 646

RESULT 55
 ABU69612
 ID ABU69612 standard; protein; 646 AA.
 XX
 AC ABU69612;
 XX
 DT 05-JUN-2003 (first entry)
 XX
 DE Human NF-kappaB associated polypeptide sequence #15.
 XX
 KW Human; nuclear factor-kappaB; NF-kappaB; immune disorder; cancer;
 KW inflammatory disorder; apoptosis; hepatic disorder; Hodgkin's lymphoma;
 KW haematopoietic tumour; hyper-IGM syndrome; viral infection; asthma;
 KW hypohidrotic ectodermal dysplasia; human immunodeficiency virus; HIV;
 KW X-linked anhidrotic ectodermal dysplasia; al incontinentia pigmenti;
 KW influenza; rheumatoid arthritis; inflammatory bowel disease; colitis;
 KW atherosclerosis; cachexia; euthyroid sick syndrome; stroke; EAE;
 KW experimental allergic encephalomyelitis; autoimmune disorder; wound;
 KW hyper immune activity; acute phase response; hypercongenital condition;
 KW birth defect; necrotic lesion; organ transplant rejection; pancreas;
 KW signal transduction; hyperproliferative disorder; diabetes mellitus;
 KW vitamin B12 malabsorption; neurological disorder; Huntington's chorea;
 KW Turner's syndrome; bacterial infection; cardiovascular disorder;
 KW infertility; psoriasis; haemolytic anaemia; antinflammatory; anti-HIV;
 KW cytostatic; hepatotropic; virucide; antirheumatic; antiarthritic;
 KW antiasthmatic; immunomodulator; antidiabetic; antiallergic;
 KW neuroprotective; immunosuppressive; vulnery; antibacterial;
 KW antiinfertility; antianaemic; antipsoriatic; cerebroprotective; cardiant;

KW	antiarteriosclerotic.	QY	238	GF--GAQGPKGSGSGPTIEVD	258
XX		Db	624	GFPGGAPPSSGSSGPTIEVD	646
OS	Homo sapiens.				
XX	WO200286076-A2.				
XX	31-OCT-2002.				
XX	19-APR-2002; 2002WO-US012636.				
XX	19-APR-2001; 2001US-0284962P.				
PR	26-APR-2001; 2001US-0286645P.				
PR	09-JAN-2002; 2002US-0346986P.				
XX	(BRIM) BRISTOL-MYERS SQUIBB CO.				
PA	Carman J, Feder J, Nadler S;				
XX	WPI; 2003-093119/08.				
XX	N-PSDB; ACA54673.				
XX	Novel NF-kappaB-associated polypeptides and polynucleotides useful for				
PT	diagnosing, treating and preventing cancer, hepatic disorders, aberrant				
PT	apoptosis, viral infections, autoimmune disorders, asthma and stroke.				
XX	Claim 6; Fig 10F; 608pp; English.				
PS					
XX	The present invention relates to the isolation of human nuclear factor-				
CC	kappaB (NF-kappaB) associated polypeptides and polynucleotides. The NF-				
CC	kappaB associated polypeptide and polynucleotide sequences are useful for				
CC	preventing, treating or ameliorating various disorders including immune				
CC	disorders, inflammatory disorders, cancers, disorders relating to				
CC	aberrant apoptosis, hepatic disorders, Hodgkin's lymphomas,				
CC	haematopoietic tumours, hyper-IGM syndromes, hypohidrotic ectodermal				
CC	dysplasia, X-linked anhidrotic ectodermal dysplasia, immunodeficiency, al				
CC	inconitencia pigmenti, viral infections (e.g. those caused by human				
CC	immunodeficiency virus (HIV), human T-cell lymphotropic virus (HTLV),				
CC	hepatitis B, hepatitis C, Epstein Barr virus (EBV), influenza),				
CC	rheumatoid arthritis, inflammatory bowel disease, colitis, asthma,				
CC	atherosclerosis, cachexia, euthyroid sick syndrome, stroke, experimental				
CC	allergic encephalomyelitis (EAE), autoimmune disorders, disorders related				
CC	to hyper immune activity, disorders related to aberrant acute phase				
CC	responses, hypercongenital conditions, birth defects, necrotic lesions,				
CC	wounds, organ transplant rejection, disorders related to aberrant signal				
CC	transduction, hyperproliferative disorders diseases of the pancreas				
CC	(e.g. diabetes mellitus, vitamin B12 malabsorption), neurological				
CC	disorders (e.g. Huntington's chorea), Turner's syndrome, bacterial				
CC	infections, cardiovascular disorders, infertility, psoriasis and				
CC	haemolytic anaemia. The present sequence represents a human NF-kappaB				
CC	associated polypeptide of the invention				
XX	Sequence 646 AA;				
SQ					
	Query Match		83.5%;	Score 1097.5;	DB 6; Length 646;
	Best Local Similarity		81.4%;	Pred. NO. 1e-82;	
	Matches 214;		Conservative 24;	Mismatches 20;	Indels 5; Gaps 3;
QY	1	KSENVQDILLDVLPLSLGLETAGVMTALIKENSTIPTKOTQITFTTSDNQPGVLIQVY	60		
Db	384	KSENVQDILLDVLPLSLGLETAGVMTALIKENSTIPTKOTQITFTTSDNQPGVLIQVY	443		
QY	61	EGERAMTKDNLLGRFELSGIPPPAGVQPIEVTFDIDANGILNVTATDKSTGKANKITI	120		
Db	444	EGERAMTKDNLLGRFELSGIPPPAGVQPIEVTFDIDANGILNVTATDKSTGKANKITI	503		
QY	121	TNDKRLSKBEETIRWVQAEKTKADEVQREVRVSKNALESYAFNMKSAVEDEGLKKGKIS	180		
Db	504	TNDKRLSKBEETIRWVQAEKTKADEVQREVRVSKNALESYAFNMKSAVEDEGLKKGKIN	563		
QY	181	EADKKVLDKCOEIVSWLDANTLAEKDEFEHKKKELEQVCNPIISGLYQGAGG-PG--PG	237		
Db	564	DEDKQKILDKCNEIINWLDKNQTAKEEPEHQKELEKVCNPIITKLQYSGAGMPGMPG	623		
	Query Match		83.5%;	Score 1097.5;	DB 6; Length 646;
	Sequence 646 AA;				
	RESULT 56				
	ABR64224				
ID	ABR64224 standard; protein; 646 AA.				
XX	AC ABR64224;				
XX	DT 15-OCT-2003 (first entry)				
XX	DE Angiogenesis protein BN0128.				
XX	Cytostatic; antirheumatic; antiarthritic; antidiabetic; ophthalmological;				
KW	antipsoriatic; antiarteriosclerotic; cardiant; vasotropic; angiogenesis;				
KW	gene therapy; vasculature; cancer; rheumatoid arthritis; psoriasis;				
KW	diabetic retinopathy; cardiovascular disease; atherosclerosis;				
KW	ischemic limb disease; coronary artery disease.				
XX	Homo sapiens.				
OS	WO2003027285-A1.				
XX	03-APR-2003.				
XX	19-SEP-2002; 2002WO-AU001282.				
XX	27-SEP-2001; 2001AU-00007973.				
PR	27-SEP-2001; 2001AU-00007974.				
PR	11-OCT-2001; 2001AU-00008210.				
PR	29-OCT-2001; 2001AU-00008532.				
PR	13-NOV-2001; 2001AU-00008838.				
PR	28-AUG-2002; 2002AU-00951032.				
XX	(BION-) BIONOMICS LTD.				
XX	Gamble JR, Hahn CN, Vadas MA;				
XX	WPI; 2003-354655/33.				
XX	N-PSDB; ACF34439.				
XX	New angiogenic genes and polypeptides, useful for diagnosing,				
PT	prognosticating or treating an angiogenesis-related disorder, e.g.				
PT	cancer, rheumatoid arthritis, diabetic retinopathy, psoriasis or				
PT	cardiovascular diseases.				
XX	Claim 15; SEQ ID NO 159; 90pp; English.				
PS					
XX	The invention relates to the isolation of novel genes (ACF34446-ACF34559)				
CC	encoding proteins (ABR64180-ABR64281) involved in the process of				
CC	angiogenesis. The nucleic acid molecules are useful in identifying and/or				
CC	obtaining full-length human genes involved in an angiogenic process. The				
CC	nucleic acid molecule, polypeptides or complexes encoded, cells or				
CC	genetically modified non-human animals derived from these are useful for				
CC	the screening of candidate pharmaceutical compounds used in treating,				
CC	angiogenesis-related disorders. They are also useful for diagnosing,				
CC	prognosticating or treating an angiogenesis-related disorder, which				
CC	involves uncontrolled or enhanced angiogenesis or is a disorder in which				
CC	a decreased vasculature is of benefit (e.g. cancer, rheumatoid arthritis,				
CC	diabetic retinopathy, psoriasis or cardiovascular diseases such as				
CC	atherosclerosis), or involves inappropriately arrested or decreased				
CC	angiogenesis or is a disorder in which an expanding vasculature is of				
CC	benefit (e.g. ischemic limb disease or coronary artery disease). The				
CC	modulator of expression or activity of the polypeptide encoded by the				
CC	nucleic acid sequence is useful for manufacturing a medicament for the				
CC	treatment of an angiogenesis-related disorder. This sequence corresponds				
CC	to one of the novel angiogenic protein				
XX	Sequence 646 AA;				
SQ					

Best Local Similarity 81.4%; Pred. No. 1e-82;		Matches 214; Conservative 24; Mismatches 20; Indels 5; Gaps 3;	
Qy	1 KSENVQDLLLLDVAPLSIGLETAGGVMTALIKRNSITPTKQTQITFTTYSNQPGLVQVY 60		
Db	384 KSENVQDLLLLDVTPSLGSETAGGVMTVLKRNITPTKQTQITFTTYSNQPGLVQVY 443		
Qy	61 EGERAMTKNNLLGRFELSGIPPPAPRGVPQIEVTFDIDANGILNVATDKSTGKANKITI 120		
Db	444 EGERAMTKNNLLGKFLTGIPPPAPRGVPQIEVTFDIDANGILNVSAVDKSTGKANKITI 503		
Qy	121 TNDKGRLSKEEIERMVQEAKEYKAEDVQERVSANKVALESYAFNMKSAYEDELKKGKIS 180		
Db	504 TNDKGRLSKEDIERMVQEAKEYKAEDKQKRDVSSKNLSLEYAFNMKATVEDEKLQKIN 563		
Qy	181 EADKKVLDKQCVISWLDANTLAEDFEHFKRLEQVNCNPIISGLYQAGG-PG--PG 237		
Db	564 DEDQKILDKCNELIINWLDKNQTAKEEPEHQQKELEKVCNPIITKLYQAGGPGMGPG 623		
Qy	238 GF--GAQPGKGGSGGPTIEVD 258		
Db	624 GFGGAGPPSGGASSGPTIEVD 646		
RESULT 57			
ID	ABU79083		
AC	ABU79083 standard; protein; 646 AA.		
AC	ABU79083;		
XX	18-JUN-2003 (first entry)		
DT	Staphylococcal heat shock protein 70, HSP-70, protein.		
DE			
XX	Superantigen; SAg; staphylococcal enterotoxin; tumour; cancer; apoptosis;		
KW	gene therapy; mammalian cell receptor; cytostatic;		
KW	tumour associated lipid; energy; T cell; antigen presenting cell; APC;		
KW	tumouricidal immunocyte; antitumour.		
XX			
OS	Staphylococcus sp.		
XX			
PN	US2002177551-A1.		
XX			
PD	28-NOV-2002.		
XX			
PF	30-MAY-2001; 2001US-00870759.		
XX			
PR	31-MAY-2000; 2000US-0208128P.		
XX			
PA	(TERM/) TERMAN D S.		
XX			
PI	Terman DS;		
XX			
DR	WPI; 2003-361759/34.		
XX			
DR	N-PSDB; ACA64714.		
XX			
PT	A mammalian cell receptor, useful in the treatment of cancer by binding		
PT	to tumour associated lipids where the binding induces energy or apoptosis		
PT	in T cells and antigen presenting cells..		
XX			
PS	Disclosure; Page; 167pp; English.		
XX			
CC	The invention relates to a mammalian cell receptor, useful in the		
CC	treatment of cancer, which binds to tumour associated lipids and induces		
CC	energy or apoptosis in the T cells and antigen presenting cells (APCs).		
CC	Also included are a mammalian cell useful in the treatment of cancer		
CC	where the receptor which binds tumour associated lipids and induces		
CC	cellular inactivation or death is deleted or functionally deactivated,		
CC	producing (M1) a tumouricidal immunocyte population in vivo in a mammal		
CC	(by allowing tumour associated lipids to contact immunocytes in which		
CC	receptors for immunosuppressive fatty acids, ceramides, glycolipids,		
CC	sphingolipids, glycosphingolipids, phosphosphingolipids, gangliosides,		
CC	sialylated glycans, lipopeptides and proteoglycolipids are inactivated or		

CC	deleted), a construct useful in the treatment of cancer comprising a		
CC	superantigen (SAG) nucleotide inserted into a virus, a mammalian T cell		
CC	useful in the treatment of cancer (where an adaptor protein which		
CC	inhibits T cell activation by tumour associated antigens is deleted or		
CC	functionally deactivated), a composition useful in the treatment of		
CC	cancer (comprising a lipid raft conjugated to a superantigen), producing		
CC	(M2) a tumouricidal immunocyte population ex vivo in a mammal (by		
CC	allowing tumour associated lipids to contact immunocytes, in which		
CC	receptors for the lipids are inactivated or deleted to produce a		
CC	tumouricidal immunocyte population, and administering the tumouricidally		
CC	activated immunocytes to the host), producing (M3) a tumouricidal APC		
CC	population ex vivo in a mammal (by allowing a tumour associated lipid to		
CC	contact APCs, in which receptors for the tumour associated lipids are		
CC	inactivated or deleted to produce a tumouricidally activated population,		
CC	and administering APCs to the host), producing a tumouricidal T cell		
CC	population ex vivo in a mammal) by allowing a tumour associated lipids to		
CC	contact T cells, in which adaptor proteins which inhibit T cell		
CC	activation by tumour associated antigens, are deleted or functionally		
CC	deactivated to produce a tumouricidal population of T cells, and		
CC	administering the tumouricidally activated T cells to the host, or		
CC	allowing a superantigen-lipid raft to contact T cells ex vivo, and		
CC	administering the tumouricidally activated T cells to the host), treating		
CC	(M5) cancer in a mammal (by administering a lipid binding molecule which		
CC	binds immunosuppressive tumour associated lipids in vivo), producing (M6)		
CC	a tumouricidal T cell population in vivo in a mammal (by allowing a		
CC	tumour associated antigen to contact immunocytes in which adaptor		
CC	proteins which inhibit T cell activation by tumour associated antigens		
CC	are deleted or functionally deactivated) and producing (M7) a		
CC	tumouricidal T cell population ex vivo in a mammal comprising allowing a		
CC	superantigen-lipid raft conjugate to contact immunocytes in vivo. The		
CC	receptors, methods and compositions are useful for treating cancers and		
CC	tumours. Bacterial superantigens are co-administered or administered as		
CC	fusion constructs with anti-tumour proteins or motifs. The present		
CC	sequence represents an anti-tumour protein which is co-administered with		
CC	or incorporated into a fusion construct with a superantigen. Note: The		
CC	sequence data for this patent did not form part of the printed		
CC	specification, but was obtained in electronic format from the US patent		
CC	office website at "seqdata.uspto.gov/sequence.html?docID=20020177551"		
XX			
SQ	Sequence 646 AA;		
Query Match 83.5%; Score 1097.5; DB 6; Length 646;			
Best Local Similarity 81.4%; Pred. No. 1e-82;			
Matches 214; Conservative 24; Mismatches 20; Indels 5; Gaps 3;			
Qy	1 KSENVQDLLLLDVAPLSIGLETAGGVMTALIKRNSITPTKQTQITFTTYSNQPGLVQVY 60		
Db	384 KSENVQDLLLLDVTPSLGSETAGGVMTVLKRNITPTKQTQITFTTYSNQPGLVQVY 443		
Qy	61 EGERAMTKNNLLGRFELSGIPPPAPRGVPQIEVTFDIDANGILNVATDKSTGKANKITI 120		
Db	444 EGERAMTKNNLLGKFLTGIPPPAPRGVPQIEVTFDIDANGILNVSAVDKSTGKANKITI 503		
Qy	121 TNDKGRLSKEEIERMVQEAKEYKAEDVQERVSANKVALESYAFNMKSAYEDELKKGKIS 180		
Db	504 TNDKGRLSKEDIERMVQEAKEYKAEDKQKRDVSSKNLSLEYAFNMKATVEDEKLQKIN 563		
Qy	181 EADKKVLDKQCVISWLDANTLAEDFEHFKRLEQVNCNPIISGLYQAGG-PG--PG 237		
Db	564 DEDQKILDKCNELIINWLDKNQTAKEEPEHQQKELEKVCNPIITKLYQAGGPGMGPG 623		
Qy	238 GF--GAQPGKGGSGGPTIEVD 258		
Db	624 GFGGAGPPSGGASSGPTIEVD 646		
RESULT 58			
ADD22402			
ID	ADD22402 standard; protein; 646 AA.		
XX			
AC	ADD22402;		
XX			
DT	15-JAN-2004 (first entry)		

XX HLA-B46 T cell recognised tumour antigenic polypeptide, SEQ NO 52.
 DE tumour antigenic peptide; cancer; vaccine; cytostatic; cytotoxic T cell;
 KW colon; mouth; lung; prostatic; gynecological; human.
 KW Homo sapiens.
 OS JP2003111595-A.
 PN 15-APR-2003.
 XX 24-JUN-2002; 2002JP-00183603.
 XX 25-JUN-2001; 2001JP-00191974.
 XX (ITOY/) ITO Y.
 XX WPI; 2003-611129/58.
 XX Novel tumor antigenic peptide or polypeptide useful for inducing
 PT cytotoxic T cells or for treating cancer such as colon, mouth, lung,
 PT prostatic or gynecological cancer.
 XX
 XX Claim 2; SEQ ID NO 52; 98pp; Japanese.
 XX The invention relates to a novel tumour antigenic peptide or polypeptide
 CC comprising a sequence selected from 99 sequences fully defined in the
 CC specification. The tumour antigenic peptide or polypeptide comprises a
 CC sequence selected from 99 sequences fully defined in the specification,
 CC where the tumour antigenic peptide preferably has a sequence of Glu-Pro-
 CC Pro-Leu-Ser-Gln-Thr-Phe, and the polypeptide preferably has a
 CC sequence comprising 393 amino acids fully defined in the specification.
 CC The invention further provides a cancer vaccine comprising a tumour
 CC antigenic peptide or polypeptide, which has cytostatic activity. A tumour
 CC antigenic peptide, polypeptide, its encoding polynucleotide, a
 CC hybridising polynucleotide, a recombinant vector containing the
 CC polynucleotide, a host transformed with the vector or an antibody are
 CC useful for screening for compounds that interact with the tumour
 CC antigenic peptide, the polypeptide or its encoding polynucleotide and
 CC increases the expression of the tumour antigenic peptide, the polypeptide
 CC or polynucleotide. The tumour antigenic peptide or the polypeptide is
 CC useful for inducing cytotoxic T cells. The tumour antigenic peptide
 CC vaccine is useful for treating cancer such as colon, mouth, lung,
 CC prostatic or gynecological cancer. The invention also provides a
 CC pharmaceutical composition useful for treating cancer. The tumour
 CC antigenic peptide or the polypeptide is useful as an antigen to create
 CC antibodies. This sequence represents one of the tumour antigenic
 CC polypeptides of the invention.

Sequence 646 AA;

Query Match 83.5%; Score 1097.5; DB 7; Length 646;
 Best Local Similarity 81.4%; Pred. No. 1e-82;
 Matches 214; Conservative 24; Mismatches 20; Indels 5; Gaps 3;
 QY 1 KSENVQDLLLDVAPLSGLGTAGVMTALIKRNTIPTKTQTFTTYSNQPGVLIQVY 60
 DB 384 KSENVQDLLLDVAPLSGLGTAGVMTALIKRNTIPTKTQTFTTYSNQPGVLIQVY 443
 QY 61 EGERAMTKNNLLGRFELSGIPAPRGVPOIEVTFDIDANGILNVATDSTGKANKITI 120
 DB 444 EGERAMTKNNLLGKGFELTGIPAPRGVPOIEVTFDIDANGILNVAVDKSTGKANKITI 503
 QY 121 TNDKGRLSKEIERMWQEAERYKAEDVQREVRSKNALESYAFNMKSAVEDGLKGGKIS 180
 DB 504 TNDKGRLSKEIERMWQEAERYKAEDKQKRDVSKNSLESYAFNMKATVEDEKLQKIN 563
 QY 181 EADKKVLDKQCVISWLDANTLAEKDFEKKLEQVNCNPIISGLYQAGG-PG--PG 237
 DB 564 DEDKQKILDKCNRIINWLDKNTAEKEFEHQKLEKVCNPIITKLYQAGGMPGMPG 623
 QY 238 GF--GAQGPKGSGSGPTIEVD 258

DB 624 GFPGGGAPSPGGASSGPTIEVD 646
 RESULT 59
 ADF43323
 ID ADF43323 standard; protein; 646 AA.
 XX ADF43323;
 AC ADF43323;
 XX 12-FEB-2004 (first entry)
 XX Superantigen associated protein seq id 43.
 XX receptor; lipid-based tumour associated antigen; cytostatic;
 KW antimicrobial; gene therapy; neoplastic disease; tumour; cancer;
 KW infectious disease.
 XX Unidentified.
 OS US2003157113-A1.
 PN 21-AUG-2003.
 PD 28-DEC-2000; 2000US-00751708.
 XX 28-DEC-1999; 99US-0173371P.
 PR (TERM/) TERMAN D S.
 XX Terman DS;
 PI WPI; 2003-787326/74.
 XX New receptor in a mammalian cell that inhibits regular activation by
 PT receptors specific for lipid-based tumor associated antigens, useful for
 PT treating a neoplastic disease or tumor, and infectious diseases.
 XX Disclosure; SEQ ID NO 43; 151pp; English.
 XX The invention describes a receptor in a mammalian cell that inhibits
 CC regular activation by receptors specific for lipid-based tumour
 CC associated antigen. The receptor has cytostatic and antimicrobial
 CC properties and is suitable for use in gene therapy. The receptors,
 CC methods and compositions are useful for treating a neoplastic disease or
 CC tumour (cancer), and infectious diseases. This sequence represents a
 CC protein associated with superantigens used to generate antitumour
 CC immunity.

Sequence 646 AA;

Query Match 83.5%; Score 1097.5; DB 7; Length 646;
 Best Local Similarity 81.4%; Pred. No. 1e-82;
 Matches 214; Conservative 24; Mismatches 20; Indels 5; Gaps 3;
 QY 1 KSENVQDLLLDVAPLSGLGTAGVMTALIKRNTIPTKTQTFTTYSNQPGVLIQVY 60
 DB 384 KSENVQDLLLDVAPLSGLGTAGVMTALIKRNTIPTKTQTFTTYSNQPGVLIQVY 443
 QY 61 EGERAMTKNNLLGRFELSGIPAPRGVPOIEVTFDIDANGILNVATDSTGKANKITI 120
 DB 444 EGERAMTKNNLLGKGFELTGIPAPRGVPOIEVTFDIDANGILNVAVDKSTGKANKITI 503
 QY 121 TNDKGRLSKEIERMWQEAERYKAEDVQREVRSKNALESYAFNMKSAVEDGLKGGKIS 180
 DB 504 TNDKGRLSKEIERMWQEAERYKAEDKQKRDVSKNSLESYAFNMKATVEDEKLQKIN 563
 QY 181 EADKKVLDKQCVISWLDANTLAEKDFEKKLEQVNCNPIISGLYQAGG-PG--PG 237
 DB 564 DEDKQKILDKCNRIINWLDKNTAEKEFEHQKLEKVCNPIITKLYQAGGMPGMPG 623
 QY 238 GF--GAQGPKGSGSGPTIEVD 258

624 GFPGGGAPPSGGASSGPTIEVD 646

Db

RESULT 61
ADJ68897
ID ADJ68897 standard; protein; 646 AA.
XX AC
XX ADJ68897;
XX DT
XX 06-MAY-2004 (first entry)
XX DE
XX Human heat mitochondrial protein as a therapeutic target SeqID703.
XX
XX mitochondrial; human; screening assay; diabetes mellitus;
XX Huntington's disease; osteoarthritis;
XX Leber's hereditary optic neuropathy; LHON;
XX mitochondrial encephalopathy lactic acidosis and stroke; MELAS;
XX myoclonic epilepsy ragged red fibre syndrome; MERRF; cancer;
XX neuroprotective; nontropic; antidiabetic; anticonvulsant; antiarthritic;
XX osteopathic; ophthalmological; cytostatic.
XX OS
XX Homo sapiens.
XX
XX W02003087768-A2.
XX
XX 23-OCT-2003.
XX PD
XX 04-APR-2003; 2003WO-US010870.
XX PF
XX 12-APR-2002; 2002US-0372843P.
XX PR
XX 17-JUN-2002; 2002US-0389987P.
XX PR
XX 20-SEP-2002; 2002US-0412418P.
XX
XX (MITO-) MITOKOR
XX (BUCK-) BUCK INST AGE RES.
XX
XX Ghosh SS, Fahy ED, Zhang B, Gibson BW, Taylor SW, Glenn GW;
XX Warnock DE;
XX WPI; 2003-845369/78.
XX
XX Identifying a mitochondrial target for drug screening assays and for
XX treating diseases associated with altered mitochondrial function,
XX comprises detecting a modified polypeptide in a sample and correlating
XX with the disease.
XX
XX Claim 1; SEQ ID NO 703; 180pp; English.
XX
XX This invention relates to novel mitochondrial targets that can be used
XX for therapeutic intervention in treating a disease associated with
XX altered mitochondrial function. Specifically, it refers to a method for
XX identifying proteins of the human heart mitochondrial proteome that are
XX useful for drug screening assays, as well as therapeutic targets. The
XX present invention describes a method for identifying such proteins that
XX can be used in the treatment of various diseases associated with altered
XX mitochondrial function including diabetes mellitus, Huntington's disease,
XX osteoarthritis, Leber's hereditary optic neuropathy (LHON), mitochondrial
XX encephalopathy lactic acidosis and stroke (MELAS), myoclonic epilepsy
XX ragged red fibre syndrome (MERRF) or cancer. Accordingly, these
XX compositions have neuroprotective, nontropic, antidiabetic,
XX anticonvulsant, antiarthritic, osteopathic, ophthalmological and
XX cytostatic activities. This polypeptide sequence is a human heart
XX mitochondrial protein of the invention.
XX
XX Sequence 646 AA;
XX

Query Match 83.5%; Score 1097.5; DB 7; Length 646;
Best Local Similarity 81.4%; Pred. No. 1e-82;
Matches 214; Conservative 24; Mismatches 20; Indels 5; Gaps 3;

Qy 1 KSNVQDLLLDVAPISLGLTETAGGVTWALIKNSITPTKQTQFTTYSNQPGVLQVY 60
384 KSNVQDLLLDVTPISLGLTETAGGVTWALIKNTIPTKQTQFTTYSNQPGVLQVY 443

Db

QY 61 EGERAMTKNNLLGRFELSGIPAPRGVPOIEVTFDIDANGILNVATDKSTGKANKITI 120
Db 444 EGERAMTKNNLLGKFLTGIPAPRGVPOIEVTFDIDANGILNVSAVDKSTGKANKITI 503
QY 121 TNDKGRLSKEEIERMVQEAERKAEDEVORERSAKNALESYAFNMKSAAVEDEGLKGIS 180
Db 504 TNDKGRLSKEDIERMVQEAERKAEDEKQDKVSSKNSLESYAFNMKAIVDEKLOGKIN 563
QY 181 EADKKVLDKQBEVTSWLDANTLAEDFEHKKKELEQVNCNPIISGLYQAGG-PG--PG 237
Db 564 DEDKQKILDKNBIINWLDKNQTAKEEHEHQKELEKVCNPIITKLYQSAGGMPGMPG 623
QY 238 GF--GAQGPKGSGSGPTIEVD 258
Db 624 GPPGGGAPPSSGSGPTIEVD 646
RESULT 62
ADE76846
ID ADE76846 standard; protein; 646 AA.
XX AC ADE76846;
XX 29-JAN-2004 (first entry)
XX Human protein expressed in a liver disorder #3.
XX human; liver disorder; hyperlipidaemia; hypertension; type II diabetes;
XX tumour; liver; inflammatory disorder; immune response disorder;
XX high-throughput screening; differential gene expression; gene therapy.
XX Homo sapiens.
XX US2003108871-A1.
XX 12-JUN-2003.
XX 30-JUL-2001; 2001US-00919039.
XX 28-JUL-2000; 2000US-0222113P.
XX (KASE/) KASER M R.
XX Kaser MR;
XX WPI; 2004-031227/03.
XX N-PSDB; ADE76845.
XX Composition comprising several cDNAs that are differentially expressed in
XX treated human C3A liver cell cultures, useful for treating liver
XX disorders.
XX Claim 1; SEQ ID NO 11; 41pp; English.
XX The invention relates to a composition comprising several cDNAs that are
XX differentially expressed in a liver disorder. The composition is useful
XX for treating liver disorder such as hyperlipidaemia, hypertension, type
XX II diabetes, tumours of the liver and disorders of the inflammatory and
XX immune response. The composition is useful for a high-throughput method
XX of screening several molecules or compounds to identify a ligand which
XX specifically binds a cDNA. A protein encoded by the cDNA is useful for a
XX high-throughput method for using a protein to screen several molecules or
XX compounds to identify at least one ligand which specifically binds the
XX protein which involves combining the protein encoded by the cDNA with
XX several of molecules or compounds under conditions to allow specific
XX binding, and detecting specific binding between the protein and a
XX molecule or compound, therefore identifying a ligand which specifically
XX binds the protein. The composition is useful for detecting and
XX quantifying differential gene expression, can be used in gene therapy, to
XX formulate prognosis and to design a treatment regimen and to monitor the
XX efficacy of treatment. The present sequence represents the amino acid
XX sequence of a protein encoded by a cDNA differentially expressed in a

CC liver disorder.
XX XX
SQ Sequence 646 AA;
Query Match 83.5%; Score 1097.5; DB 8; Length 646;
Best Local Similarity 81.4%; Pred. No. ie-82; Indels 5; Gaps 3;
Matches 214; Conservative 24; Mismatches 20;
QY 1 KSENVQDILLDLVPLSLGLETAGGVMTALIKRNSIPTKQTIQFTTYSNQPGLIQVY 60
Db 384 KSENVQDILLDLVPLSLGLETAGGVMTALIKRNTTPTKQTIQFTTYSNQPGLIQVY 443
QY 61 EGERAMTKNNLLGRFELSGIPAPRGVPOIEVTFDIDANGILNVATDKSTGKANKITI 120
Db 444 EGERAMTKNNLLGKFLTGIPAPRGVPOIEVTFDIDANGILNVSAVDKSTGKANKITI 503
QY 121 TNDKGRLSKEEIERMVQEAERKAEDEVORERSAKNALESYAFNMKSAAVEDEGLKGIS 180
Db 504 TNDKGRLSKEDIERMVQEAERKAEDEKQDKVSSKNSLESYAFNMKAIVDEKLOGKIN 563
QY 181 EADKKVLDKQBEVTSWLDANTLAEDFEHKKKELEQVNCNPIISGLYQAGG-PG--PG 237
Db 564 DEDKQKILDKNBIINWLDKNQTAKEEHEHQKELEKVCNPIITKLYQSAGGMPGMPG 623
QY 238 GF--GAQGPKGSGSGPTIEVD 258
Db 624 GPPGGGAPPSSGSGPTIEVD 646
RESULT 63
ADN04484
ID ADN04484 standard; protein; 646 AA.
XX AC ADN04484;
XX 01-JUL-2004 (first entry)
XX Antipsoriatic protein sequence #435.
XX antipsoriatic; gene therapy; psoriasis; diagnosis.
XX Homo sapiens.
XX WO2004028479-A2.
XX 08-APR-2004.
XX 25-SEP-2003; 2003WO-US030907.
XX 25-SEP-2002; 2002US-0414006P.
XX (GETH) GENENTECH INC.
XX Bodary S, Clark H, Jackman J, Schoenfeld J, Williams PM, Wood WT;
XX Wu TD;
XX WPI; 2004-305105/28.
XX N-PSDB; ADN04483.
XX New PRO nucleic acid or polypeptide, useful for preparing a
XX pharmaceutical composition for diagnosing or treating psoriasis in a
XX mammal.
XX Claim 9; SEQ ID NO 878; 3069pp; English.
XX The invention relates to novel polynucleotide and polypeptides for
XX treating psoriasis or a sequence having at least 80% identity to the
XX above sequences. The nucleic acid is useful for preparing a composition
XX for diagnosing or treating psoriasis in a mammal. This sequence
XX corresponds to one of the polypeptides of the invention.
XX Sequence 646 AA;

Query Match 83.5%; Score 1097.5; DB 8; Length 646;
 Best Local Similarity 81.4%; Pred. No. 1e-82;
 Matches 214; Conservative 24; Mismatches 20; Indels 5; Gaps 3;

QY 1 KSNVQDLLLLDVAPLSGLGTAGGVTALIKNSTIPTKQTOIFTTYSNQPGVLIQVY 60
 DB 384 KSNVQDLLLLDVAPLSGLGTAGGVTALIKNSTIPTKQTOIFTTYSNQPGVLIQVY 443

QY 61 EGERAMTKONLLGRFELSGIPAPRGVPOIETVTFDIDANGILNVATDKSTGKANKITI 120
 DB 444 EGERAMTKONLLGRFELSGIPAPRGVPOIETVTFDIDANGILNVATDKSTGKANKITI 503

QY 121 TNDKGRLSKEEIERMVQEAKEYAEDVQERVSNAKNALESYAFNMKSVADEGLKGKIS 180
 DB 504 TNDKGRLSKEEIERMVQEAKEYAEDVQERVSNAKNALESYAFNMKSVADEGLKGKIN 563

QY 181 EADKKVLDKQEVISWLDANTLAEKDEFEHKELEQVNCNPIISGLYQAGG-PG--PG 237
 DB 564 DEDKQKILDKCNEIINWLDKNTAEEFEHKELEQVNCNPIITKLYQAGGMPGMPG 623

QY 238 GF--GAQGPKGSGSGPTIEVD 258
 DB 624 GPFPGGAPPSGGSGPTIEVD 646

RESULT 64
 ADQ91627
 ID ADQ91627 standard; protein; 646 AA.
 AC ADQ91627;
 XX
 DT 07-OCT-2004 (first entry)
 DE Human heat shock cognate protein 70 (HSC70).
 XX Human; heat shock cognate protein 70; HSC70; multidrug resistance;
 KW cytotstatic; cancer; vaccine; gene therapy.
 XX Homo sapiens.
 XX WO2004061458-A2.
 XX 22-JUL-2004.
 XX 15-DEC-2003; 2003WO-18006416.
 XX 03-JAN-2003; 2003US-0438012P.
 XX (AURE-) AURELIUM BIOPHARMA INC.
 XX Georges E, Serfass L, Bonneau A, Dallaire P;
 XX WPI: 2004-553396/53.
 XX N-PSDB; ADQ91628.
 XX GENBANK; AAK17898.
 XX Detecting multidrug resistance/multidrug resistance potential in test
 PT neoplastic cell, by measuring heat shock cognate 70 protein level in test
 PT cell, comparing level of protein expression in test cell and non-
 PT resistant neoplastic cell.
 XX Claim 44; SEQ ID NO 1; 166pp; English.
 XX The present sequence is the protein sequence of human heat shock cognate
 CC protein 70 (HSC70). The invention is based on the discovery that HSC70, a
 CC normally intracellular protein, is expressed in full length on the cell
 CC surface of neoplastic cells and damaged cells, and is expressed more
 CC abundantly on the cell surfaces of multidrug resistant (MDR) neoplastic
 CC cells and MDR damaged cells. Although lower levels of HSC70 are expressed
 CC on the cell surface of drug-sensitive neoplastic cells, in contrast to
 CC other cell surface MDR markers such as P-glycoprotein, HSC70 is expressed
 CC in only negligible amounts on the cell surface of normal cells of the
 CC body. Thus, the invention provides a method for detecting multidrug

CC resistance in a test neoplastic cell by measuring the level of cell
 CC surface-expressed HSC70 protein. The neoplastic cell is especially a
 CC breast cancer, ovarian cancer, myeloma, lymphoma, melanoma, sarcoma,
 CC leukemia, retinoblastoma, hepatoma, glioma, mesothelioma or carcinoma
 CC cancer cell, or from a tissue selected from blood, bone marrow, spleen,
 CC lymph node, liver, thymus, kidney, brain, skin, gastrointestinal tract,
 CC eye, breast, prostate and ovary. The invention also provides a cell
 CC surface HSC70-targeted agent for treatment or prevention of an MDR
 CC neoplasm. This may include an HSC70 binding component and a therapeutic
 CC component such as a chemotherapeutic agent or radioisotope. Vaccines for
 CC treating or preventing MDR neoplasms comprise a HSC70 polypeptide or, in
 CC the case of DNA vaccines, a nucleic acid sequence encoding HSC70.
 XX Sequence 646 AA;
 SQ

Query Match 83.5%; Score 1097.5; DB 8; Length 646;
 Best Local Similarity 81.4%; Pred. No. 1e-82;
 Matches 214; Conservative 24; Mismatches 20; Indels 5; Gaps 3;

QY 1 KSNVQDLLLLDVAPLSGLGTAGGVTALIKNSTIPTKQTOIFTTYSNQPGVLIQVY 60
 DB 384 KSNVQDLLLLDVAPLSGLGTAGGVTALIKNSTIPTKQTOIFTTYSNQPGVLIQVY 443

QY 61 EGERAMTKONLLGRFELSGIPAPRGVPOIETVTFDIDANGILNVATDKSTGKANKITI 120
 DB 444 EGERAMTKONLLGRFELSGIPAPRGVPOIETVTFDIDANGILNVATDKSTGKANKITI 503

QY 121 TNDKGRLSKEEIERMVQEAKEYAEDVQERVSNAKNALESYAFNMKSVADEGLKGKIS 180
 DB 504 TNDKGRLSKEEIERMVQEAKEYAEDVQERVSNAKNALESYAFNMKSVADEGLKGKIN 563

QY 181 EADKKVLDKQEVISWLDANTLAEKDEFEHKELEQVNCNPIISGLYQAGG-PG--PG 237
 DB 564 DEDKQKILDKCNEIINWLDKNTAEEFEHKELEQVNCNPIITKLYQAGGMPGMPG 623

QY 238 GF--GAQGPKGSGSGPTIEVD 258
 DB 624 GPFPGGAPPSGGSGPTIEVD 646

RESULT 65
 ADQ89812
 ID ADQ89812 standard; protein; 646 AA.
 AC ADQ89812;
 XX
 DT 21-OCT-2004 (first entry)
 DE Antagonist of cell cycle progression polypeptide #121.
 XX Cytostatic; cancer; cell division cycle; mitosis; meiosis;
 KW cell cycle progression.
 XX Homo sapiens.
 XX WO2004063362-A2.
 XX 29-JUL-2004.
 XX 31-DEC-2003; 2003WO-GB005635.
 XX 10-JAN-2003; 2003US-0439123P.
 XX 06-MAY-2003; 2003US-0468402P.
 XX (CYCL-) CYCLACEL LTD.
 XX Glover D, Bell G, Frenz L, Midgley C;
 XX WPI: 2004-544089/52.
 XX N-PSDB; ADQ89811.
 XX New cell cycle progression genes and proteins for modulating cell cycle
 PT progression in cells, for preventing, treating or diagnosing cell

XX PR 29-OCT-2002; 2002US-0422472P.
XX PA (GETH) GENENTECH INC.
XX PI Aggarwal S, Clark H, Gurney AL, Schoenfeld J, Williams PM;
XX PI Wood WI, Wu TD;
XX DR N-PSDB; ADP54907.
XX DR WPI; 2004-376182/35.
XX PT New PRO polynucleotides and polypeptides, useful in useful in diagnosing
XX PT and treating an immune related disease, e.g. systemic lupus
XX PT erythematosus, rheumatoid arthritis, diabetes mellitus or asthma and in
XX PT stimulating an immune response.
XX PS Claim 1; SEQ ID NO 884; 3009pp; English.
XX CC The present invention describes an isolated PRO nucleic acid (1). Also
XX CC described: (1) a vector comprising (1); (2) a host cell comprising the
XX CC vector of (1); (3) a process for producing a PRO polypeptides; (4) an
XX CC isolated PRO polypeptide; (5) a chimeric molecule comprising the
XX CC polypeptide of (4) fused to a heterologous amino acid sequence; (6) an
XX CC antibody which specifically binds to a polypeptide of (4); (7) a
XX CC composition of matter comprising a polypeptide of (4), an agonist or
XX CC antagonist of the polypeptide or an antibody that binds to the
XX CC polypeptide in combination with a carrier; (8) an article of manufacture
XX CC comprising a container, a label on the container and a composition of
XX CC matter of (7); (9) a method of treating an immune related disease in a
XX CC mammal; (10) a method for determining the presence of a PRO polypeptide
XX CC in a sample suspected of having the polypeptide; (11) a method of
XX CC diagnosing an immune related disease or an inflammatory immune response
XX CC in a mammal; (12) a method of identifying a compound that inhibits or
XX CC mimics the activity of or expression of a gene encoding a PRO polypeptide
XX CC ; and (13) a method of stimulating the immune response in a mammal. The
XX CC PRO sequences have anti-allergic, anti-inflammatory, antipsoriatic,
XX CC anti-asthmatic, anti-diabetic, anti-rheumatoid, antipsoriatic,
XX CC anti-rheumatic, antithyroid, CNS, dermatological, gastrointestinal,
XX CC haemostatic, hepatotropic, immunostimulant, immunosuppressive, muscular,
XX CC nephrotropic, neuroprotective, osteopathic, respiratory, vasotropic and
XX CC virucide activities, and can be used in gene therapy. The nucleic acid
XX CC (1) and the encoded polypeptides, compositions, kits and methods are
XX CC useful in diagnosing and treating an immune related disease and in
XX CC stimulating an immune response. The present sequence represents a human
XX CC PRO protein from the present invention.
XX SQ Sequence 646 AA;

Query Match 83.5%; Score 1097.5; DB 8; Length 646;
Best Local Similarity 81.4%; Pred. No. 1e-82;
Matches 214; Conservative 24; Mismatches 20; Indels 5; Gaps 3;
QY 1 KSENVQDILLVAPISLGLTAGGVMTALIKNSITPTKQTQITFTYSDNQGVLIQVY 60
DB 384 KSENVQDILLVAPISLGLTAGGVMTALIKNSITPTKQTQITFTYSDNQGVLIQVY 443
QY 61 EGERAMTKDNNLLGRPELSGIPAPRGVPOIETVFDIDANGILNVATDKSTGKANKITI 120
DB 444 EGERAMTKDNNLLGRPELSGIPAPRGVPOIETVFDIDANGILNVATDKSTGKANKITI 503
QY 121 TNDKGRLSKEEIERWQAEKYKAEDEVRERVSNAKNALSYAFNMKSAVEDGLGKGIS 180
DB 504 TNDKGRLSKEEIERWQAEKYKAEDEVRERVSNAKNALSYAFNMKSAVEDGLGKGIS 563
QY 181 EADKKVLDKQEVISWLDANTLAEKDFEHEKLEQVNCNPIISGLYQAGG-PG--PG 237
DB 564 DEBKQKILDKCNRIINWLDKXNTAEKEEFHQKELEKVCNPIITKLYQAGGMPGMPG 623
QY 238 GF--GAQGPKGSGSGPTIEVD 258
DB 624 GFFGGGAPPSSGGASGPTIEVD 646

RESULT 68
ADP24120
ID ADP24120 standard; protein; 646 AA.
XX AC ADP24120;
XX AC ADP24120;
XX DT 18-NOV-2004 (first entry)
XX DE PRO polypeptide SEQ ID NO:1298.
XX KW PRO; anti-inflammatory; antiarthritic; antirheumatic; immunosuppressive;
XX KW osteopathic; antidiabetic; dermatological; antipsoriatic; antiallergic;
XX KW antiasthmatic; hepatotropic; respiratory; gene therapy; immune system.
XX OS Unidentified.
XX PN WQ2004041170-A2.
XX PD 21-MAY-2004.
XX PF 30-OCT-2003; 2003WO-US034312.
XX PR 01-NOV-2002; 2002US-0423394P.
XX PA (GETH) GENENTECH INC.
XX PI Clark H, Schoenfeld J, Van Lookeren M, Williams PM, Wood WI;
XX PI Wu TD;
XX DR WPI; 2004-419628/39.
XX DR N-PSDB; ADP24119.
XX DR New PRO polypeptides and polynucleotides, useful for treating e.g.
XX PT erythematosus, rheumatoid arthritis, diabetes mellitus, immune-mediated
XX PT renal disease, or demyelinating diseases of the central or peripheral
XX PT nervous system.
XX PS Claim 7; SEQ ID NO 1298; 2940pp; English.
XX CC The invention relates to a novel isolated nucleic acid and the PRO
XX CC polypeptide encoded by it. A protein of the invention has
XX CC anti-inflammatory, antiarthritic, antirheumatic, immunosuppressive,
XX CC osteopathic, antidiabetic, dermatological, antipsoriatic, antiallergic,
XX CC antiasthmatic, hepatotropic, and respiratory activity. A polynucleotide
XX CC of the invention may have a use in gene therapy. The PRO polypeptide, its
XX CC agonist, antagonist, or antibody that specifically binds to the
XX CC polypeptide is useful for treating an immune related disorder such as
XX CC systemic lupus erythematosus, rheumatoid arthritis, osteoarthritis,
XX CC juvenile chronic arthritis, a spondyloarthropathy, systemic sclerosis, an
XX CC idiopathic inflammatory myopathy, Sjogren's syndrome, systemic
XX CC vasculitis, sarcoidosis, autoimmune haemolytic anaemia, autoimmune
XX CC thrombocytopenia, thyroiditis, diabetes mellitus, immune-mediated renal
XX CC disease, a demyelinating disease of the central or peripheral nervous
XX CC system, idiopathic demyelinating polyneuropathy, Guillain-Barre syndrome,
XX CC a chronic inflammatory demyelinating polyneuropathy, a hepatobiliary
XX CC disease, infectious or autoimmune chronic active hepatitis, primary
XX CC biliary cirrhosis, granulomatous hepatitis, sclerosing cholangitis,
XX CC inflammatory bowel disease, gluten-sensitive enteropathy, Whipple's
XX CC disease, an autoimmune or immune-mediated skin disease, a bullous skin
XX CC disease, erythema multiforme, contact dermatitis, psoriasis, an allergic
XX CC disease, asthma, allergic rhinitis, atopic dermatitis, food
XX CC hypersensitivity, urticaria, an immunologic disease of the lung,
XX CC eosinophilic pneumonia, idiopathic pulmonary fibrosis, hypersensitivity
XX CC pneumonitis, a transplantation associated disease, graft rejection or
XX CC graft-versus-host disease. The present sequence represents a PRO protein
XX CC of the invention.
XX SQ Sequence 646 AA;

Query Match 83.5%; Score 1097.5; DB 8; Length 646;
Best Local Similarity 81.4%; Pred. No. 1e-82;
Matches 214; Conservative 24; Mismatches 20; Indels 5; Gaps 3;

OS Aequorea victoria.
OS Mammalia.
OS Chimeric.
XX WO2000050872-A2.
XX 31-AUG-2000.
XX 25-FEB-2000; 2000WO-US004794.
XX 26-FEB-1999; 99US-0122152P.
PR 08-MAR-1999; 99US-0123399P.
PR 12-JUL-1999; 99US-00352171.
XX (CELL-) CELLOMICS INC.
XX
XX Giuliano KA, Kapur R;
XX WPI; 2000-594086/56.
DR N-PSDB; AAA93443.
XX
XX Automated cell-based characterization of toxin by contacting cells
PT containing luminescent reporter molecules with test substance and
PT analyzing optically.
XX
XX Example 11; Page 315-318; 336pp; English.
XX
XX The invention relates to systems, methods and reagents for cell-based
CC screening or detection of compounds which affect particular biological
CC functions. The methods of the invention utilise fluorescent bioreactor
CC molecules which, when acted on by a compound of interest, cause an
CC alteration in the cellular distribution of at least the fluorescent
CC moiety. In one embodiment, the biosensors comprise heat shock proteins
CC (HSPs) fused to a fluorescent protein (e.g., jellyfish green fluorescent
CC protein (GFP), or derivatives thereof). Such biosensors are located in
CC the cytoplasm, but on stress activation translocate to the nucleus. In
CC another embodiment bioreactor proteins can be used to detect protease
CC activity. Such protease bioreactor fusion proteins comprise one or more
CC fluorescent proteins; a recognition signal which is cleaved by the
CC protease; and at least one cellular localisation signal. The latter two
CC components may be components of a single protein which is acted upon by
CC the protease, or may be from heterologous sources. Due to the
CC localisation signal, the bioreactor protein is localised to a particular
CC region of the cell. Once acted on by the protease of interest, the
CC fluorescent protein is cleaved from the localisation sequence, and is
CC free to migrate to other locations within the cell. The presence of a
CC second localisation signal attached to the fluorescent protein enables
CC the fluorescent protein to be directed to a different cellular
CC compartment after cleavage of the protease recognition sequence. The
CC change in distribution of the fluorescent protein can be detected using
CC imaging methods with a high degree of spatial resolution. The methods and
CC biosensors of the invention can be used to investigate a wide range of
CC cellular activities and to screen compounds which modulate these
CC activities. Biosensors containing a recognition site for caspase, for
CC example, may be used for the screening of compounds which modulate
CC apoptosis, while biosensors containing other protease recognition sites
CC may be used for the detection of proteolytic toxins (such as anthrax
CC lethal factor). The method provides improved target validation and
CC candidate compound optimisation by combining many cell screening formats
CC with fluorescence-based molecular reagents and computer-based feature
CC extraction, data analysis and automation, resulting in increased quantity
CC and speed of data collection and faster evaluation of drug candidates.
CC Sequences AAB22860-B22876 and AAB22936-B22941 represent biosensor fusion
CC proteins produced in an exemplification of the invention. (Updated on 12-
CC SEP-2003 to standardise OS field)
XX
XX Sequence 890 AA;
SQ
Query Match 83.5%; Score 1097.5; DB 3; Length 890;
Best Local Similarity 81.4%; Pred. No. 1.6e-82;
Matches 214; Conservative
XX 1 KSENVQDLLLDVAPLSLGTAGGVMTALKRNSTIPTKTQTFTTYSNQPGVLQVY 60

Db 628 KSENVQDLLLDVAPLSLGTAGGVMTALKRNSTIPTKTQTFTTYSNQPGVLQVY 687
Qy 61 EGERAMTKONNLLGRFELSGIPPPAPRGVPOIEVTFDIDANGILNVATATDKSTGKANKITI 120
Db 688 EGERAMTKONNLLGKFLTGIPPPAPRGVPOIEVTFDIDANGILNVSAVDSTGKANKITI 747
Qy 121 TNDKRLSKKEIERMVOEAEKYKAEDVQERVSQAKNALESYAFNMKSAVEDEGLKQKIS 180
Db 748 TNDKRLSKKEDIERMVOEAEKYKAEDKQKRDVSSKNSLESYAFNMKATVEDEKLQKGIN 807
Qy 181 EADKKVLDKQCVISWLDANTLAEDKDFEHKELEOVNPIISGLYQAGG-PG--PG 237
Db 808 DEDKQKILDKCNELIINWLDKQNTAEKEEFHQKLEKVCNPIITKLYQAGGMPGMPG 867
Qy 238 GF--GAQPGKSGSGPTIEVD 258
Db 868 GFGGGAGPPSGGASSGPTIEVD 890
XX
XX RESULT 71
XX ABG94501
ID ABG94501 standard; protein; 890 AA.
XX
XX AC ABG94501;
XX
XX DT 27-NOV-2002 (first entry)
XX
XX DE Protease biosensor related biosensor #3.
XX
XX KW Detection; classification; identification; toxin detection; protease;
KW ADP-ribosylating toxin; cytotoxic phospholipase; exfoliative toxin;
XX toxic threat agent.
XX
XX OS Synthetic.
XX
XX PN US6416959-B1.
XX
XX PD 09-JUL-2002.
XX
XX PF 25-FEB-2000; 2000US-00513783.
XX
XX PR 27-FEB-1997; 97US-00810983.
PR 27-FEB-1998; 98US-00031271.
PR 26-FEB-1999; 99US-0122152P.
PR 08-MAR-1999; 99US-0123399P.
PR 12-JUL-1999; 99US-00352171.
PR 31-AUG-1999; 99US-0151797P.
PR 17-SEP-1999; 99US-00398965.
PR 29-OCT-1999; 99US-00430656.
PR 01-DEC-1999; 99US-0168408P.
XX
XX (GIUL/) GIULIANO K.
XX (KAPU/) KAPUR R.
XX
XX Giuliano K, Kapur R;
XX
XX WPI; 2002-634730/68.
DR N-PSDB; ABS71562.
XX
XX Automated cell-based toxin detection, classification, and/or
PT identification by treating cells involves use of three classes of
PT luminescent reporter molecules such as detectors, classifiers or
PT identifiers.
XX
XX Example 11; Col 291-296; 214pp; English.
XX
XX The invention describes methods of automated detection, classification
CC and identification comprising treating cells containing luminescent
CC reporter molecules (I) in array of locations with a test substance, where
CC (I) are detectors, classifiers or identifiers, imaging cells in each
CC location to obtain luminescent signals and converting optical information
CC into digital data to interpret presence of toxins in the test substance.

CC The method are useful for detection of toxins chosen from proteases, ADP-
 CC ribosylating toxins, cytotoxic phospholipases, and exfoliative toxins.
 CC Three classes of cell-based luminescent reporter molecules such as
 CC detectors, classifiers and identifiers are described and serve as
 CC reporters of toxic threat agents. The first two levels of
 CC characterisation ensure a rapid readout of toxin class without
 CC sacrificing the ability to detect many new mutant toxins or dissect
 CC several complex mixtures of known toxins. This is the amino acid sequence
 CC of a biosensor associated with the protease biosensor of the invention
 XX
 SQ Sequence 890 AA;

Query Match 83.5%; Score 1097.5; DB 5; Length 890;
 Best Local Similarity 81.4%; Pred. No. 1.6e-82;
 Matches 214; Conservative 24; Mismatches 20; Indels 5; Gaps 3;
 QY 1 KSENVQDLLLDVAPISLGLTETAGGVTALIKNSIPIPTQIQTFTYSDNQPGVLIQVY 60
 DB 628 KSENVQDLLLDVAPISLGLTETAGGVTALIKNSIPIPTQIQTFTYSDNQPGVLIQVY 697
 QY 61 EGERAMTKNNLGRPELSGIPAPRGVPOIEVTFDIDANGILNVATDKSTGKANKITI 120
 DB 688 EGERAMTKNNLGRPELSGIPAPRGVPOIEVTFDIDANGILNVATDKSTGKANKITI 747
 QY 121 TNDKGRLSKEEIERMVQAEKYKAEDVQRRVSAKNALESYAFNMKSAVEDGLKGGKIS 180
 DB 748 TNDKGRLSKEEIERMVQAEKYKAEDVQRRVSAKNALESYAFNMKSAVEDGLKGGKIS 807
 QY 181 EADKKVLDKQEVISWLDANTLAEDKFEHKELEVOVCPNPIISGLYQAGG-PG--PG 237
 DB 808 DEDKQKILDKCNRIINWLDKNTAEKEEFHQKELEKVCNPIITKLYQAGGMPGMPG 867
 QY 238 GF--GAQGPKGSGSGPTIEVD 258
 DB 868 GFPGGAGPPSGGSGPTIEVD 890

RESULT 72
 ADM05456
 ID ADM05456 standard; protein; 250 AA.
 AC ADM05456;
 DT 20-MAY-2004 (first entry)
 XX Human protein of the invention SEQ ID NO:4141.
 XX human; gene therapy; diagnostic marker; pharmaceutical.
 OS Homo sapiens.
 XX
 XX EF1347046-A1.
 XX
 XX 24-SEP-2003.
 XX
 XX 12-APR-2002; 2002EP-00008400.
 XX
 XX 22-MAR-2002; 2002JP-00137785.
 XX
 XX (REAS-) RES ASSOC BIOTECHNOLOGY.
 XX
 XX Isogai T, Sugiyama T, Otsuki T, Wakamatsu A, Sato H, Ishii S;
 XX Yamamoto J, Isono Y, Hio Y, Otsuka K, Nagai K, Irie R, Tamechika I;
 XX Seki N, Yoshikawa T, Otsuka M, Nagahari K, Masuho Y;
 XX
 XX WPI; 2003-723558/69.
 DR N-PSDB; ADM03013.
 XX
 XX New polynucleotides and polypeptides are useful in gene therapy, for
 XX developing a diagnostic marker or medicines for regulating their
 XX expression and activity, or as a target of gene therapy.
 XX
 XX Claim 1; SEQ ID NO 4141; 305pp; English.

XX The invention relates to a novel human polynucleotide and the encoded
 CC polypeptide. A polynucleotide of the invention may have a use in gene
 CC therapy. An oligonucleotide of the invention ADM06202-ADM06773 is useful
 CC as a primer for synthesizing the polynucleotide or as a probe for
 CC detecting the polynucleotide. The polynucleotides ADM0316-ADM03758 are
 CC useful in gene therapy, for developing a diagnostic marker or medicines
 CC for regulating their expression and activity, or as a target of gene
 CC therapy. The proteins ADM03759-ADM06201 encoded by the polynucleotides
 CC are useful as pharmaceutical agents. The present sequence represents a
 CC protein sequence of the invention.
 XX
 SQ Sequence 250 AA;

Query Match 83.5%; Score 1097; DB 7; Length 250;
 Best Local Similarity 100.0%; Pred. No. 3.3e-83;
 Matches 213; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 46 TTYSDNQPGVLIQVYGERAMTKNNLGRFELSGIPAPRGVPOIEVTFDIDANGILNV 105
 DB 38 TTYSDNQPGVLIQVYGERAMTKNNLGRFELSGIPAPRGVPOIEVTFDIDANGILNV 97
 QY 106 TATDKSTGKANKITITNDKGRLSKEEIERMVQAEKYKAEDVQRRVSAKNALESYAFN 165
 DB 98 TATDKSTGKANKITITNDKGRLSKEEIERMVQAEKYKAEDVQRRVSAKNALESYAFN 157
 QY 166 MKSAVEDGLKGGKISADKKVLDKQEVISWLDANTLAEDKFEHKELEVOVCPNPIIS 225
 DB 158 MKSAVEDGLKGGKISADKKVLDKQEVISWLDANTLAEDKFEHKELEVOVCPNPIIS 217
 QY 226 GLYQAGGPGPGFGAQQPGKGGSGPTIEVD 258
 DB 218 GLYQAGGPGPGFGAQQPGKGGSGPTIEVD 250

RESULT 73
 ADS85121
 ID ADS85121 standard; protein; 646 AA.
 AC ADS85121;
 DT 18-NOV-2004 (first entry)
 XX Mouse atopic dermatitis-related protein sequence SeqID123.
 XX atopic dermatitis; gene expression level; skin; inflammation; rash;
 XX dermatological; anti-inflammatory; antipsoriatic; psoriasis; mouse;
 XX murine.
 OS Mus musculus.
 XX
 XX WO2004031386-A1.
 XX
 XX 15-APR-2004.
 XX
 XX 01-AUG-2003; 2003WO-JP009808.
 XX
 XX 06-AUG-2002; 2002JP-00229318.
 XX
 XX 14-MAY-2003; 2003JP-00136543.
 XX
 XX (GENO-) GENOX RES INC.
 XX (UYJU-) UNIV JUNTENDO.
 XX
 XX Itoh M, Ogawa K, Shinagawa A, Sudo H, Ogawa H, Ra C;
 XX Mitsuishi K;
 XX
 XX WPI; 2004-330185/30.
 DR N-PSDB; ADS85120.
 XX
 XX Determination of difference in expression level of specified genes in
 XX inflamed and non-inflamed skin sites for diagnosis and examination of
 XX atopic dermatitis and psoriasis.

PS	Example 1; SEQ ID NO 123; 61pp; Japanese.	PT	treated human C3A liver cell cultures, useful for treating liver disorders.
XX		XX	
CC	This invention relates to a novel method for the examination of atopic dermatitis in which the expression level of specified genes in specimens of skin taken from inflamed (rash) areas and non-inflamed areas is compared and the presence of increased or reduced expression in the inflamed areas determined. The invention may be useful for the development of compounds with a dermatological, antiinflammatory or antipsoriatic activity acting as inhibitors and stimulators of genes involved in atopic dermatitis and psoriasis. The invention may be useful for treatment, prevention, diagnosis and assessment of atopic dermatitis and psoriasis. The present sequence is that of an atopic dermatitis-related protein which was used in the exemplification of the invention.	CC	The invention relates to a composition comprising several cDNAs that are differentially expressed in a liver disorder. The composition is useful for treating liver disorder such as hyperlipidaemia, hypertension, type II diabetes, tumours of the liver and disorders of the inflammatory and immune response. The composition is useful for a high-throughput method of screening several cDNAs or compounds to identify a ligand which specifically binds a cDNA. A protein encoded by the cDNA is useful for a high-throughput method for using a protein to screen several molecules or compounds to identify at least one ligand which specifically binds the protein which involves combining the protein encoded by the cDNA with several of molecules or compounds under conditions to allow specific binding, and detecting specific binding between the protein and a molecule or compound, therefore identifying a ligand which specifically binds the protein. The composition is useful for detecting and quantifying differential gene expression, can be used in gene therapy, to formulate prognosis and to design a treatment regimen and to monitor the efficacy of treatment. The present sequence represents the amino acid sequence of a protein encoded by a cDNA differentially expressed in a liver disorder.
XX		XX	
SQ	Sequence 646 AA;	SQ	Sequence 641 AA;
	Query Match 83.3%; Score 1094.5; DB 8; Length 646;		Query Match 83.2%; Score 1093; DB 8; Length 641;
	Best Local Similarity 81.4%; Pred. No. 1.8e-82;		Best Local Similarity 81.5%; Pred. No. 2.4e-82;
	Matches 214; Conservative 23; Mismatches 21; Indels 5; Gaps 3;		Matches 216; Conservative 16; Mismatches 17; Indels 16; Gaps 2;
QY	1 KSENVQDLLLLDVAPLSGLGLETAGGVTALIKRNSTIPTKQIIFTTYSNPGVLIQY 60	QY	1 KSENVQDLLLLDVAPLSGLGLETAGGVTALIKRNSTIPTKQIIFTTYSNPGVLIQY 60
DB	384 KSENVQDLLLLDVAPLSGLGLETAGGVTALIKRNSTIPTKQIIFTTYSNPGVLIQY 443	DB	386 KSENVQDLLLLDVAPLSGLGLETAGGVTALIKRNSTIPTKQIIFTTYSNPGVLIQY 445
QY	61 EGERAMTKDNNLLGRFELSGIPAPRGVQIEVTFDIDANGILNVATDKSTGKANKITI 120	QY	61 EGERAMTKDNNLLGRFELSGIPAPRGVQIEVTFDIDANGILNVATDKSTGKANKITI 120
DB	444 EGERAMTKDNNLLGRFELSGIPAPRGVQIEVTFDIDANGILNVATDKSTGKANKITI 503	DB	446 EGERAMTKDNNLLGRFELSGIPAPRGVQIEVTFDIDANGILNVATDKSTGKANKITI 505
QY	121 TNDKGRLSKEETIERMVQAEKYKAEDVQERVSNAKNALESYAFNMKSABVEDEGLGKIS 180	QY	121 TNDKGRLSKEETIERMVQAEKYKAEDVQERVSNAKNALESYAFNMKSABVEDEGLGKIS 180
DB	504 TNDKGRLSKEETIERMVQAEKYKAEDVQERVSNAKNALESYAFNMKSABVEDEGLGKIS 563	DB	506 TNDKGRLSKEETIERMVQAEKYKAEDVQERVSNAKNALESYAFNMKSABVEDEGLGKIS 565
QY	181 EADKKKKVLDKQEVISWLDANTLAEDKDEFEHKKRKELEQVNCNPIISGLYQAGG-PG--PG 237	QY	181 EADKKKKVLDKQEVISWLDANTLAEDKDEFEHKKRKELEQVNCNPIISGLYQAGGPG 240
DB	564 DEDQKILDKCNEIISWLDKQNTAEKEEFHQKLEKVCNPIITKLYQSGAGGMPG 623	DB	566 ESDKNKILDKCNEIISWLEVNQAEKDEPDHKKRKELEQVNCNPIITKLYQG-----G 616
QY	238 GP--GAGPKGGSGSGPTIEVD 258	QY	241 AOGPKGGSG-----SGPTIEVD 258
DB	624 GPPGGGAPPSSGSGPTIEVD 646	DB	617 CTGPACGTGYVPGRPATGPTIEVD 641
RESULT 74		RESULT 75	
AD76908		ADD18948	
ID	ADE76908 standard; protein; 641 AA.	ID	ADD18948 standard; protein; 650 AA.
AC	AC	AC	AC
XX	ADE76908;	XX	ADD18948;
XX		XX	
DT	29-JAN-2004 (first entry)	DT	15-JAN-2004 (first entry)
DE	Human protein expressed in a liver disorder #22.	DE	Human disease related protein SeqID437.
XX	human; liver disorder; hyperlipidaemia; hypertension; type II diabetes;	XX	human; disease state; cytostatic; antiinflammatory; ophthalmological;
KW	tumour; liver; inflammatory disorder; immune response disorder;	KW	antiartherosclerotic; vulnary; gene therapy;
KW	high-throughput screening; differential gene expression; gene therapy.	KW	hypoxia-regulated condition; tumorigenesis; angiogenesis; apoptosis;
XX		KW	inflammation; erythropoiesis; glycolysis; gluconeogenesis;
OS	Homo sapiens.	KW	glucose transportation; catecholamine synthesis; iron transport;
XX		KW	nitric oxide synthesis; cancer; ischaemic condition; reperfusion injury;
PN	US2003108871-A1.	KW	retinopathy; neonatal stress; pre-eclampsia; atherosclerosis;
XX		XX	inflammatory condition; wound healing.
PD	12-JUN-2003.	OS	Homo sapiens.
XX		XX	
PF	30-JUL-2001; 2001US-00919039.		
PR	28-JUL-2000; 2000US-0222113P.		
XX			
PA	(KASE/) KASER M R.		
XX			
PI	Kaser MR;		
XX			
DR	WPI; 2004-031227/03.		
DR	N-PSDB; ADE76907.		
XX			
FT	Composition comprising several cDNAs that are differentially expressed in		

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PN WO2003018621-A2.
XX
XX
PD 06-MAR-2003.
XX
XX PF 23-AUG-2002; 2002WO-GB003892.
XX
XX PR 23-AUG-2001; 2001GB-00020558.
PR 05-OCT-2001; 2001GB-00024037.
XX
XX PA (OXFO-) OXFORD BIOMEDICA UK LTD.
XX
XX PI Kingsman SM, White J, Ward NR, Harris RA, Naylor S, Mundy CR;
XX WPI; 2003-290046/28.
XX DR N-PSDB; ADD18949.
XX
XX New substantially purified polypeptide, useful for diagnosing or treating
PT a hypoxia-regulated condition, such as cancer, ischemia, reperfusion
PT injury, retinopathy, pre-eclampsia, atherosclerosis, inflammation, or
PT wound healing.
XX
XX PS Claim 25; SEQ ID NO 437; 424pp; English.
XX
XX This invention relates to novel human genes and gene product which are
CC implicated in certain disease states. Compounds which modulate the
CC proteins of the invention may have cytostatic, antiinflammatory,
CC ophthalmological, antiarteriosclerotic or vulnary activities. The
CC sequences of the invention may be useful for gene therapy. The invention
CC may be useful for diagnosing or treating a hypoxia-regulated condition,
CC such as tumorigenesis, angiogenesis, apoptosis, inflammation,
CC erythropoiesis, or the biological response to hypoxia conditions
CC including processes such as glycolysis, gluconeogenesis, glucose
CC transport, catecholamine synthesis, iron transport or nitric oxide
CC synthesis. The disease includes cancer, ischemic conditions, reperfusion
CC injury, retinopathy, neonatal stress, pre-eclampsia, atherosclerosis,
CC inflammatory conditions or wound healing. The present sequence is that of
CC a disease related protein of the invention.
XX
XX Sequence 650 AA;
XX
XX Query Match 83.1%; Score 1091.5; DB 7; Length 650;
XX Best Local Similarity 79.8%; Pred. No. 3.3e-82;
XX Matches 213; Conservative 25; Mismatches 20; Indels 9; Gaps 3;
XX
QY 1 KSENVQDLLLDVAPLSGLGTAGGVMTALIKRNTIPTKQTQFTTYSNQPGLVIQVY 60
DB 384 KSENVQDLLLDVTPLSGLGTAGGVMTVLKRNTPKQTQFTTYSNQPGLVIQVY 443
QY 61 EGERAMTKDNNLLGRFELSGIPAPRGVQPIEVTFDIDANGILNVATDKSTGKANKITI 120
DB 444 EGERAMTKDNNLLGKFLTGIPAPRGVQPIEVTFDIDANGILNVSAVDKSTGKANKITI 503
QY 121 TNDKGRLSKEIERMVOEAKYKAEDVQERVSAKNALESYAFNMKSAVEDGLGKGKIS 180
DB 504 TNDKGRLSKEDIEMVOEAKYKAEDKQDKVSSKNLSKSYAFNMKATVDEKLGKIN 563
QY 181 EADKKVLDKQCVISWLDANTLAEDFEHKKLEQVNCNPIISGLYQAGG-----PG 235
DB 564 DEDKQKILDKCNEIINWLDKNQTAKEEFHKKLEQVNCNPIITKLYQAGGMPGMPG 623
QY 236 --PGGP--GAQGPKGSGSGPTIEVD 258
DB 624 GMPGGPFGGAPPSPGSGSGPTIEVD 650
XX
XX RESULT 76
XX ADD18946
XX ID ADD18946 standard; protein; 650 AA.
XX AC
XX AC ADD18946;
XX DX
XX DT 15-JAN-2004 (first entry)
XX
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Human disease related protein SeqID435.

human; disease state; cytostatic; antiinflammatory; ophthalmological; antiarteriosclerotic; vulnary; gene therapy; hypoxia-regulated condition; tumorigenesis; angiogenesis; apoptosis; inflammation; erythropoiesis; glycolysis; gluconeogenesis; glucose transport; catecholamine synthesis; iron transport; nitric oxide synthesis; cancer; ischemic condition; reperfusion injury; retinopathy; neonatal stress; pre-eclampsia; atherosclerosis; inflammatory condition; wound healing.

Homo sapiens.

WO2003018621-A2.

06-MAR-2003.

23-AUG-2002; 2002WO-GB003892.

23-AUG-2001; 2001GB-00020558.

05-OCT-2001; 2001GB-00024037.

(OXFO-) OXFORD BIOMEDICA UK LTD.

Kingsman SM, White J, Ward NR, Harris RA, Naylor S, Mundy CR; WPI; 2003-290046/28.

N-PSDB; ADD18947.

New substantially purified polypeptide, useful for diagnosing or treating a hypoxia-regulated condition, such as cancer, ischemia, reperfusion injury, retinopathy, pre-eclampsia, atherosclerosis, inflammation, or wound healing.

Claim 25; SEQ ID NO 435; 424pp; English.

This invention relates to novel human genes and gene product which are implicated in certain disease states. Compounds which modulate the proteins of the invention may have cytostatic, antiinflammatory, ophthalmological, antiarteriosclerotic or vulnary activities. The sequences of the invention may be useful for gene therapy. The invention may be useful for diagnosing or treating a hypoxia-regulated condition, such as tumorigenesis, angiogenesis, apoptosis, inflammation, erythropoiesis, or the biological response to hypoxia conditions including processes such as glycolysis, gluconeogenesis, glucose transport, catecholamine synthesis, iron transport or nitric oxide synthesis. The disease includes cancer, ischemic conditions, reperfusion injury, retinopathy, neonatal stress, pre-eclampsia, atherosclerosis, inflammatory conditions or wound healing. The present sequence is that of a disease related protein of the invention.

Sequence 650 AA;

Query Match 83.1%; Score 1091.5; DB 7; Length 650; Best Local Similarity 79.8%; Pred. No. 3.3e-82; Matches 213; Conservative 25; Mismatches 20; Indels 9; Gaps 3;

1 KSENVQDLLLDVAPLSGLGTAGGVMTALIKRNTIPTKQTQFTTYSNQPGLVIQVY 60

384 KSENVQDLLLDVTPLSGLGTAGGVMTVLKRNTPKQTQFTTYSNQPGLVIQVY 443

61 EGERAMTKDNNLLGRFELSGIPAPRGVQPIEVTFDIDANGILNVATDKSTGKANKITI 120

444 EGERAMTKDNNLLGKFLTGIPAPRGVQPIEVTFDIDANGILNVSAVDKSTGKANKITI 503

121 TNDKGRLSKEIERMVOEAKYKAEDVQERVSAKNALESYAFNMKSAVEDGLGKGKIS 180

504 TNDKGRLSKEDIEMVOEAKYKAEDKQDKVSSKNLSKSYAFNMKATVDEKLGKIN 563

181 EADKKVLDKQCVISWLDANTLAEDFEHKKLEQVNCNPIISGLYQAGG-----PG 235

564 DEDKQKILDKCNEIINWLDKNQTAKEEFHKKLEQVNCNPIITKLYQAGGMPGMPG 623

--PGGP--GAQGPKGSGSGPTIEVD 258

GMPGGPFGGAPPSPGSGSGPTIEVD 650

RESULT 76

ADD18946

ID ADD18946 standard; protein; 650 AA.

AC

AC ADD18946;

DX

DT 15-JAN-2004 (first entry)


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CC ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 641 AA;
Query Match 82.7%; Score 1087; DB 7; Length 641;
Best Local Similarity 83.5%; Pred. No. 7.7e-82;
Matches 218; Conservative 17; Mismatches 18; Indels 8; Gaps 3;
QY 1 KSENVQDLLLLDVAPLSLGLTAGGVTALIKRNSTIPTKQIQTFTTSDNPGVLIQY 60
DB 386 KSEKVDLLLLDVAPLSLGLTAGGVTALIKRNSTIPTKQIQTFTTSDNPGVLIQY 445
QY 61 EGERAMTKDNLGRFELSGIPAPRGVQIETVFDIDANGILNVTATDKSTGKANKITI 120
DB 446 EGERAMTRDNLGRFDLTGIPAPRGVQIETVFDIDANGILNVTATDKSTGKANKITI 505
QY 121 TNDKGRLSKEEIERMVQEAERYKAEDVQERVSAAKNALESYAFNMKSASVDEGLKDKIS 180
DB 506 TNDKGRLSKEEIERMVQEAERYKAEDVQERVSAAKNALESYAFNMKSASVDEGLKDKIS 565
QY 181 EADKKVLDKQCVISWLDANTLAEKDFEHRKELEQVCNPIISGLYQ-GAGGP--GPG 237
DB 566 ESDKKKILDKCEVLSWLEAQAEKDFHKKRKELENMNCNPIITKLYQSGCTGPTCAPG 625
QY 238 GFCAQGPKGSGSGPTIEVD 258
DB 626 -----YTPGARITGPTIEVD 641
RESULT 79
ADD48986
ID ADD48986 standard; protein; 641 AA.
XX
AC ADD48986;
XX
XX 02-DEC-2004 (revised)
DT 29-JAN-2004 (first entry)
XX
XX Rat Protein P55063, SEQ ID NO 14698.
DE
XX Rat; pain; neuronal tissue; gene therapy; spinal segmental nerve injury;
XX chronic constriction injury; CCI; spared nerve injury; SNI; Chung.
XX
XX Rattus norvegicus.
OS
OS Unidentified.
XX
XX WO2003016475-A2.
XX
XX 27-FEB-2003.
XX
XX 14-AUG-2002; 2002WO-US025765.
XX
XX 14-AUG-2001; 2001US-0312147P.
PR
XX 01-NOV-2001; 2001US-0346382P.
PR
XX 26-NOV-2001; 2001US-0333347P.
XX
XX (GEO ) GEN HOSPITAL CORP.
PA
XX (FARB ) BAYER AG.
XX
XX Woolf C, D'urso D, Befort K, Costigan M;
XX
XX WPI; 2003-268312/26.
DR
XX GENBANK; P55063.
XX
XX New composition comprising two or more isolated polypeptides, useful for
PT preparing a medicament for treating pain in an animal.
XX
XX Example 1; Page; 1017pp; English.
XX
XX The invention discloses a composition comprising two or more isolated rat
CC or human polynucleotides or a polynucleotide which represents a fragment,
CC derivative or allelic variation of the nucleic acid sequence. Also
CC claimed are a vector comprising the novel polynucleotide, a host cell
CC
```

```
CC comprising the vector, a method for identifying a nucleotide sequence
CC which is differentially regulated in an animal subjected to pain and a
CC kit to perform the method, an array, a method for identifying an agent
CC that increases or decreases the expression of the polynucleotide sequence
CC that is differentially expressed in neuronal tissue of a first animal
CC subjected to pain, a method for identifying a compound which regulates
CC the expression of a polynucleotide sequence which is differentially
CC expressed in an animal subjected to pain, a method for identifying a
CC compound that regulates the activity of one or more of the
CC polynucleotides, a method for producing a pharmaceutical composition, a
CC method for identifying a compound or small molecule that regulates the
CC activity in an animal of one or more of the polypeptides given in the
CC specification, a method for identifying a compound useful in treating
CC pain and a pharmaceutical composition comprising the one or more
CC polypeptides or their antibodies. The polynucleotide or the compound that
CC modulates its activity is useful for preparing a medicament for treating
CC pain (e.g. spinal segmental nerve injury (Chung), chronic constriction
CC injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene
CC therapy). The sequence presented is a rat protein (described in Table 3
CC of the specification) which is differentially expressed during pain.
CC Note: The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic form directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 641 AA;
Query Match 82.7%; Score 1087; DB 7; Length 641;
Best Local Similarity 83.5%; Pred. No. 7.7e-82;
Matches 218; Conservative 17; Mismatches 18; Indels 8; Gaps 3;
QY 1 KSENVQDLLLLDVAPLSLGLTAGGVTALIKRNSTIPTKQIQTFTTSDNPGVLIQY 60
DB 386 KSEKVDLLLLDVAPLSLGLTAGGVTALIKRNSTIPTKQIQTFTTSDNPGVLIQY 445
QY 61 EGERAMTKDNLGRFELSGIPAPRGVQIETVFDIDANGILNVTATDKSTGKANKITI 120
DB 446 EGERAMTRDNLGRFDLTGIPAPRGVQIETVFDIDANGILNVTATDKSTGKANKITI 505
QY 121 TNDKGRLSKEEIERMVQEAERYKAEDVQERVSAAKNALESYAFNMKSASVDEGLKDKIS 180
DB 506 TNDKGRLSKEEIERMVQEAERYKAEDVQERVSAAKNALESYAFNMKSASVDEGLKDKIS 565
QY 181 EADKKVLDKQCVISWLDANTLAEKDFEHRKELEQVCNPIISGLYQ-GAGGP--GPG 237
DB 566 ESDKKKILDKCEVLSWLEAQAEKDFHKKRKELENMNCNPIITKLYQSGCTGPTCAPG 625
QY 238 GFCAQGPKGSGSGPTIEVD 258
DB 626 -----YTPGARITGPTIEVD 641
RESULT 80
ADD48287
ID ADD48287 standard; protein; 641 AA.
XX
AC ADD48287;
XX
XX 02-DEC-2004 (revised)
DT 29-JAN-2004 (first entry)
XX
XX Rat Protein P55063, SEQ ID NO 13985.
DE
XX Rat; pain; neuronal tissue; gene therapy; spinal segmental nerve injury;
XX chronic constriction injury; CCI; spared nerve injury; SNI; Chung.
XX
XX Rattus norvegicus.
OS
OS Unidentified.
XX
XX WO2003016475-A2.
XX
XX 27-FEB-2003.
XX
XX 14-AUG-2002; 2002WO-US025765.
XX
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XX 14-AUG-2001; 2001US-0312147P.
PR 01-NOV-2001; 2001US-0346382P.
PR 26-NOV-2001; 2001US-0333347P.
XX (GEO) GEN HOSPITAL CORP.
PA (FARB) BAYER AG.
XX Woolf C, D'urso D, Befort K, Costigan M;
XX WPI; 2003-268312/26.
DR GENBANK; P55063.
XX New composition comprising two or more isolated polypeptides, useful for
PT preparing a medicament for treating pain in an animal.
XX Example 1; Page; 1017pp; English.
XX The invention discloses a composition comprising two or more isolated rat
CC or human polynucleotides or a polynucleotide which represents a fragment,
CC derivative or allelic variation of the nucleic acid sequence. Also
CC claimed are a vector comprising the novel polynucleotide, a host cell
CC comprising the vector, a method for identifying a nucleotide sequence
CC which is differentially regulated in an animal subjected to pain and a
CC kit to perform the method, an array, a method for identifying an agent
CC that increases or decreases the expression of the polynucleotide sequence
CC subjected to pain, a method for identifying a compound which regulates
CC the expression of a polynucleotide sequence which is differentially
CC expressed in an animal subjected to pain, a method for identifying a
CC compound that regulates the activity of one or more of the
CC polynucleotides, a method for producing a pharmaceutical composition, a
CC method for identifying a compound or small molecule that regulates the
CC activity in an animal of one or more of the polypeptides given in the
CC specification, a method for identifying a compound useful in treating
CC pain and a pharmaceutical composition comprising the one or more
CC polypeptides or their antibodies. The polynucleotide or the compound that
CC modulates its activity is useful for preparing a medicament for treating
CC pain (e.g. spinal segmental nerve injury (SNI)) in an animal (e.g. gene
CC injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene
CC therapy). The sequence presented is a rat protein (described in Table 3
CC of the specification) which is differentially expressed during pain.
CC Note: The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic form directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences.
XX Sequence 641 AA;
SQ
Query Match 82.7%; Score 1087; DB 7; Length 641;
Best Local Similarity 83.5%; Pred. No. 7.7e-82;
Matches 218; Conservative 17; Mismatches 18; Indels 8; Gaps 3;
QY 1 KSENVODLLLDVAPLSGLTAGGVTALIKRNSTIPTKQTOIFTYSDNPGVLIQVY 60
DB 386 KSEKVDLLLDVAPLSGLTAGGVTALIKRNSTIPTKQTOIFTYSDNPGVLIQVY 445
QY 61 EGERAMTKDNLLGRFELSGIPAPRGVQIEVTFDIDANGILNVTATDKSTGKANKITI 120
DB 446 EGERAMTRDNNLLGRFDLGIAPAPRGVQIEVTFDIDANGILNVTAMDKSTGKANKITI 505
QY 121 TNDKGLSKKEEIERMVOEAKYKAEDVQERVSARNALESYAFNMKSVADEGLGKGIS 180
DB 506 TNDKGLSKKEEIERMVOEAKYKAEDVQERVSARNALESYAFNMKSVADEGLGKGIS 565
QY 181 EADKKVLDKCOEIVSWLDANTLAEDREHKELEQVNCNPIISGLYQ-GAGGP--GPG 237
DB 566 ESDKKKILDKCSVLNLEQVLAEDREHKELEQVNCNPIISGLYQ-GAGGP--GPG 625
QY 238 GFCAQPGKSGSGPTIEVD 258
DB 626 -----YTPGRARTGPTIEVD 641

RESULT 81
ADD45650
ID ADD45650 standard; protein; 641 AA.
XX ADD45650;
AC ADD45650;
XX 29-JAN-2004 (first entry)
DT Rat Protein CAA54424, SEQ ID NO 11317.
XX Rat; pain; neuronal tissue; gene therapy; spinal segmental nerve injury;
XX Chronic constriction injury; CCI; spared nerve injury; SNI; Chung.
OS Rattus norvegicus.
XX WO2003016475-A2.
XX 27-FEB-2003.
PD 14-AUG-2002; 2002WO-US025765.
XX 14-AUG-2001; 2001US-0312147P.
PR 01-NOV-2001; 2001US-0346382P.
PR 26-NOV-2001; 2001US-0333347P.
XX (GEO) GEN HOSPITAL CORP.
PA (FARB) BAYER AG.
XX Woolf C, D'urso D, Befort K, Costigan M;
XX WPI; 2003-268312/26.
DR GENBANK; CAA54424.
XX New composition comprising two or more isolated polypeptides, useful for
PT preparing a medicament for treating pain in an animal.
XX Claim 1; Page; 1017pp; English.
XX The invention discloses a composition comprising two or more isolated rat
CC or human polynucleotides or a polynucleotide which represents a fragment,
CC derivative or allelic variation of the nucleic acid sequence. Also
CC claimed are a vector comprising the novel polynucleotide, a host cell
CC comprising the vector, a method for identifying a nucleotide sequence
CC which is differentially regulated in an animal subjected to pain and a
CC kit to perform the method, an array, a method for identifying an agent
CC that increases or decreases the expression of the polynucleotide sequence
CC that is differentially expressed in neuronal tissue of a first animal
CC subjected to pain, a method for identifying a compound which regulates
CC the expression of a polynucleotide sequence which is differentially
CC expressed in an animal subjected to pain, a method for identifying a
CC compound that regulates the activity of one or more of the
CC polynucleotides, a method for producing a pharmaceutical composition, a
CC method for identifying a compound or small molecule that regulates the
CC activity in an animal of one or more of the polypeptides given in the
CC specification, a method for identifying a compound useful in treating
CC pain and a pharmaceutical composition comprising the one or more
CC polypeptides or their antibodies. The polynucleotide or the compound that
CC modulates its activity is useful for preparing a medicament for treating
CC pain (e.g. spinal segmental nerve injury (SNI)) in an animal (e.g. gene
CC injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene
CC therapy). The sequence presented is a rat protein (described in Table 3
CC of the specification) which is differentially expressed during pain.
CC Note: The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic form directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences.
XX Sequence 641 AA;
SQ
Query Match 82.7%; Score 1087; DB 7; Length 641;
Best Local Similarity 83.5%; Pred. No. 7.7e-82;
Matches 218; Conservative 17; Mismatches 18; Indels 8; Gaps 3;
QY 1 KSENVODLLLDVAPLSGLTAGGVTALIKRNSTIPTKQTOIFTYSDNPGVLIQVY 60
DB 386 KSEKVDLLLDVAPLSGLTAGGVTALIKRNSTIPTKQTOIFTYSDNPGVLIQVY 445
QY 61 EGERAMTKDNLLGRFELSGIPAPRGVQIEVTFDIDANGILNVTATDKSTGKANKITI 120
DB 446 EGERAMTRDNNLLGRFDLGIAPAPRGVQIEVTFDIDANGILNVTAMDKSTGKANKITI 505
QY 121 TNDKGLSKKEEIERMVOEAKYKAEDVQERVSARNALESYAFNMKSVADEGLGKGIS 180
DB 506 TNDKGLSKKEEIERMVOEAKYKAEDVQERVSARNALESYAFNMKSVADEGLGKGIS 565
QY 181 EADKKVLDKCOEIVSWLDANTLAEDREHKELEQVNCNPIISGLYQ-GAGGP--GPG 237
DB 566 ESDKKKILDKCSVLNLEQVLAEDREHKELEQVNCNPIISGLYQ-GAGGP--GPG 625
QY 238 GFCAQPGKSGSGPTIEVD 258
DB 626 -----YTPGRARTGPTIEVD 641

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Db 386 KSEKVDLLLDVAPLSGLTAGVMTVLKRNSTPTKQTFITYSDNQPGLVLIQVY 445
QY 61 EGERAMTKDNLLGRFELSGIPAPRGVPOIEVTFDIDANGILNVATATDKSTGKANKITI 120
Db 446 EGERAMTRDNLLGRFELSGIPAPRGVPOIEVTFDIDANGILNVATATDKSTGKANKITI 505
QY 121 TNDKGRLSKEETERMVQEAKEYKAEDVORERSVAKNALESYAFNMKSAAVEDEGLKGIS 180
Db 506 TNDKGRLSKEETERMVQEAKEYKAEDVORERSVAKNALESYAFNMKSAAVEDEGLKGIS 565
QY 181 EADKKVLDKCOEIVSWLDANTLAERKDEFEHKKRKELEQVNCNPIISGLYQAGG-PG 237
Db 566 ESDKKILDKCEVLSWLEANQAEKEEFHKKRKELENCNPIITKLYQSGCTGPTCAPG 625
QY 238 GFQAQPKGSGSGPTIEEVD 258
Db 626 -----YTPGRARTGPTIEEVD 641

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RESULT 82
 AAR03927
 ID AAR03927 standard; protein; 646 AA.
 AC AAR03927;
 XX
 XX 27-AUG-2003 (revised)
 DT 30-AUG-1990 (first entry)
 XX
 XX Rat HSP (rathsp70).
 XX
 XX Hsp70; heat shock protein; Trypanosoma cruzi; vaccines; HSP.
 XX
 XX Rattus rattus.
 OS
 XX
 XX WO9002564-A.
 PN
 XX
 PD 22-MAR-1990.
 XX
 XX 12-SEP-1988; 88US-00243474.
 PF
 XX 12-SEP-1988; 88US-00243474.
 PR
 XX
 XX (CODON).
 PA
 XX Dragon E, Faulds D, Sias S;
 PI
 XX WPI; 1990-115820/15.
 DR
 XX
 XX Proteins homologous to heat shock proteins of Trypanosoma cruzi - used in
 PT vaccines and diagnosis for species of e.g. muco-plasma or mycobacteria.
 XX
 XX Disclosure; Fig 2.1-2.14; 86pp; English.

Fig. 2 provides an alignment of heat shock proteins from a variety of
 organisms: 1. M. hyopneumoniae (Mhyhep70 - AAR03922); 2. Bacillus
 megaterium (Emehsp70 - AAR03923); 3. E. coli (dnaK - AAR03924); 4. T.
 cruzi (tc70kd - AAR03925); 5. T. cruzi (AAR03926); 6. Rat rattus
 (rathsp70 - AAR03927); 7. Xenopus laevis (xl170 - AAR03928); 8. Homo
 sapiens (huhsp70 - AAR03929); 9. Gallus gallus (chkhsp70 - AAR03930);
 10. Zea mays (mzehep70 - AAR03931); 11. Serratia marcescens (smahsp70 -
 AAR03932). The proteins having homology to hsp's of T. cruzi can be used
 in vaccines and diagnosis involving e.g. Trypanosoma, Mycoplasma and
 Mycobacteria species. (Updated on 27-AUG-2003 to correct OS field.)

XX Sequence 646 AA;
 Query Match 82.5%; Score 1084.5; DB 2; Length 646;
 Best Local Similarity 81.0%; Pred. No. 1.3e-81;
 Matches 213; Conservative 22; Mismatches 22; Indels 5; Gaps 3;

QY 1 KSENVQDLLLDVAPLSGLTAGVMTVLKRNSTPTKQTFITYSDNQPGLVLIQVY 60

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Db 384 KSENVQDLLLDVAPLSGLTAGVMTVLKRNSTPTKQTFITYSDNQPGLVLIQVY 443
QY 61 EGERAMTKDNLLGRFELSGIPAPRGVPOIEVTFDIDANGILNVATATDKSTGKANKITI 120
Db 444 EGERAMTKDNLLGRFELSGIPAPRGVPOIEVTFDIDANGILNVATATDKSTGKANKITI 503
QY 121 TNDKGRLSKEETERMVQEAKEYKAEDVORERSVAKNALESYAFNMKSAAVEDEGLKGIS 180
Db 504 TNDKGRLSKEETERMVQEAKEYKAEDVORERSVAKNALESYAFNMKSAAVEDEGLKGIS 563
QY 181 EADKKVLDKCOEIVSWLDANTLAERKDEFEHKKRKELEQVNCNPIISGLYQAGG-PG 237
Db 564 ESDKKILDKCEVLSWLEANQAEKEEFHKKRKELENCNPIITKLYQSGCTGPTCAPG 623
QY 238 GFQAQPKGSGSGPTIEEVD 258
Db 624 GFPGGAPPGSGSGPTIEEVD 646

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RESULT 83
 ADM05931
 ID ADM05931 standard; protein; 413 AA.
 AC ADM05931;
 XX
 XX 20-MAY-2004 (first entry)
 DT
 XX Human protein of the invention SEQ ID NO:4616.
 DE
 XX human; gene therapy; diagnostic marker; pharmaceutical.
 XX
 XX Homo sapiens.
 OS
 XX EP1347046-A1.
 PN
 XX 24-SEP-2003.
 PD
 XX 12-APR-2002; 2002EP-00008400.
 PF
 XX 22-MAR-2002; 2002JP-00137785.
 PR
 XX (REAS-) RES ASSOC BIOTECHNOLOGY.
 PA
 XX Isogai T, Sugiyama T, Otsuki T, Wakamatsu A, Sato H, Ishii S;
 PI Yamamoto J, Isono Y, Hio Y, Otsuka K, Nagai K, Irie R, Tameschika I;
 PI Seki N, Yoshikawa T, Otsuka M, Nagahari K, Masuho Y;
 XX WPI; 2003-723558/69.
 DR N-PSDB; ADM03488.
 DR
 XX New polynucleotides and polypeptides are useful in gene therapy, for
 PT developing a diagnostic marker or medicines for regulating their
 PT expression and activity, or as a target of gene therapy.
 XX
 XX Claim 1; SEQ ID NO 4616; 305pp; English.

The invention relates to a novel human polynucleotide and the encoded
 polypeptide. A polynucleotide of the invention may have a use in gene
 therapy. An oligonucleotide of the invention ADM06202-ADM06773 is useful
 as a primer for synthesizing the polynucleotide or as a probe for
 detecting the polynucleotide. The polynucleotides ADM01316-ADM03758 are
 useful in gene therapy, for developing a diagnostic marker or medicines
 for regulating their expression and activity, or as a target of gene
 therapy. The proteins ADM03759-ADM06201 encoded by the polynucleotides
 are useful as pharmaceutical agents. The present sequence represents a
 protein sequence of the invention.

XX Sequence 413 AA;
 Query Match 80.6%; Score 1059.5; DB 7; Length 413;
 Best Local Similarity 79.1%; Pred. No. 8.6e-80;
 Matches 204; Conservative 24; Mismatches 25; Indels 5; Gaps 1;

QY 1 KSENVODLLLDVAPLSGLGLETAGGVTALIKNSTIPTKQTOIFTTYSNQPGVLIQVY 60
 DB 161 KSENVODLLLDVAPLSGLGLETAGGVTPLIKRNTIPTKQTOIFTTYSNQSSVLQVY 220
 QY 61 EGERAMTKDNLLGRFELSGIPAPRGVPQIEVTFDIDANGILNVTATDKSTGKANKITI 120
 DB 221 EGERAMTKDNLLGRFELSGIPAPRGVPQIEVTFDIDANGILNVTAAADKSTGKANKITI 280
 QY 121 TNDKGRSLKEEIERMVQAEKRYKAEDVQREVSNAKNALESYAFNMKSAVEDGLGKGIS 180
 DB 281 TNDKGRSLKDDIDRMVQAEKRYKSEDEANRDRVAANKNALESYTYNIKQTVDEDEKLKGIS 340
 QY 181 EADKKVLDKQCVISWLDANTLAEDKDFEHHKKELEQVNCNPIISGLYQAGGPGPGGFG 240
 DB 341 EQDKNKILDKQCVINWLDNRQMAEKDEYEHKQKELERVCNPIISKLYQGGPGGGGGGG 400
 QY 241 AQPGKGGSGGPTIEVD 258
 DB 401 S-----GASGGPTIEVD 413

RESULT 84
 ADE63493
 ID ADE63493 standard; protein; 639 AA.
 XX
 AC ADE63493;
 XX
 DT 29-JAN-2004 (first entry)
 XX
 DE Human Protein P54652, SEQ ID NO 9437.
 XX
 KW Human; pain; neuronal tissue; gene therapy;
 KW spinal segmental nerve injury; chronic constriction injury; CCI;
 KW spared nerve injury; SNI; Chung.
 XX
 OS Homo sapiens.
 XX
 PN WO2003016475-A2.
 XX
 PD 27-FEB-2003.
 XX
 PF 14-AUG-2002; 2002WO-US025765.
 XX
 PR 14-AUG-2001; 2001US-0312147P.
 PR 01-NOV-2001; 2001US-0346382P.
 PR 26-NOV-2001; 2001US-0333347P.
 XX
 PA (GEHO) GEN HOSPITAL CORP.
 PA (FARB) BAYER AG.
 XX
 PI Woolf C, D'urso D, Belfort K, Costigan M;
 XX
 DR WPI; 2003-268312/26.
 DR GENBANK; P54652.
 XX
 PT New composition comprising two or more isolated polypeptides, useful for
 PT preparing a medicament for treating pain in an animal.
 XX
 PS Claim 1; Page; 1017pp; English.
 XX

The invention discloses a composition comprising two or more isolated rat
 CC or human polynucleotides or a polynucleotide which represents a fragment,
 CC derivative or allelic variation of the nucleic acid sequence. Also
 CC claimed are a vector comprising the novel polynucleotide, a host cell
 CC comprising the vector, a method for identifying a nucleotide sequence
 CC which is differentially regulated in an animal subjected to pain and a
 CC kit to perform the method, an array, a method for identifying an agent
 CC that increases or decreases the expression of the polynucleotide sequence
 CC that is differentially expressed in neuronal tissue of a first animal
 CC subjected to pain, a method for identifying a compound which regulates
 CC the expression of a polynucleotide sequence which is differentially
 CC expressed in an animal subjected to pain, a method for identifying a
 CC compound that regulates the activity of one or more of the

CC polynucleotides, a method for producing a pharmaceutical composition, a
 CC method for identifying a compound or small molecule that regulates the
 CC activity in an animal of one or more of the polypeptides given in the
 CC specification, a method for identifying a compound useful in treating
 CC pain and a pharmaceutical composition comprising the one or more
 CC polypeptides or their antibodies. The polynucleotide or the compound that
 CC modulates its activity is useful for preparing a medicament for treating
 CC pain (e.g. spinal segmental nerve injury (Chung), chronic constriction
 CC injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene
 CC therapy). The sequence presented is a human protein (shown in Table 2 of
 CC the specification) which is differentially expressed during pain. Note:
 CC The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic form directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences.

XX Sequence 639 AA;

Query Match 80.6%; Score 1059.5; DB 7; Length 639;
 Best Local Similarity 79.1%; Pred. No. 1.5e-79;
 Matches 204; Conservative 24; Mismatches 25; Indels 5; Gaps 1;

QY 1 KSENVODLLLDVAPLSGLGLETAGGVTALIKNSTIPTKQTOIFTTYSNQPGVLIQVY 60
 DB 387 KSENVODLLLDVAPLSGLGLETAGGVTPLIKRNTIPTKQTOIFTTYSNQSSVLQVY 446
 QY 61 EGERAMTKDNLLGRFELSGIPAPRGVPQIEVTFDIDANGILNVTATDKSTGKANKITI 120
 DB 447 EGERAMTKDNLLGRFELSGIPAPRGVPQIEVTFDIDANGILNVTAAADKSTGKANKITI 506
 QY 121 TNDKGRSLKEEIERMVQAEKRYKAEDVQREVSNAKNALESYAFNMKSAVEDGLGKGIS 180
 DB 507 TNDKGRSLKDDIDRMVQAEKRYKSEDEANRDRVAANKNALESYTYNIKQTVDEDEKLKGIS 566
 QY 181 EADKKVLDKQCVISWLDANTLAEDKDFEHHKKELEQVNCNPIISGLYQAGGPGPGGFG 240
 DB 567 EQDKNKILDKQCVINWLDNRQMAEKDEYEHKQKELERVCNPIISKLYQGGPGGGGGGG 626
 QY 241 AQPGKGGSGGPTIEVD 258
 DB 627 S-----GASGGPTIEVD 639

RESULT 85

ADJ69917

ID ADJ69917 standard; protein; 639 AA.

XX

AC ADJ69917;

XX

DT 06-MAY-2004 (first entry)

XX

DE Human heat mitochondrial protein as a therapeutic target SeqID1723.

XX

KW mitochondrial; human; screening assay; diabetes mellitus;

KW Huntington's disease; osteoarthritis;

KW Leber's hereditary optic neuropathy; LHON;

KW mitochondrial encephalopathy lactic acidosis and stroke; MELAS;

KW myoclonic epilepsy ragged red fibre syndrome; MERRF; cancer;

KW neuroprotective; nootropic; antidiabetic; anticonvulsant; antiarthritic;

KW osteopathic; ophthalmological; cytostatic.

XX

OS Homo sapiens.

XX

PN WO2003087768-A2.

XX

PD 23-OCT-2003.

XX

PF 04-APR-2003; 2003WO-US010870.

XX

PR 12-APR-2002; 2002US-0372843P.

XX

PR 17-JUN-2002; 2002US-0389987P.

XX

PR 20-SEP-2002; 2002US-0412418P.

XX

PA (MITO-) MITOKOR.

PA (BUCK-) BUCK INST AGE RES.
 XX Ghosh SS, Fahy ED, Zhang B, Gibson BW, Taylor SW, Glenn GM;
 PI Warnock DE;
 XX WPI; 2003-845369/78.
 XX Identifying a mitochondrial target for drug screening assays and for
 PT treating diseases associated with altered mitochondrial function,
 PT comprises detecting a modified polypeptide in a sample and correlating
 PT with the disease.
 XX Claim 1; SEQ ID NO 1723; 180pp; English.
 XX This invention relates to novel mitochondrial targets that can be used
 CC for therapeutic intervention in treating a disease associated with
 CC altered mitochondrial function. Specifically, it refers to a method for
 CC identifying proteins of the human heart mitochondrial proteome that are
 CC useful for drug screening assays, as well as therapeutic targets. The
 CC present invention describes a method for identifying such proteins that
 CC can be used in the treatment of various diseases associated with altered
 CC mitochondrial function including diabetes mellitus, Huntington's disease,
 CC osteoarthritis, Leber's hereditary optic neuropathy (LHON), mitochondrial
 CC encephalopathy lactic acidosis and stroke (MELAS), myoclonic epilepsy
 CC ragged red fibre syndrome (MERRF) or cancer. Accordingly, these
 CC compositions have neuroprotective, nootropic, antidiabetic,
 CC anticonvulsant, antiarthritic, osteopathic, ophthalmological and
 CC cytotatic activities. This polypeptide sequence is a human heart
 CC mitochondrial protein of the invention.
 XX SQ Sequence 639 AA;
 Query Match 80.6%; Score 1059.5; DB 7; Length 639;
 Best Local Similarity 79.1%; Pred. No. 1.5e-79;
 Matches 204; Conservative 24; Mismatches 25; Indels 5; Gaps 1;
 QY 1 KSENVQDLLLDVAPLSLGLTAGGVMTALIKRNSTPTKQTQIFFTYSDNQPGVLIQVY 60
 DB 387 KSENVQDLLLDVTPLSLGLTAGGVMTPLIKNTTPTKQTFTTYSNQSSVLVQVY 446
 QY 61 EGERAMTKNNLLGRFELSIPAPRGVQIETVTFDIDANGILNVTATDKSTGKANKITI 120
 DB 447 EGERAMTKNNLLGKFDLTGIPAPRGVQIETVTFDIDANGILNVTADKSTGKANKITI 506
 QY 121 TNDKGRLSKEEIERMWQEAERYKAEDVQERVSAAKNALSVAFNPKMSAVEDEGLGKGIS 180
 DB 507 TNDKGRLSKDDIDRMVQEAERYKSEDEANDRVAANKNALESYTYNIQTVEDEKLKGIS 566
 QY 181 EADKKVLDKQCEVISWLDANTLAKEDEFEHKKKELEQVNCNPIISGLYQAGGPGGPGF 240
 DB 567 EQDKNKILDKQCEVINWLDNRQMAEKDEYEHKQKELERVNCNPIISKLYQGGPGGGGGG 626
 QY 241 AQPGKGGSGSGPTIEVD 258
 DB 627 S-----GASGGPTIEVD 639
 RESULT 86
 ADJ69887
 ID ADJ69887 standard; protein; 639 AA.
 XX
 XX ADJ69887;
 AC
 AC
 DT 06-MAY-2004 (first entry)
 XX
 XX Human heat mitochondrial protein as a therapeutic target SeqID1693.
 DE
 DE
 KW mitochondrial; human; screening assay; diabetes mellitus;
 KW Huntington's disease; osteoarthritis;
 KW Leber's hereditary optic neuropathy; LHON;
 KW mitochondrial encephalopathy lactic acidosis and stroke; MELAS;
 KW myoclonic epilepsy ragged red fibre syndrome; MERRF; cancer;
 KW neuroprotective; nootropic; antidiabetic; anticonvulsant; antiarthritic;

KW osteopathic; ophthalmological; cytostatic.
 XX Homo sapiens.
 XX WO2003087768-A2.
 XX 23-OCT-2003.
 XX 04-APR-2003; 2003WO-US010870.
 XX 12-APR-2002; 2002US-0372843P.
 XX 17-JUN-2002; 2002US-0389987P.
 XX 20-SEP-2002; 2002US-0412418P.
 XX (MITO-) MITOKOR.
 XX (BUCK-) BUCK INST AGE RES.
 XX Ghosh SS, Fahy ED, Zhang B, Gibson BW, Taylor SW, Glenn GM;
 PI Warnock DE;
 XX WPI; 2003-845369/78.
 XX Identifying a mitochondrial target for drug screening assays and for
 PT treating diseases associated with altered mitochondrial function,
 PT comprises detecting a modified polypeptide in a sample and correlating
 PT with the disease.
 XX Claim 1; SEQ ID NO 1693; 180pp; English.
 XX This invention relates to novel mitochondrial targets that can be used
 CC for therapeutic intervention in treating a disease associated with
 CC altered mitochondrial function. Specifically, it refers to a method for
 CC identifying proteins of the human heart mitochondrial proteome that are
 CC useful for drug screening assays, as well as therapeutic targets. The
 CC present invention describes a method for identifying such proteins that
 CC can be used in the treatment of various diseases associated with altered
 CC mitochondrial function including diabetes mellitus, Huntington's disease,
 CC osteoarthritis, Leber's hereditary optic neuropathy (LHON), mitochondrial
 CC encephalopathy lactic acidosis and stroke (MELAS), myoclonic epilepsy
 CC ragged red fibre syndrome (MERRF) or cancer. Accordingly, these
 CC compositions have neuroprotective, nootropic, antidiabetic,
 CC anticonvulsant, antiarthritic, osteopathic, ophthalmological and
 CC cytotatic activities. This polypeptide sequence is a human heart
 CC mitochondrial protein of the invention.
 XX SQ Sequence 639 AA;
 Query Match 80.6%; Score 1059.5; DB 7; Length 639;
 Best Local Similarity 79.1%; Pred. No. 1.5e-79;
 Matches 204; Conservative 24; Mismatches 25; Indels 5; Gaps 1;
 QY 1 KSENVQDLLLDVAPLSLGLTAGGVMTALIKRNSTPTKQTQIFFTYSDNQPGVLIQVY 60
 DB 387 KSENVQDLLLDVTPLSLGLTAGGVMTPLIKNTTPTKQTFTTYSNQSSVLVQVY 446
 QY 61 EGERAMTKNNLLGRFELSIPAPRGVQIETVTFDIDANGILNVTATDKSTGKANKITI 120
 DB 447 EGERAMTKNNLLGKFDLTGIPAPRGVQIETVTFDIDANGILNVTADKSTGKANKITI 506
 QY 121 TNDKGRLSKEEIERMWQEAERYKAEDVQERVSAAKNALSVAFNPKMSAVEDEGLGKGIS 180
 DB 507 TNDKGRLSKDDIDRMVQEAERYKSEDEANDRVAANKNALESYTYNIQTVEDEKLKGIS 566
 QY 181 EADKKVLDKQCEVISWLDANTLAKEDEFEHKKKELEQVNCNPIISGLYQAGGPGGPGF 240
 DB 567 EQDKNKILDKQCEVINWLDNRQMAEKDEYEHKQKELERVNCNPIISKLYQGGPGGGGGG 626
 QY 241 AQPGKGGSGSGPTIEVD 258
 DB 627 S-----GASGGPTIEVD 639
 RESULT 87

ADN04525
 ID ADN04525 standard; protein; 639 AA.
 AC ADN04525;
 XX
 DT 01-JUL-2004 (first entry)
 XX
 DE Antipsoriatic protein sequence #455.
 XX
 KW antipsoriatic; gene therapy; psoriasis; diagnosis.
 XX
 OS Homo sapiens.
 XX
 PN WO2004028479-A2.
 XX
 PD 08-APR-2004.
 XX
 PF 25-SEP-2003; 2003WO-US030907.
 XX
 PR 25-SEP-2002; 2002US-0414006P.
 XX
 PA (GETH) GENENTECH INC.
 XX
 PI Bodary S, Clark H, Jackman J, Schoenfeld J, Williams PM, Wood W;
 PI Wu TD;
 XX
 DR WPI; 2004-305105/28.
 DR N-PSDB; ADN04524.
 XX
 PT New PRO nucleic acid or polypeptide, useful for preparing a
 PT pharmaceutical composition for diagnosing or treating psoriasis in a
 PT mammal.
 XX
 PS Claim 9; SEQ ID NO 919; 3069pp; English.
 XX
 CC The invention relates to novel polynucleotide and polypeptides for
 CC treating psoriasis or a sequence having at least 80% identity to the
 CC above sequences. The nucleic acid is useful for preparing a composition
 CC for diagnosing or treating psoriasis in a mammal. This sequence
 CC corresponds to one of the polypeptides of the invention.
 XX
 SQ Sequence 639 AA;

Query Match 80.6%; Score 1059.5; DB 8; Length 639;
 Best Local Similarity 79.1%; Pred. No. 1.5e-79;
 Matches 204; Conservative 24; Mismatches 25; Indels 5; Gaps 1;

QY 1 KSENVQDLILLDVAPLSGLGLETAGGVTALIKRNTIPTKQTQIFTTYSNQSGVLIOVY 60
 DB 387 KSENVQDLILLDVTPLSGLGLETAGGVTPLIKRNTIPTKQTQIFTTYSNQSGVLIOVY 446
 QY 61 EGERAMTKNNLLGRFELSGIPAPRGVPOIEVTFDIDANGILNVTATDKSTGKANKITI 120
 DB 447 EGERAMTKNNLLGKFDLTGIPAPRGVPOIEVTFDIDANGILNVTADSTGKANKITI 506
 QY 121 TNDKGRLSKEIEIRMVQEAERYKAEDEVQRRVSAKNALESYAFNMKMSAVEDGLKGIS 180
 DB 507 TNDKGRLSKDDIDRMVQEAERYKSEDEANRDRVAANKNALESYTYNIQTVEDEKLRGKIS 566
 QY 181 EADKKVLDKQCVISWLDANTLAEKDEFEHKKKELEQVNCNPIISGLYQGAGPGPGGFG 240
 DB 567 EQDKNKILDKQCVINWLDNRQNAEKDEYEHKKKELEQVNCNPIISGLYQGAGPGPGGFG 626
 QY 241 AQGPKGGSGSGPTIEVD 258
 DB 627 S-----GASGGPTIEVD 639

RESULT 88
 AAR43002
 ID AAR43002 standard; protein; 633 AA.
 XX
 AC AAR43002;

XX
 DT 25-MAR-2003 (revised)
 XX
 DE 20-MAY-1994 (first entry)
 XX
 DE Mouse SLIP1 homologue HSC70B.
 XX
 KW Sulphoglycolipid immobilising protein 1; sperm plasma membrane;
 KW mouse homologue; HSC70B; mammalian; infertility; mycoplasma;
 KW anti-SLIP1 antibody.
 XX
 OS Mus musculus.
 XX
 PN WO9321954-A1.
 XX
 PD 11-NOV-1993.
 XX
 PF 22-APR-1993; 93WO-US0003816.
 XX
 PR 24-APR-1992; 92US-00873961.
 XX
 PA (BERL-) BERLEX LAB INC.
 PA (OTTA-) OTTAWA CIVIC HOSPITAL.
 XX
 PI Paulds DH, Lingwood CA, Tanphaichitr N;
 XX
 DR WPI; 1993-368422/46.
 XX
 CC Mammalian fertilisation decrease for detecting and treating infertility -
 CC using sulpho glyco lipid immobilising protein 1-sulphated-glyco moiety
 CC interfering compsn., for mycoplasma infection treatment.
 XX
 PS Claim 2; Page 60-62; 77pp; English.
 XX
 CC The likelihood of mammalian fertilisation is decreased by contacting a
 CC gamete with a sulphoglycolipid immobilising protein 1 (SLIP1)/ sulphated
 CC glyco-moiety interfering composition. The interfering compsn. is e.g.
 CC SLIP1 (or analogues such as the mouse SLIP1 analogue "HSC70B" comprising
 CC the amino acid sequence AAR43002). SLIP1 binds to
 CC sulphogalactosylglycerolipid (SGG), a testicular glycolipid, and to
 CC sulphogalactosyl ceramide. (Updated on 25-MAR-2003 to correct PN field.)
 XX
 SQ Sequence 633 AA;

Query Match 80.3%; Score 1054.5; DB 2; Length 633;
 Best Local Similarity 79.1%; Pred. No. 3.9e-79;
 Matches 204; Conservative 23; Mismatches 20; Indels 11; Gaps 2;

QY 1 KSENVQDLILLDVAPLSGLGLETAGGVTALIKRNTIPTKQTQIFTTYSNQSGVLIOVY 60
 DB 387 KSENVQDLILLDVTPLSGLGLETAGGVTPLIKRNTIPTKQTQIFTTYSNQSGVLIOVY 446
 QY 61 EGERAMTKNNLLGRFELSGIPAPRGVPOIEVTFDIDANGILNVTATDKSTGKANKITI 120
 DB 447 EGERAMTKNNLLGKFDLTGIPAPRGVPOIEVTFDIDANGILNVTADSTGKANKITI 506
 QY 121 TNDKGRLSKEIEIRMVQEAERYKAEDEVQRRVSAKNALESYAFNMKMSAVEDGLKGIS 180
 DB 507 TNDKGRLSKDDIDRMVQEAERYKSEDEANRDRVAANKNALESYTYNIQTVEDEKLRGKIS 566
 QY 181 EADKKVLDKQCVISWLDANTLAEKDEFEHKKKELEQVNCNPIISGLYQGAGPGPGGFG 240
 DB 567 EQDKNKILDKQCVINWLDNRQNAEKDEYEHKKKELEQVNCNPIISGLYQGAGPGPGGFG 620
 QY 241 AQGPKGGSGSGPTIEVD 258
 DB 621 -----GSSGGPTIEVD 633

RESULT 89
 ADE63491
 ID ADE63491 standard; protein; 633 AA.
 XX
 AC ADE63491;

QY 61 EGERAMTKDNNLLGRFELSGIPAPRGVPOIEVTFDIDANGILNVATDKSTGKANKITI 120
 DB 445 EGERAMTKDNNLLGRFELSGIPAPRGVPOIEVTFDIDANGILNVATDKSTGKANKITI 504
 QY 121 TNDKGRLSKEEIERMVOEAEKYKAEDVQREVRSYAKNALESYAFNMKSAVEDGLGKIS 180
 DB 505 TNDKGRLSKEDIKQVQAEKYKADDDAQERVDKNALESYAFNLKSMVEDENVKGKIS 564
 QY 181 EADKKVLDKQEVISWLDANTLAEDFEHKEKELEQVNCNPIISGLYQAGAGPG--PGG 238
 DB 565 DEDKRTISEKCTQVSWLENNQLAEKEEYAFQOKLEKVCQPIITKLYQG-GVPGGVPGG 623
 QY 239 P-----GAQPKGSGSGPTIEVD 258
 DB 624 MPGSSCGAQAQNGN-SGPTIEVD 647
 RESULT 91
 AAR03930
 ID AAR03930 standard; protein; 634 AA.
 XX
 AC AAR03930;
 DT 30-AUG-1990 (first entry)
 XX
 DE Gallus gallus HSP (chkhsp70).
 XX
 KW Hsp70; heat shock protein; Trypanosoma cruzi; vaccines; HSP.
 XX
 OS Gallus gallus.
 XX
 FH Key Location/Qualifiers
 FT Misc-difference 634
 FT /note= "residue given as "O" in specification"
 XX
 PN W09002564-A.
 XX
 PD 22-MAR-1990.
 XX
 PF 12-SEP-1988; 88US-00243474.
 XX
 PR 12-SEP-1988; 88US-00243474.
 XX
 PA (CODON-) CODON.
 XX
 PI Dragon E, Faulds D, Sias S;
 XX
 DR WPI; 1990-115820/15.
 XX
 PT Proteins homologous to heat shock proteins of Trypanosoma cruzi - used in
 PT vaccines and diagnosis for species of e.g. muco-plasma or mycobacteria.
 XX
 PS Disclosure; Fig 2.1-2.14; 86pp; English.
 XX
 CC According to the legend of Fig 2, the G. gallus HSP sequence has 635
 CC amino acid residues, the sequence itself has only 634, including "O" (?)
 CC at position 634. Fig. 2 provides an alignment of heat shock proteins from
 CC a variety of organisms: 1. M.hypopneumoniae (Mhysp70 - AAR03922); 2.
 CC Bacillus megaterium (Bmehsp70 - AAR03923); 3. E. coli (dnaK - AAR03924);
 CC 4. T. cruzi (tc70kd - AAR03925); 5. T. cruzi (AAR03926); 6. Rat rattus
 CC (rathsp70 - AAR03927); 7. Xenopus laevis (xl170 - AAR03928); 8. Homo
 CC sapiens (humhsp70 - AAR03929); 9. Gallus gallus (chkhsp70 - AAR03930);
 CC 10. Zea mays (mzehsp70 - AAR03931); 11. Serratia marcescens (smahsp70 -
 CC AAR03932). The proteins having homology to hsp's of T. cruzi can be used
 CC in vaccines and diagnosis involving e.g. Trypanosoma, Mycoplasma and
 CC Mycobacteria species
 XX
 SQ Sequence 634 AA;

Query Match 78.88; Score 1035.5; DB 2; Length 634;
 Best Local Similarity 79.58; Pred. No. 1.5e-77;
 Matches 205; Conservative 23; Mismatches 19; Indels 11; Gaps 3;

QY 1 KSENVQDLLLLDVAPISLGLETAGGVTALIKNSTIPTKQTOIFTTYSNQPGVLIQVY 60
 DB 387 KSENVQDLLLLDVAPISLGLETAGGVTALIKNSTIPTKQTOIFTTYSNQSSVLQVY 446
 QY 61 EGERAMTKDNNLLGRFELSGIPAPRGVPOIEVTFDIDANGILNVATDKSTGKANKITI 120
 DB 447 EGERAMTKDNNLLGRFELSGIPAPRGVPOIEVTFDIDANGILNVATDKSTGKANKITI 506
 QY 121 TNDKGRLSKEEIERMVOEAEKYKAEDVQREVRSYAKNALESYAFNMKSAVEDGLGKIS 180
 DB 507 TNDKGRLSKDDIDRMVQAEKYKAEDANRDRVCAKNLSLEYTYNMKQTVDEDEKLKGKIS 566
 QY 181 EADKKVLDKQEVISWLDANTLAEDFEHKEKELEQVNCNPIISGLYQAGAGPGGPG 240
 DB 567 DQDKQKVLQKQEVISWLDNRQNAEKEVEHKEKELEKCNPIVTVKLYQAGAGA-----G 620
 QY 241 AQGPKGSGSGPTIEVD 258
 DB 621 A-----GGSG-GPTIEVD 633
 RESULT 92
 ADN23580
 ID ADN23580 standard; protein; 640 AA.
 XX
 AC ADN23580;
 DT 02-DEC-2004 (first entry)
 XX
 DE Bacterial polypeptide #6233.
 XX
 KW Recombinant DNA construct; transformed plant; improved plant property;
 KW cold tolerance; heat tolerance; drought tolerance; herbicide; osmosis;
 KW pathogen tolerance; pest tolerance; plant disease resistance;
 KW cell cycle pathway modification; plant growth regulator;
 KW homologous recombination; seed oil yield; protein yield; carbohydrate;
 KW nitrogen; phosphorus; photosynthesis; lignin; galactomannan;
 KW bacterial polypeptide.
 XX
 OS Bacteria.
 XX
 PN US2003233675-A1.
 XX
 PD 18-DEC-2003.
 XX
 PF 20-FEB-2003; 2003US-00369493.
 XX
 PR 21-FEB-2002; 2002US-0360039P.
 XX
 PA (CAOY/) CAO Y.
 PA (HINK/) HINKLE G J.
 PA (SLAT/) SLATER S C.
 PA (CHEN/) CHEN X.
 PA (GOLD/) GOLDMAN B S.
 XX
 CC Cao Y, Hinkle GJ, Slater SC, Chen X, Goldman BS;
 CC WPI; 2004-061375/06.
 XX
 CC New recombinant DNA construct comprising a promoter positioned to provide
 CC for expression of a polynucleotide encoding a polypeptide from a
 CC microbial source, useful for producing plants with improved properties.
 XX
 PS Claim 1; SEQ ID NO 6233; 122pp; English.
 XX
 CC The invention relates to a recombinant DNA construct comprising a
 CC promoter functional in a plant cell, where the promoter is positioned to
 CC provide for expression of a polynucleotide encoding a polypeptide from a
 CC microbial source. The invention also relates to a transformed plant
 CC comprising the recombinant DNA construct and a method of producing a
 CC transformed plant having an improved property. The plant is a crop plant
 CC such as maize or soybean. The method of producing a transformed plant
 CC having an improved property comprises transforming a plant with the

CC recombinant DNA construct and growing the transformed plant, where the
 CC polynucleotide or polypeptide is useful for improving plant properties.
 CC The recombinant DNA construct is useful for producing plants with
 CC improved plant properties, e.g. improved cold, heat or drought tolerance,
 CC tolerance to herbicides, extreme osmotic conditions, pathogens or pests,
 CC increased resistance to plant disease, better growth rate by modification
 CC of the cell cycle pathway with plant growth regulators, increased rate of
 CC homologous recombination, modified seed oil or protein yield and/or
 CC content, improved yield by modification of carbohydrate, nitrogen or
 CC phosphorus use and/or uptake, by modification of photosynthesis or by
 CC providing improved plant growth and development under at least one stress
 CC condition. Improved lignin production or improved galactomannan
 CC production. This sequence represents a bacterial polypeptide used in the
 CC scope of the invention. Note: The sequence data for this patent did not
 CC form part of the printed specification but was obtained in electronic
 CC format from USPTO at seqdata.uspto.gov/sequence.html.

XX Sequence 640 AA;

Query Match 78.7%; Score 1034; DB 8; Length 640;
 Best Local Similarity 77.9%; Pred. No. 2e-77;
 Matches 201; Conservative 21; Mismatches 34; Indels 2; Gaps 1;
 QY 1 KSNVODLLLDVAPLSGLGTAGGVTALIKRNTPTKQTQFTTYSNDQPGVLIQVY 60
 DB 385 KSEAVQDLLLLDVAPLSGLGTAGGVTALIKRNTPTKQTQFTTYSNDQPGVLIQVY 444
 QY 61 EGERAMTKDNLLGRFELSGIPAPRGVQPIEVTFDIDANGILNVATDKSTGKANKITI 120
 DB 445 EGERAMTKDNLLGRFELSGIPAPRGVQPIEVTFDIDANGILNVATDKSTGKANKITI 504
 QY 121 TNDKGRLSKEEIERMVQEAQKAEDEVQREVRSNAKNALESYAFNMKSAVEDEGLKGLKIS 180
 DB 505 TNDKGRLSKDDIERMVNEAEKQKADDEAQRIGAKNGLSEYAFNLKQTIIDEKLDKIS 564
 QY 181 EADKKVLDKQCVISWLDANTLAEDKDEPHKKELEQVNCNPIISGLYQAGGPGG 240
 DB 565 PEDKKKIEDKCDRLKWLDSNQTAKEEFHQKLEGLANPIISKLYQAGGAPPG--A 622
 QY 241 ACPGKPGSGSGPTIEVD 258
 DB 623 ACPGAGGAGGPTIEVD 640

RESULT 94
 AAR03928
 ID AAR03928 standard; protein; 647 AA.

XX AAR03928;
 XX 30-AUG-1990 (first entry)
 XX Xenopus laevis HSP (xl70).
 XX Hsp70; heat shock protein; Trypanosoma cruzi; vaccines; HSP.
 XX Xenopus laevis.
 XX WO9002564-A.
 XX 22-MAR-1990.
 XX 12-SEP-1988; 88US-00243474.
 XX 12-SEP-1988; 88US-00243474.
 XX (CODON) CODON.
 XX Dragon E, Faulds D, Sias S;
 XX WPI; 1990-115820/15.
 XX Proteins homologous to heat shock proteins of Trypanosoma cruzi - used in

PT vaccines and diagnosis for species of e.g. muco-plasma or mycobacteria.
 XX Disclosure; Fig 2.1-2.14; 86pp; English.
 XX Fig. 2 provides an alignment of heat shock proteins from a variety of
 CC organisms: 1. M.hypneumonidae (Mhynsp70 - AAR03922); 2. Bacillus
 CC megaterium (Bmehsp70 - AAR03923); 3. E. coli (dnaK - AAR03924); 4. T.
 CC cruzi (tc70kd - AAR03925); 5. T. cruzi (AAR03926); 6. Rat rattus
 CC (rathsp70 - AAR03927); 7. Xenopus laevis (xl70 - AAR03928); 8. Homo
 CC sapiens (humhsp70 - AAR03929); 9. Gallus gallus (chkhsp70 - AAR03930);
 CC 10. Zea mays (mzhsp70 - AAR03931); 11. Serratia marcescens (smahsp70 -
 CC AAR03932). The proteins having homology to hsp's of T. cruzi can be used
 CC in vaccines and diagnosis involving e.g. Trypanosoma, Mycoplasma and
 CC Mycobacteria species
 XX Sequence 647 AA;

Query Match 78.5%; Score 1031.5; DB 2; Length 647;
 Best Local Similarity 78.1%; Pred. No. 3.3e-77;
 Matches 207; Conservative 26; Mismatches 23; Indels 9; Gaps 4;
 QY 1 KSNVODLLLDVAPLSGLGTAGGVTALIKRNTPTKQTQFTTYSNDQPGVLIQVY 60
 DB 385 KSNVODLLLDVAPLSGLGTAGGVTALIKRNTPTKQTQFTTYSNDQPGVLIQVY 444
 QY 61 EGERAMTKDNLLGRFELSGIPAPRGVQPIEVTFDIDANGILNVATDKSTGKANKITI 120
 DB 445 EGERAMTKDNLLGRFELSGIPAPRGVQPIEVTFDIDANGILNVATDKSTGKANKITI 504
 QY 121 TNDKGRLSKEEIERMVQEAQKAEDEVQREVRSNAKNALESYAFNMKSAVEDEGLKGLKIS 180
 DB 505 TNDKGRLSKDDIERMVNEAEKQKADDEAQRIGAKNGLSEYAFNLKQTIIDEKLDKIS 564
 QY 181 EADKKVLDKQCVISWLDANTLAEDKDEPHKKELEQVNCNPIISGLYQAGGPG--PGG 238
 DB 565 DEBKRTISKCTQVVISWLNQLAKEEYAFQKLEKVCQPIITKLYOG-GVPGGVPGG 623
 QY 239 F-----GAQPGKSGSGPTIEVD 258
 DB 624 MPGSSCGAQAQGGN-SGPTIEVD 647

RESULT 94
 ABB60514
 ID ABB60514 standard; protein; 651 AA.

XX ABB60514;
 XX 26-MAR-2002 (first entry)
 XX Drosophila melanogaster polypeptide SRQ ID NO 8334.
 XX Drosophila melanogaster polypeptide SRQ ID NO 8334.
 XX Drosophila; developmental biology; cell signalling; insecticide;
 XX pharmaceutical.
 XX Drosophila melanogaster.
 XX WO200171042-A2.
 XX 27-SEP-2001.
 XX 23-MAR-2001; 2001WO-US009231.
 XX 23-MAR-2000; 2000US-0191637P.
 XX 11-JUL-2000; 2000US-00614150.
 XX (PEKE) PE CORP NY.
 XX Venter JC, Adams M, Li PWD, Myers EW;
 XX WPI; 2001-656860/75.
 XX N-PSDB; ABL04617.

PT New isolated nucleic acid detection reagent for detecting 1000 or more
PT genes from Drosophila and for elucidating cell signaling and cell-cell
XX interactions.
XX
XX Disclosure; SEQ ID NO 8334; 21pp + Sequence Listing; English.
XX
XX The invention relates to an isolated nucleic acid detection reagent
CC capable of detecting 1000 or more genes from Drosophila. The invention is
CC useful in developmental biology and in elucidating cell signaling and
CC cell-cell interactions in higher eukaryotes for the development of
CC insecticides, therapeutics and pharmaceutical drugs. The invention
CC discloses genomic DNA sequences (AB116176-ABL30511), expressed DNA
CC sequences (AB101840-ABL16175) and the encoded proteins (ABB57737-
CC ABB72072). The sequence data for this patent did not form part of the
CC printed specification, but was obtained in electronic format directly
CC from WIPO at fip.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 651 AA;

Query Match 78.4%; Score 1030; DB 4; Length 651;
Best Local Similarity 74.3%; Pred. No. 4.5e-77;
Matches 199; Conservative 28; Mismatches 31; Indels 10; Gaps 2;

QY 1 KSENVODLLLDVAPLSGLGAGTGTALIKRNTSTPTKQTQFTTYSNQPGLVIOVY 60
DB 384 KQEVQDLLLLDVTPLSGLGAGTGTALIKRNTSTPTKQTQFTTYSNQPGLVIOVY 443

QY 61 EGERAMTKDNLLGRFELSGIPAPRGVPOIEVTFDIDANGILNVTATDKSTGKANKITI 120
DB 444 EGERAMTKDNLLGRFELSGIPAPRGVPOIEVTFDIDANGILNVTALERTSTNKENKITI 503

QY 121 TNDKGRLSKEEIERMVQAEKYKAEDVQERVSANNALESYAFNMKSAVEDGLKGIKIS 180
DB 504 TNDKGRLSKEDIERMVNEAEKYRNEDEKQETIAAKNGLESYCFNMKATLDEDNLTKIS 563

QY 181 EADKKVLDKQEVISWLDANTLAEDFEHKKKELEQVCNPIISGLYOGA-----G 232
DB 564 DSDRTTILDKCNETIKWLDANLADKEEYEHKQKELEGCVCNPIITKLYOGAGFPFGMPG 623

QY 233 GPG--PGGFGAQPCKGGSGGPTIEVD 258
DB 624 GPGMGGAAGAAGAAGAGGAGPTIEVD 651

RESULT 96
ADQ89618
ID ADQ89618 standard; protein; 651 AA.
AC ADQ89618;
XX
XX 21-OCT-2004 (first entry)
XX Antagonist of cell cycle progression polypeptide #24.
XX
XX Cytostatic; cancer; cell division cycle; mitosis; meiosis;
KW cell cycle progression.
XX
XX Drosophila melanogaster.
XX
XX WO2004063362-A2.
XX
XX 29-JUL-2004.
XX
XX 31-DEC-2003; 2003WO-GB005635.
XX
XX 10-JAN-2003; 2003US-0439123P.
PR 06-MAY-2003; 2003US-0468402P.
XX
XX (CYCL-) CYCLACEL LTD.
XX
XX Glover D, Bell G, Frenz L, Midgley C;
PI WPI; 2004-544089/52.
XX
XX

DR N-PSDB; ADQ89617.
XX
XX New cell cycle progression genes and proteins for modulating cell cycle
PT progression in cells, for preventing, treating or diagnosing cell
PT proliferative diseases (e.g. cancer) or for identifying modulators of
PT mitosis or meiosis.
XX
XX Claim 2; SEQ ID NO 48; 461pp; English.
XX
XX The present invention relates to a polynucleotide for preventing,
CC treating or diagnosing a disease in an individual. The composition or the
CC polypeptide, polynucleotide or RNA precursor, or antibody is useful for
CC diagnosing, preventing or treating diseases (e.g. cell proliferative
CC diseases such as cancer) in an individual. These may also be used for
CC identifying substances capable of binding to or modulating the function
CC of the polypeptide, capable of affecting the function of the
CC corresponding gene, or capable of inhibiting the cell division cycle or
CC cell cycle progression, preferably mitosis and/or meiosis. The present
CC sequence represents an antagonist of cell cycle progression protein
XX
SQ Sequence 651 AA;

Query Match 78.4%; Score 1030; DB 8; Length 651;
Best Local Similarity 74.3%; Pred. No. 4.5e-77;
Matches 199; Conservative 28; Mismatches 31; Indels 10; Gaps 2;

QY 1 KSENVODLLLDVAPLSGLGAGTGTALIKRNTSTPTKQTQFTTYSNQPGLVIOVY 60
DB 384 KQEVQDLLLLDVTPLSGLGAGTGTALIKRNTSTPTKQTQFTTYSNQPGLVIOVY 443

QY 61 EGERAMTKDNLLGRFELSGIPAPRGVPOIEVTFDIDANGILNVTATDKSTGKANKITI 120
DB 444 EGERAMTKDNLLGRFELSGIPAPRGVPOIEVTFDIDANGILNVTALERTSTNKENKITI 503

QY 121 TNDKGRLSKEEIERMVQAEKYKAEDVQERVSANNALESYAFNMKSAVEDGLKGIKIS 180
DB 504 TNDKGRLSKEDIERMVNEAEKYRNEDEKQETIAAKNGLESYCFNMKATLDEDNLTKIS 563

QY 181 EADKKVLDKQEVISWLDANTLAEDFEHKKKELEQVCNPIISGLYOGA-----G 232
DB 564 DSDRTTILDKCNETIKWLDANLADKEEYEHKQKELEGCVCNPIITKLYOGAGFPFGMPG 623

QY 233 GPG--PGGFGAQPCKGGSGGPTIEVD 258
DB 624 GPGMGGAAGAAGAAGAGGAGPTIEVD 651

RESULT 96
AAM48711
ID AAM48711 standard; protein; 643 AA.
AC AAM48711;
XX
XX 21-MAR-2002 (first entry)
XX Human schizophrenia/SCZ associated protein HSP70B SEQ ID NO 2.
XX
XX Human; chromosome 1q22; SCZ; schizophrenia; in utero screening;
KW gene therapy; heat shock protein 70B; HSP70B.
XX
XX Homo sapiens.
OS
XX WO200190412-A1.
XX
XX 29-NOV-2001.
PD
XX 23-APR-2001; 2001WO-US013086.
PF
XX 21-APR-2000; 2000US-0198900P.
PR
XX (RUTF) UNIV RUTGERS STATE NEW JERSEY.
XX
XX

PI Bzrustowicz LM, Bassett AS;
 XX WPI; 2002-083121/11.
 DR N-PSDB; ABA96361.
 DR
 XX
 PT Diagnosing susceptibility to schizophrenia comprises determining presence
 PT of allele of linked polymorphic marker on chromosome 1q22 and linked to
 PT variant form of SCZ gene associated with schizophrenia phenotype.
 XX
 XX Claim 20; Page 70; 83pp; English.
 XX
 XX The invention relates to diagnosing susceptibility to schizophrenia in a
 CC patient comprising determining the presence/absence of an allele of a
 CC polymorphic marker in the DNA of a patient, where the polymorphic marker
 CC is within the chromosome segment 1q22 bordered by DIS2705, DIS1679 and
 CC linked to the DNA segment SCZ having a variant form associated with
 CC phenotype of schizophrenia, where the allele is in phase with the variant
 CC form of SCZ and the presence of the allele indicates susceptibility to
 CC schizophrenia. The method can be used for in utero screening of fetuses
 CC for the presence of a variant SCZ allele. Identification of such
 CC variations offers the possibility of gene therapy and for couples known
 CC to be at risk of giving rise to an affected progeny, diagnosis can be
 CC combined with in vitro reproduction procedures to identify an embryo
 CC having wild-type SCZ alleles before implantation. Screening children
 CC shortly after birth allows administration of appropriate treatment at an
 CC early stage of detection. The genetic tests provide a highly accurate
 CC assay for diagnosing schizophrenia and schizophrenia susceptibility. The
 CC SCZ gene encodes a previously isolated sequence encoding human heat shock
 CC protein 70B (HSP70B, GenBank Accession Number NM002155)
 XX
 XX Sequence 643 AA;
 Query Match 77.0%; Score 1012; DB 5; Length 643;
 Best Local Similarity 74.4%; Pred. No. 1.4e-75;
 Matches 192; Conservative 33; Mismatches 33; Indels 0; Gaps 0;
 QY 1 KSENVQDLLLLDVAPLSLGLTAGGVTALIKRNSTPTKQTQFTTYSNDQPGVLIQVY 60
 DB 386 KCEKVQDLLLLDVAPLSLGLTAGGVTALIKRNSTPTKQTQFTTYSNDQPGVLIQVY 445
 QY 61 EGERAMTKDNLLGRFELSGIPAPRGVPOIETVFDANGILNVATDSTGKANKITI 120
 DB 446 EGERAMTKDNLLGRFELSGIPAPRGVPOIETVFDANGILNVATDSTGKANKITI 505
 QY 121 TNDKGRLSKEEIERMVOEAKYKAEDVQERVSAKNALYESAFNMKSAVEDGLKGIS 180
 DB 506 TNDKGRLSKEEVERMWEAEQYKAEDQAQDRVAKNLSLEAHVHVKGSLQESLRDKIP 565
 QY 181 EADKKVLDKQCEVISWLDANTLAEKDFEHRKKELEQVCNPIISGLYQAGGPGGFG 240
 DB 566 EEDRRKMQDKREVLAHNLAEKHEVEYHQKRELEQICRPFIIFSLYGGPGVPGGSSCG 625
 QY 241 AQPGKGGSGSGPTIEEVD 258
 DB 626 TQARQDGPSTGPTIEEVD 643
 RESULT 97
 ADD18650
 ID ADD18650 standard; protein; 643 AA.
 AC
 XX
 XX ADD18650;
 DT 15-JAN-2004 (first entry)
 XX Human disease related protein SeqID81.
 DE
 XX human; disease state; cytostatic; antiinflammatory; ophthalmological;
 KW antiarteriosclerotic; vulnary; gene therapy;
 KW hypoxia-regulated condition; tumorigenesis; angiogenesis; apoptosis;
 KW inflammation; erythropoiesis; glycolysis; gluconeogenesis;
 KW glucose transportation; catecholamine synthesis; iron transport;
 KW nitric oxide synthesis; cancer; ischaemic condition; reperfusion injury;

KW retinopathy; neonatal stress; pre-eclampsia; atherosclerosis;
 KW inflammatory condition; wound healing.
 OS Homo sapiens.
 XX WO2003018621-A2.
 XX
 PD 06-MAR-2003.
 XX
 PF 23-AUG-2002; 2002WO-CB003892.
 XX
 XX 23-AUG-2001; 2001GB-00020558.
 PR 05-OCT-2001; 2001GB-00024037.
 XX
 PA (OXFO-) OXFORD BIOMEDICA UK LTD.
 XX
 PI Kingsman SM, White J, Ward NR, Harris RA, Naylor S, Mundy CR;
 DR WPI; 2003-290046/28.
 DR N-PSDB; ADD18651.
 XX
 XX New substantially purified polypeptide, useful for diagnosing or treating
 PT a hypoxia-regulated condition, such as cancer, ischemia, reperfusion
 PT injury, retinopathy, pre-eclampsia, atherosclerosis, inflammation, or
 PT wound healing.
 PS
 PS Claim 25; SEQ ID NO 81; 424pp; English.
 XX
 XX This invention relates to novel human genes and gene product which are
 CC implicated in certain disease states. Compounds which modulate the
 CC proteins of the invention may have cytostatic, antiinflammatory,
 CC ophthalmological, antiarteriosclerotic or vulnary activities. The
 CC sequences of the invention may be useful for gene therapy. The invention
 CC may be useful for diagnosing or treating a hypoxia-regulated condition,
 CC such as tumorigenesis, angiogenesis, apoptosis, inflammation,
 CC erythropoiesis, or the biological response to hypoxia conditions
 CC including processes such as glycolysis, gluconeogenesis, glucose
 CC transportation, catecholamine synthesis, iron transport or nitric oxide
 CC synthesis. The disease includes cancer, ischaemic conditions, reperfusion
 CC injury, retinopathy, neonatal stress, pre-eclampsia, atherosclerosis,
 CC inflammatory conditions or wound healing. The present sequence is that of
 CC a disease related protein of the invention.
 XX
 XX Sequence 643 AA;
 Query Match 77.0%; Score 1012; DB 7; Length 643;
 Best Local Similarity 74.4%; Pred. No. 1.4e-75;
 Matches 192; Conservative 33; Mismatches 33; Indels 0; Gaps 0;
 QY 1 KSENVQDLLLLDVAPLSLGLTAGGVTALIKRNSTPTKQTQFTTYSNDQPGVLIQVY 60
 DB 386 KCEKVQDLLLLDVAPLSLGLTAGGVTALIKRNSTPTKQTQFTTYSNDQPGVLIQVY 445
 QY 61 EGERAMTKDNLLGRFELSGIPAPRGVPOIETVFDANGILNVATDSTGKANKITI 120
 DB 446 EGERAMTKDNLLGRFELSGIPAPRGVPOIETVFDANGILNVATDSTGKANKITI 505
 QY 121 TNDKGRLSKEEIERMVOEAKYKAEDVQERVSAKNALYESAFNMKSAVEDGLKGIS 180
 DB 506 TNDKGRLSKEEVERMWEAEQYKAEDQAQDRVAKNLSLEAHVHVKGSLQESLRDKIP 565
 QY 181 EADKKVLDKQCEVISWLDANTLAEKDFEHRKKELEQVCNPIISGLYQAGGPGGFG 240
 DB 566 EEDRRKMQDKREVLAHNLAEKHEVEYHQKRELEQICRPFIIFSLYGGPGVPGGSSCG 625
 QY 241 AQPGKGGSGSGPTIEEVD 258
 DB 626 TQARQDGPSTGPTIEEVD 643
 RESULT 98
 ADE77039
 ID ADE77039 standard; protein; 643 AA.

XX AC ADE77039;
XX DT 29-JAN-2004 (first entry)
XX DE Human protein expressed in a liver disorder #57.
XX KW human; liver disorder; hyperlipidaemia; hypertension; type II diabetes;
XX KW tumour; liver; inflammatory disorder; immune response disorder;
XX KW high-throughput screening; differential gene expression; gene therapy.
XX OS Homo sapiens.
XX PN US2003108871-A1.
XX PD 12-JUN-2003.
XX PF 30-JUL-2001; 2001US-00919039.
XX PR 28-JUL-2000; 2000US-0222113P.
XX PA (KASE/) KASER M R.
XX PI Kaser MR;
XX DR WPI; 2004-031227/03.
XX DR N-PSDB; ADE77038.
XX PT Composition comprising several cDNAs that are differentially expressed in
XX PT treated human C3A liver cell cultures, useful for treating liver
XX disorders.
XX PS Claim 1; SEQ ID NO 204; 41pp; English.
XX CC The invention relates to a composition comprising several cDNAs that are
XX CC differentially expressed in a liver disorder. The composition is useful
XX CC for treating liver disorder such as hyperlipidaemia, hypertension, type
XX CC II diabetes, tumours of the liver and disorders of the inflammatory and
XX CC immune response. The composition is useful for a high-throughput method
XX CC of screening several molecules or compounds to identify a ligand which
XX CC specifically binds a cDNA. A protein encoded by the cDNA is useful for a
XX CC high-throughput method for using a protein to screen several molecules or
XX CC compounds to identify at least one ligand which specifically binds the
XX CC protein which involves combining the protein encoded by the cDNA with
XX CC several of molecules or compounds under conditions to allow specific
XX CC binding, and detecting specific binding between the protein and a
XX CC molecule or compound, therefore identifying a ligand which specifically
XX CC binds the protein. The composition is useful for detecting and
XX CC quantifying differential gene expression, can be used in gene therapy, to
XX CC formulate prognosis and to design a treatment regimen and to monitor the
XX CC efficacy of treatment. The present sequence represents the amino acid
XX CC sequence of a protein encoded by a cDNA differentially expressed in a
XX CC liver disorder.
XX SQ Sequence 643 AA;
Query Match 77.0%; Score 1012; DB 8; Length 643;
Best Local Similarity 74.4%; Pred. No. 1.4e-75;
Matches 192; Conservative 33; Mismatches 33; Indels 0; Gaps 0;
QY 1 KSENVQDLLLLDVAPLSLGLTAGGVTALIKNSTIPTKTQITFTTYSNQPGLVIQY 60
DB 386 KCEKVQDLLLLDVAPLSLGLTAGGVTTLIQRNATIPKTQTFTTYSNQPGLVIQY 445
QY 61 EGERAMTKNNLLGRFELSGIPAPRGVQIETFTDANGILNVATDSTCKANKITI 120
DB 446 EGERAMTKNNLLGRFELSGIPAPRGVQIETFTDANGILNVATDSTCKANKITI 505
QY 121 TNDKGRLSKEEIERVWQEAQYKAEDVQREVSQAKNALESYAFNMKSAYEDELGKGIS 180
DB 506 TNDKGRLSKEEVERWVHEAQYKAEDQAQRDRVAQKNSLEAHVHVYKSGLSQESLRDKIP 565
QY 181 EADKKVLDKQCEVISWLDANTLAEKDFEHRKELEQVCNPIISGLYQAGGPGGFG 240

DB 566 EEDRRKXQDKCREVLAWLHNLAEKEEYEHQRELEQICRPIFSRLYGGPGVPGSSCG 625
QY 241 AQGPKGSGSGGPTIREVD 258
DB 626 TQARQGDPTGTPIIEVD 643
RESULT 99
ADP12947
ID ADP12947 standard; protein; 643 AA.
XX AC ADP12947;
XX DT 12-AUG-2004 (first entry)
XX DE Protein encoding reference mRNA sequence #32.
XX KW transplant rejection; immune system; rheumatoid arthritis; lupus;
XX KW inflammatory bowel disease; multiple sclerosis; HIV; AIDS.
XX OS Homo sapiens.
XX PN WO2004042346-A2.
XX PD 21-MAY-2004.
XX PF 24-APR-2003; 2003WO-US012946.
XX PR 24-APR-2002; 2002US-00131831.
XX PR 20-DEC-2002; 2002US-00325899.
XX PA (EXPR-) EXPRESSION DIAGNOSTICS INC.
XX PI Wohlgemuth J, Fry K, Woodward R, Ly N, Prentice J, Morris M;
XX PI Rosenberg S;
XX DR WPI; 2004-400724/37.
XX PT Diagnosing or monitoring transplant rejection, e.g. heart, kidney, liver,
XX PT pancreas, pancreatic islet, lung, bone marrow or stem cell transplant
XX PT rejection, in an individual, comprises detecting the expression level of
XX PT the genes.
XX PS Claim 65; SEQ ID NO 2956; 1762pp; English.
XX CC The present invention relates to diagnosing or monitoring transplant
XX CC rejection, e.g. cardiac or kidney transplant rejection, in an individual
XX CC comprises detecting the expression level of one or more genes. The
XX CC methods, system and kits are useful in diagnosing or monitoring
XX CC transplant rejection, e.g. heart, kidney, liver, pancreas, pancreatic
XX CC islet, lung, bone marrow or stem cell transplant rejection,
XX CC xenotransplant rejection or mechanical organ replacement rejection, in an
XX CC individual. The method is also useful in assessing the immune status of
XX CC an individual. The methods are also useful in diagnosing and monitoring
XX CC diseases that involve the immune system, e.g. rheumatoid arthritis,
XX CC lupus, inflammatory bowel diseases, multiple sclerosis, HIV/AIDS or
XX CC viral, bacterial or fungal infection. The present sequence represents a
XX CC protein encoded by an mRNA sequence of the invention which show altered
XX CC expression in renal transplantation and expression.
XX SQ Sequence 643 AA;
Query Match 77.0%; Score 1012; DB 8; Length 643;
Best Local Similarity 74.4%; Pred. No. 1.4e-75;
Matches 192; Conservative 33; Mismatches 33; Indels 0; Gaps 0;
QY 1 KSENVQDLLLLDVAPLSLGLTAGGVTALIKNSTIPTKTQITFTTYSNQPGLVIQY 60
DB 386 KCEKVQDLLLLDVAPLSLGLTAGGVTTLIQRNATIPKTQTFTTYSNQPGLVIQY 445
QY 61 EGERAMTKNNLLGRFELSGIPAPRGVQIETFTDANGILNVATDSTCKANKITI 120

Db 446 EGERAMTKDNLLGRFELSGIPAPRGVQIEVTFDIDANGILSVTATDRSTGKANKITI 505
 Qy 121 TNDKGRLSKEEIERMVOEAKYKAEDVQERVSANKNALESYAFNMKSAVEDGLGKGIS 180
 Db 506 TNDKGRLSKEEVERMWEAEQYKAEDBAQDRVAANKNSLEAHVHVKGSLQESLRDKIP 565
 Qy 181 EADKKVLDRCQEVISWLDANTLAEDKDFPHKRELEQVCNPIISGLYQAGGPGPGFG 240
 Db 566 EEDRRKMQDKCREVLAWLHNLQAEKEEYEHQKRELEICRPIFSRLYGGPGVPGGSSCG 625
 Qy 241 AQGPKGGSGSGPTIEVD 258
 Db 626 TQARQGDPTSGPTIEVD 643

RESULT 100

ADRI4395

ID ADRI4395 standard; protein; 643 AA.

XX AC ADRI4395;

XX DT 21-OCT-2004 (first entry)

XX DE Human NF-kappaB pathway-associated protein SeqID396.

XX KW NF-kappaB pathway; anti-inflammatory; cytostatic; hepatotropic; virucide;

XX KW antiarthritic; antirheumatic; gastrointestinal-Gen; antiasthmatic;

XX KW antiarteriosclerotic; immunomodulator; cerebroprotective; vasotropic;

XX KW immunosuppressive; vulnerary; gene therapy; immune disorder;

XX KW inflammatory disorder; NF-kappaB regulation; cancer; aberrant apoptosis;

XX KW hepatic disorder; Hodgkin's lymphoma; haematopoietic tumour;

XX KW hyper-IgM syndrome; hypohidrotic ectodermal dysplasia;

XX KW X-linked anhidrotic ectodermal dysplasia; immunodeficiency;

XX KW viral infection; HIV-1; HTLV-1; hepatitis B; hepatitis C; EBV; influenza;

XX KW rheumatoid arthritis; inflammatory bowel disease; colitis; ascemia;

XX KW atherosclerosis; cachexia; euthyroid sick syndrome; stroke; EAE;

XX KW autoimmune disorder; hyper immune activity;

XX KW aberrant acute phase response; hypercongenital condition; birth defect;

XX KW necrotic lesion; wound; organ transplant rejection;

XX KW aberrant signal transduction; proliferating disorder; cancer;

XX KW HIV propagation; human.

XX OS Homo sapiens.

XX PN WO2004065577-A2.

XX PD 05-AUG-2004.

XX 13-JAN-2004; 2004WO-US000798.

XX 14-JAN-2003; 2003US-0440068P.

XX 12-MAY-2003; 2003US-0469757P.

XX (BRIM) BRISTOL-MYERS SQUIBB CO.

XX Nadler SG, Neubauer MG, Feder JN, Carman J;

XX WPI; 2004-562168/54.

XX N-PSDB; ADRI4394.

XX New isolated polynucleotides and polypeptides associated with NF-kappaB

XX pathway, useful for diagnosing, treating, or preventing disorders or

XX diseases associated with NF-kappaB pathway.

XX Claim 6; SEQ ID NO 396; 237pp; English.

XX This invention relates to the novel association of protein sequences (and

XX the genes which encode them) to the NF-kappaB pathway. The invention may

XX be useful for the production of compounds with an antiinflammatory,

XX cytostatic, hepatotropic, virucide, antiarthritic, antirheumatic,

XX gastrointestinal-Gen, antiasthmatic, antiarteriosclerotic,

XX immunomodulator, cerebroprotective, vasotropic, immunosuppressive or

CC vulnary activity or for gene therapy. The proteins and nucleotides are
 CC useful for diagnosing, preventing, treating, or ameliorating conditions
 CC or diseases associated with the NF-kappaB pathway. The condition is an
 CC immune disorder, an inflammatory disorder, an inflammatory disorder
 CC related to aberrant NF-kappaB regulation, cancer, aberrant apoptosis,
 CC hepatic disorders, Hodgkin's lymphomas, haematopoietic tumours, hyper-IgM
 CC syndromes, hypohidrotic ectodermal dysplasia, X-linked anhidrotic
 CC ectodermal dysplasia, immunodeficiency, viral infections, HIV-1, HTLV-1,
 CC hepatitis B, hepatitis C, EBV, influenza, viral replication, host cell
 CC survival, evasion of immune responses, rheumatoid arthritis, inflammatory
 CC bowel disease, colitis, asthma, atherosclerosis, cachexia, euthyroid sick
 CC syndrome, stroke, EAE, autoimmune disorders, disorders related to hyper
 CC immune activity, disorders related to aberrant acute phase responses,
 CC hypercongenital conditions, birth defects, necrotic lesions, wounds,
 CC organ transplant rejection, conditions related to organ transplant
 CC rejection, disorders related to aberrant signal transduction,
 CC proliferating disorders, cancers and HIV propagation in cells infected
 CC with other viruses. The present sequence is that of a human protein which
 CC is subject to the novel association with the NF-kappaB pathway of the
 CC invention. Note: This sequence does not appear in the specification but
 CC was obtained by the indexer from Genbank.

XX SQ Sequence 643 AA;

Query Match 77.0%; Score 1012; DB 8; Length 643;

Best Local Similarity 74.4%; Pred. NO. 1.4e-75;

Matches 192; Conservative 33; Mismatches 33; Indels 0; Gaps 0;

Qy 1 KSENVODLLLDVAPLSGLGTAGGVTALIKRNSIPTKQTIFTYSDNPGVLIQVY 60
 Db 386 KCEKVODLLLDVAPLSGLGTAGGVTALIKRNSIPTKQTIFTYSDNPGVLIQVY 445
 Qy 61 EGERAMTKDNLLGRFELSGIPAPRGVQIEVTFDIDANGILSVTATDRSTGKANKITI 120
 Db 446 EGERAMTKDNLLGRFELSGIPAPRGVQIEVTFDIDANGILSVTATDRSTGKANKITI 505
 Qy 121 TNDKGRLSKEEIERMVOEAKYKAEDVQERVSANKNALESYAFNMKSAVEDGLGKGIS 180
 Db 506 TNDKGRLSKEEVERMWEAEQYKAEDBAQDRVAANKNSLEAHVHVKGSLQESLRDKIP 565
 Qy 181 EADKKVLDRCQEVISWLDANTLAEDKDFPHKRELEQVCNPIISGLYQAGGPGPGFG 240
 Db 566 EEDRRKMQDKCREVLAWLHNLQAEKEEYEHQKRELEICRPIFSRLYGGPGVPGGSSCG 625
 Qy 241 AQGPKGGSGSGPTIEVD 258
 Db 626 TQARQGDPTSGPTIEVD 643

Search completed: April 6, 2005, 17:20:53

Job time : 184 secs

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OM protein - protein search, using sw model

Run on: April 6, 2005, 17:16:54 ; Search time 43 Seconds
(without alignments)
447.894 Million cell updates/sec

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Perfect score: 1314
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Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database :

Issued Patents AA:*
1: /cgn2_6/ptodata/1/iaa/5A COMB.pep.*
2: /cgn2_6/ptodata/1/iaa/5B COMB.pep.*
3: /cgn2_6/ptodata/1/iaa/6A COMB.pep.*
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5: /cgn2_6/ptodata/1/iaa/PTUS COMB.pep.*
6: /cgn2_6/ptodata/1/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1314	100.0	641	4	US-09-919-039-146
2	1249	95.1	244	4	US-09-440-367-2
3	1097.5	83.5	646	4	US-09-919-039-11
4	1097.5	83.5	890	4	US-09-513-783A-174
5	1097.5	83.5	894	4	US-09-949-016-10605
6	1094.5	83.3	646	1	US-08-441-139-14
7	1093	83.2	641	4	US-09-919-039-73
8	1059.5	80.6	639	4	US-09-949-016-7028
9	1059.5	80.6	664	4	US-09-949-016-8177
10	1012	77.0	643	4	US-09-919-039-204
11	1009	76.8	643	3	US-08-797-358B-3
12	864.5	65.8	315	1	US-08-257-073-7
13	824	62.7	312	4	US-09-270-767-32060
14	824	62.7	312	4	US-09-270-767-47277
15	742.5	56.5	655	4	US-09-632-538C-36
16	724	55.1	666	1	US-08-441-139-16
17	717	54.6	654	1	US-08-441-139-11
18	717	54.6	654	4	US-09-919-172-54
19	717	54.6	654	4	US-09-919-039-260
20	716	54.5	692	4	US-09-248-796A-19789
21	705	53.7	682	1	US-08-441-139-2
22	703	53.5	253	4	US-09-581-001B-8
23	678	51.6	663	1	US-08-441-139-7
24	634	48.2	679	1	US-08-441-139-5
25	536.5	40.8	430	4	US-09-902-540-13248
26	531.5	40.4	625	4	US-09-501-097A-9
27	531.5	40.4	723	4	US-09-501-097A-20

28	531.5	40.4	724	4	US-09-613-303-45	Sequence 45, Appl
29	531.5	40.4	724	4	US-10-267-311-45	Sequence 45, Appl
30	530	40.3	618	4	US-09-603-208A-32	Sequence 32, Appl
31	526.5	40.1	618	4	US-09-603-208A-34	Sequence 34, Appl
32	525.5	40.0	711	4	US-09-613-303-41	Sequence 41, Appl
33	525.5	40.0	711	4	US-10-267-311-41	Sequence 41, Appl
34	524.5	39.9	539	4	US-09-710-279-888	Sequence 888, App
35	524.5	39.9	616	3	US-09-134-001C-3646	Sequence 3646, App
36	518	39.4	187	6	5196523-13	Patent No. 5196523
37	518	39.4	187	6	5196523-13	Patent No. 5196523
38	517	39.3	663	4	US-09-438-185A-505	Sequence 505, App
39	509.5	38.8	649	3	US-09-066-047-5	Sequence 5, Appli
40	500	38.1	636	4	US-09-540-236-2873	Sequence 2873, Ap
41	497	37.8	679	1	US-08-214-583-2	Sequence 2, Appli
42	489.5	37.3	516	4	US-09-248-796A-17736	Sequence 17736, A
43	488.5	37.2	199	4	US-09-581-001B-7	Sequence 7, Appli
44	488	37.1	208	4	US-09-248-796A-17615	Sequence 17615, A
45	488	37.1	660	4	US-09-328-352-4932	Sequence 4932, Ap
46	486	37.0	92	4	US-09-440-367-3	Sequence 3, Appli
47	484	36.8	562	4	US-09-207-388-14	Sequence 14, Appl
48	484	36.8	642	4	US-09-207-388-15	Sequence 15, Appl
49	484	36.8	662	4	US-09-207-388-16	Sequence 16, Appl
50	482.5	36.7	641	1	US-08-441-139-4	Sequence 4, Appli
51	480.5	36.6	657	4	US-09-352-991A-27358	Sequence 27358, A
52	480	36.5	569	4	US-09-302-540-12527	Sequence 12527, A
53	472	35.9	607	2	US-08-472-534-5	Sequence 5, Appli
54	472	35.9	607	2	US-09-207-388-13	Sequence 13, Appl
55	472	35.9	612	4	US-09-583-110-4651	Sequence 4651, Ap
56	471	35.8	607	4	US-09-107-433-3621	Sequence 3621, Ap
57	471	35.8	307	3	US-08-858-207A-481	Sequence 481, App
58	469	35.7	638	4	US-09-489-039A-8996	Sequence 8996, Ap
59	468.5	35.7	641	4	US-09-543-681A-6258	Sequence 6258, Ap
60	463	35.2	196	4	US-09-581-001B-9	Sequence 9, Appli
61	462.5	35.2	187	4	US-09-248-796A-17616	Sequence 17616, A
62	460.5	35.0	536	4	US-09-107-532A-6930	Sequence 6930, Ap
63	453.5	34.5	281	4	US-09-134-000C-3432	Sequence 3432, Ap
64	448.5	34.1	549	4	US-09-248-796A-19897	Sequence 19897, A
65	448.5	34.1	600	6	5240706-1	Patent No. 5240706
66	448.5	34.1	600	6	5240706-1	Patent No. 5240706
67	445	33.9	168	1	US-08-441-139-10	Sequence 10, Appl
68	443	33.7	539	4	US-09-198-452A-543	Sequence 543, App
69	406	30.9	132	4	US-09-270-767-42542	Sequence 42542, A
70	400	30.4	654	4	US-09-248-796A-17735	Sequence 17735, A
71	393	29.9	298	4	US-09-902-540-15923	Sequence 15923, A
72	379	28.8	96	4	US-09-248-796A-17616	Sequence 17616, A
73	376	28.6	192	4	US-09-581-001B-10	Sequence 10, Appl
74	354.5	27.0	623	4	US-09-252-991A-22906	Sequence 22906, A
75	334	25.4	622	4	US-09-540-236-3242	Sequence 3242, Ap
76	333	25.3	621	4	US-09-489-039A-11583	Sequence 11583, A
77	328	25.0	623	4	US-09-543-681A-7673	Sequence 7673, Ap
78	319.5	24.3	620	4	US-09-328-352-7730	Sequence 7730, Ap
79	285	21.7	415	4	US-09-207-388-12	Sequence 12, Appl
80	254	19.3	183	4	US-09-556-877-301	Sequence 301, App
81	254	19.3	183	4	US-09-620-412C-301	Sequence 301, App
82	254	19.3	183	4	US-09-598-419-301	Sequence 301, App
83	248.5	18.9	136	3	US-09-183-861-49	Sequence 49, Appl
84	248.5	18.9	136	3	US-09-022-765-49	Sequence 49, Appl
85	248.5	18.9	136	4	US-09-551-974A-49	Sequence 49, Appl
86	248.5	18.9	136	4	US-09-565-501A-49	Sequence 49, Appl
87	248.5	18.9	136	4	US-09-639-206A-49	Sequence 49, Appl
88	248.5	18.9	136	4	US-09-874-923-49	Sequence 49, Appl
89	234.5	17.8	535	4	US-09-902-540-15138	Sequence 15138, A
90	226.5	17.2	506	4	US-09-902-540-14235	Sequence 14235, A
91	223	17.0	69	4	US-09-581-001B-6	Sequence 6, Appli
92	217	16.5	690	4	US-09-902-540-10349	Sequence 10349, A
93	216	16.4	1027	4	US-09-902-540-11750	Sequence 11750, A
94	201	15.3	714	2	US-08-472-534-3	Sequence 3, Appli
95	193.5	14.7	222	4	US-09-581-001B-11	Sequence 11, Appl
96	190.5	14.5	608	4	US-09-902-540-14034	Sequence 14034, A
97	184	14.0	56	6	5196523-12	Patent No. 5196523
98	184	14.0	56	6	5196523-12	Patent No. 5196523
99	165	12.6	337	4	US-09-710-279-1876	Sequence 1876, Ap
100	119	9.1	941	4	US-09-513-783A-172	Sequence 172, App

ALIGNMENTS

RESULT 1
US-09-919-039-146
; Sequence 146, Application US/09919039
; Patent No. 6727066
; GENERAL INFORMATION:
; APPLICANT: Kaber, Matthew R.
; TITLE OF INVENTION: GENES EXPRESSED IN TREATED HUMAN C3A LIVER CELL CULTURES
; FILE REFERENCE: PA-0035 US
; CURRENT APPLICATION NUMBER: US/09/919,039
; CURRENT FILING DATE: 2002-09-09
; PRIOR APPLICATION NUMBER: 60/222,113
; PRIOR FILING DATE: 2000-07-28
; NUMBER OF SEQ ID NOS: 401
; SOFTWARE: PERL Program
; SEQ ID NO 146
; LENGTH: 641
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. 6727066 1678695CD1
US-09-919-039-146

Query Match 100.0%; Score 1314; DB 4; Length 641;
Best Local Similarity 100.0%; Pred. No. 6.1e-113;
Matches 258; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 KSENVODLLLDVAPLSGLGTAGGVMTALIKENSTIPTKTQTFITYSDNQPGVLIQVY 60
DB 384 KSENVODLLLDVAPLSGLGTAGGVMTALIKENSTIPTKTQTFITYSDNQPGVLIQVY 443
QY 61 EGERAMTKONLLGRFELSGLIPAPRGVPQIEVTFDIDANGILNVTATDKSTGKANKITI 120
DB 444 EGERAMTKONLLGRFELSGLIPAPRGVPQIEVTFDIDANGILNVTATDKSTGKANKITI 503
QY 121 TNDKGRLSKEIEIRMWQEAKEYKADEVQERVSANNALESYAFNMKSAVEDSLGKGIS 180
DB 504 TNDKGRLSKEIEIRMWQEAKEYKADEVQERVSANNALESYAFNMKSAVEDSLGKGIS 563
QY 181 EADKKVLDKQCEVISWLDANTLAEKDPEFHKRKELEQVNCNPIISGLYQAGGPGGFG 240
DB 564 EADKKVLDKQCEVISWLDANTLAEKDPEFHKRKELEQVNCNPIISGLYQAGGPGGFG 623
QY 241 AQGPKGSGSGPTIEVD 258
DB 624 AQGPKGSGSGPTIEVD 641

RESULT 2
US-09-440-967-2
; Sequence 2, Application US/09440967
; Patent No. 6730302
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; TITLE OF INVENTION: INTRACELLULAR TARGETED DELIVERY OF COMPOUNDS BY 70 KD HEAT SHOCK
; FILE REFERENCE: DB8
; CURRENT APPLICATION NUMBER: US/09/440,967
; CURRENT FILING DATE: 1999-11-16
; PRIOR APPLICATION NUMBER: 60/109,872
; PRIOR FILING DATE: 1998-11-24
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: Patent in version 3.0
; SEQ ID NO 2
; LENGTH: 244
; TYPE: PRT
; ORGANISM: Homo Sapien
US-09-440-967-2

Query Match 95.1%; Score 1249; DB 4; Length 244;
Best Local Similarity 100.0%; Pred. No. 1.6e-107;
Matches 244; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 15 PLSLGLGTAGGVMTALIKENSTIPTKTQTFITYSDNQPGVLIQVYEGERAMTKONLLG 74
DB 1 PLSLGLGTAGGVMTALIKENSTIPTKTQTFITYSDNQPGVLIQVYEGERAMTKONLLG 60
QY 75 RPELSGIPAPRGVPQIEVTFDIDANGILNVTATDKSTGKANKITITNDKGRLSKEIEIR 134
DB 61 RPELSGIPAPRGVPQIEVTFDIDANGILNVTATDKSTGKANKITITNDKGRLSKEIEIR 120
QY 135 MVQEAKEYKADEVQERVSANNALESYAFNMKSAVEDSLGKGISADKKVLDKQCEV 194
DB 121 MVQEAKEYKADEVQERVSANNALESYAFNMKSAVEDSLGKGISADKKVLDKQCEV 180
QY 195 ISWLDANTLAEKDPEFHKRKELEQVNCNPIISGLYQAGGPGGFGAQGPKGSGSGPTI 254
DB 181 ISWLDANTLAEKDPEFHKRKELEQVNCNPIISGLYQAGGPGGFGAQGPKGSGSGPTI 240
QY 255 EEVD 258
DB 241 EEVD 244

RESULT 3
US-09-919-039-11
; Sequence 11, Application US/09919039
; Patent No. 6727066
; GENERAL INFORMATION:
; APPLICANT: Kaber, Matthew R.
; TITLE OF INVENTION: GENES EXPRESSED IN TREATED HUMAN C3A LIVER CELL CULTURES
; FILE REFERENCE: PA-0035 US
; CURRENT APPLICATION NUMBER: US/09/919,039
; CURRENT FILING DATE: 2002-09-09
; PRIOR APPLICATION NUMBER: 60/222,113
; PRIOR FILING DATE: 2000-07-28
; NUMBER OF SEQ ID NOS: 401
; SOFTWARE: PERL Program
; SEQ ID NO 11
; LENGTH: 646
; TYPE: PRT
; ORGANISM: Homo sapiens
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. 6727066 1545176CD1
US-09-919-039-11

Query Match 83.5%; Score 1097.5; DB 4; Length 646;
Best Local Similarity 81.4%; Pred. No. 6.5e-93;
Matches 214; Conservative 24; Mismatches 20; Indels 5; Gaps 3;
QY 1 KSENVODLLLDVAPLSGLGTAGGVMTALIKENSTIPTKTQTFITYSDNQPGVLIQVY 60
DB 384 KSENVODLLLDVAPLSGLGTAGGVMTALIKENSTIPTKTQTFITYSDNQPGVLIQVY 443
QY 61 EGERAMTKONLLGRFELSGLIPAPRGVPQIEVTFDIDANGILNVTATDKSTGKANKITI 120
DB 444 EGERAMTKONLLGRFELSGLIPAPRGVPQIEVTFDIDANGILNVTATDKSTGKANKITI 503
QY 121 TNDKGRLSKEIEIRMWQEAKEYKADEVQERVSANNALESYAFNMKSAVEDSLGKGIS 180
DB 504 TNDKGRLSKEIEIRMWQEAKEYKADEVQERVSANNALESYAFNMKSAVEDSLGKGIS 563
QY 181 EADKKVLDKQCEVISWLDANTLAEKDPEFHKRKELEQVNCNPIISGLYQAGGPGGFG 237
DB 564 EADKKVLDKQCEVISWLDANTLAEKDPEFHKRKELEQVNCNPIISGLYQAGGPGGFG 623
QY 238 GF--GAQGPKGSGSGPTIEVD 258
DB 624 GF--GAQGPKGSGSGPTIEVD 646

RESULT 4

US-09-513-783A-174
 ; Sequence 174, Application US/09513783A
 ; Patent No. 6416959
 ; GENERAL INFORMATION:
 ; APPLICANT: Giuliano, Kenneth A.
 ; APPLICANT: Kapur, Ravi
 ; TITLE OF INVENTION: A System for Cell Based Screening
 ; FILE REFERENCE: 97-022-L1
 ; CURRENT APPLICATION NUMBER: US/09/513,783A
 ; CURRENT FILING DATE: 2000-02-25
 ; NUMBER OF SEQ ID NOS: 180
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 174
 ; LENGTH: 890
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; OTHER INFORMATION: Description of Artificial Sequence: GFP-HSC70
 US-09-513-783A-174

Query Match 83.5%; Score 1097.5; DB 4; Length 890;
 Best Local Similarity 81.4%; Pred. No. 1e-92;
 Matches 214; Conservative 24; Mismatches 20; Indels 5; Gaps 3;

QY 1 KSENVQDLLLLDVAPLSLGLTAGGVTALIKRNSTIPTKTQITFTTYSNQPGLVIQVY 60
 DB 628 KSENVQDLLLLDVAPLSLGLTAGGVTALIKRNTTPTKTQITFTTYSNQPGLVIQVY 687
 QY 61 EGERAMTKONLLGRPELSGIPAPRGVQIETVFDIDANGILNVATDKSTCKANKITI 120
 DB 688 EGERAMTKONLLGKGFELTGIPAPRGVQIETVFDIDANGILNVSAVDKSTCKENKITI 747
 QY 121 TNDKGRLSKEEIERMVOEAEKYAEDEVORERSAKNALESYAFNMKSAVEDGLKGKIS 180
 DB 748 TNDKGRLSKEDIEMVQAEKYAEDEKQDKVSSKNSLESYAFNMKATVEDEKLQKIN 807
 QY 181 EADKKVKLDKQEVISWLDANTLAEDPEHKEKELEQVNCNPIISGLYQAGG-PG--PG 237
 DB 808 DEDKQKILDKCNEIINWLDKNQTAEEKEFEHQKELEKVCNPIITKLYQAGGMPGMPG 867
 QY 238 GP--GAQPGKGGSGGPTIEVD 258
 DB 868 GPPGGGAPPSSGGSSGPTIEVD 890

RESULT 5

US-09-949-016-10605
 ; Sequence 10605, Application US/09949016
 ; Patent No. 6812339
 ; GENERAL INFORMATION:
 ; APPLICANT: VENTER, J. Craig et al.
 ; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
 ; FILE REFERENCE: CL001307
 ; CURRENT APPLICATION NUMBER: US/09/949,016
 ; CURRENT FILING DATE: 2000-04-14
 ; PRIOR APPLICATION NUMBER: 60/241,755
 ; PRIOR FILING DATE: 2000-10-20
 ; PRIOR APPLICATION NUMBER: 60/237,768
 ; PRIOR FILING DATE: 2000-10-03
 ; PRIOR APPLICATION NUMBER: 60/231,498
 ; PRIOR FILING DATE: 2000-09-08
 ; NUMBER OF SEQ ID NOS: 207012
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 10605
 ; LENGTH: 894
 ; TYPE: PRT
 ; ORGANISM: Human
 US-09-949-016-10605

Query Match 83.5%; Score 1097.5; DB 4; Length 894;
 Best Local Similarity 81.4%; Pred. No. 1e-92;

Matches 214; Conservative 24; Mismatches 20; Indels 5; Gaps 3;
 QY 1 KSENVQDLLLLDVAPLSLGLTAGGVTALIKRNSTIPTKTQITFTTYSNQPGLVIQVY 60
 DB 632 KSENVQDLLLLDVAPLSLGLTAGGVTALIKRNTTPTKTQITFTTYSNQPGLVIQVY 691
 QY 61 EGERAMTKONLLGRPELSGIPAPRGVQIETVFDIDANGILNVATDKSTCKANKITI 120
 DB 692 EGERAMTKONLLGKGFELTGIPAPRGVQIETVFDIDANGILNVSAVDKSTCKENKITI 751
 QY 121 TNDKGRLSKEEIERMVOEAEKYAEDEVORERSAKNALESYAFNMKSAVEDGLKGKIS 180
 DB 752 TNDKGRLSKEDIEMVQAEKYAEDEKQDKVSSKNSLESYAFNMKATVEDEKLQKIN 811
 QY 181 EADKKVKLDKQEVISWLDANTLAEDPEHKEKELEQVNCNPIISGLYQAGG-PG--PG 237
 DB 812 DEDKQKILDKCNEIINWLDKNQTAEEKEFEHQKELEKVCNPIITKLYQAGGMPGMPG 871
 QY 238 GP--GAQPGKGGSGGPTIEVD 258
 DB 872 GPPGGGAPPSSGGSSGPTIEVD 894

RESULT 6

US-08-441-139-14
 ; Sequence 14, Application US/08441139
 ; Patent No. 5773245
 ; GENERAL INFORMATION:
 ; APPLICANT: Wittrup, Dr. Karl D.
 ; APPLICANT: Robinson, Anne S.
 ; TITLE OF INVENTION: METHODS FOR INCREASING SECRETION OF RECOMBINANTLY EXPRESSED PROTEINS
 ; TITLE OF INVENTION: RECOMBINANTLY EXPRESSED PROTEINS
 ; NUMBER OF SEQUENCES: 20
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: SCULLY, SCOTT, MURPHY & PRESSER
 ; STREET: 400 Garden City Plaza
 ; CITY: Garden City
 ; STATE: NY
 ; COUNTRY: USA
 ; ZIP: 11530
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/441,139
 ; FILING DATE: 15-MAY-1995
 ; CLASSIFICATION: 435
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/089,997
 ; FILING DATE: 06-JUL-1993
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Digiglio, Frank S.
 ; REGISTRATION NUMBER: 31,346
 ; REFERENCE/DOCKET NUMBER: 8646
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 516-742-4343
 ; TELEFAX: 516-742-4366
 ; TELEX: 230 901 SANS UR
 ; INFORMATION FOR SEQ ID NO: 14:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 646 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 US-08-441-139-14

Query Match 83.3%; Score 1094.5; DB 1; Length 646;
 Best Local Similarity 81.4%; Pred. No. 1.2e-92;
 Matches 214; Conservative 23; Mismatches 21; Indels 5; Gaps 3;
 QY 1 KSENVQDLLLLDVAPLSLGLTAGGVTALIKRNSTIPTKTQITFTTYSNQPGLVIQVY 60

Db 384 KSENVQDLLLLDVTPSLGLETAGVMTALIKRNTTPTKQTQITLITYSDNQPGVLIQVY 443
QY 61 EGERAMTKDNNLLGRFELSGIPAPRGVPOIEVTFDIDANGILNVATDKSTGKANKITI 120
Db 444 EGERAMTKDNNLLGKFLGTGIPAPRGVPOIEVTFDIDANGILNVSAVDKSTGKANKITI 503
QY 121 TNDKGRLSKEIEIRWVQAEAKYKAEDVQREVRSKNALESYAFNMKSAVEDGLGKGIS 180
Db 504 TNDKGRLSKEDIERWVQAEAKYKAEDQKRDQVSSKNSLESYAFNMKATVEDEKJQCKIN 563
QY 181 EADKKVKLDKQCEVISWLDANTLAEDFEHKKRKELEQVNCNPIISGLYQAGG-PG--PG 237
Db 564 EADKKVKLDKQCEVISWLDANTLAEDFEHKKRKELEQVNCNPIISGLYQAGG-PG--PG 237
QY 238 GP--GAQPKGGSGGPTIEVD 258
Db 624 GFGGGGAPPSGGSSGPTIEVD 646

RESULT 7
US-09-919-039-73
; Sequence 73, Application US/09919039
; Patent No. 6727066
; GENERAL INFORMATION:
; APPLICANT: Kaser, Matthew R.
; TITLE OF INVENTION: GENES EXPRESSED IN TREATED HUMAN C3A LIVER CELL CULTURES
; FILE REFERENCE: PA-0035 US
; CURRENT APPLICATION NUMBER: US/09/919,039
; CURRENT FILING DATE: 2002-09-09
; PRIOR APPLICATION NUMBER: 60/222,113
; PRIOR FILING DATE: 2000-07-28
; NUMBER OF SEQ ID NOS: 401
; SOFTWARE: PERL Program
; SEQ ID NO 73
; LENGTH: 641
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No. 6727066 701484CD1
US-09-919-039-73

Query Match 83.2%; Score 1093; DB 4; Length 641;
Best Local Similarity 81.5%; Pred. No. 1.7e-92;
Matches 216; Conservative 16; Mismatches 17; Indels 16; Gaps 2;
QY 1 KSENVQDLLLLDVAPLSGLGLETAGVMTALIKRNTTPTKQTQITFTYSDNQPGVLIQVY 60
Db 386 KSENVQDLLLLDVAPLSGLGLETAGVMTALIKRNTTPTKQTQITFTYSDNQPGVLIQVY 445
QY 61 EGERAMTKDNNLLGRFELSGIPAPRGVPOIEVTFDIDANGILNVATDKSTGKANKITI 120
Db 446 EGERAMTKDNNLLGRFELSGIPAPRGVPOIEVTFDIDANGILNVATDKSTGKANKITI 505
QY 121 TNDKGRLSKEIEIRWVQAEAKYKAEDVQREVRSKNALESYAFNMKSAVEDGLGKGIS 180
Db 506 TNDKGRLSKEIEIRWVQAEAKYKAEDVQREVRSKNALESYAFNMKSAVEDGLGKGIS 565
QY 181 EADKKVKLDKQCEVISWLDANTLAEDFEHKKRKELEQVNCNPIISGLYQAGGPGGPG 240
Db 566 ESDKNKILDKQCEVISWLDANTLAEDFEHKKRKELEQVNCNPIISGLYQAGGPGGPG 240
QY 241 AQGPKGGSG-----SGPTIEVD 258
Db 617 CTGPACGFGYVPGRPATGPTIEVD 641

RESULT 8
US-09-949-016-7028
; Sequence 7028, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:

; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7028
; LENGTH: 639
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-7028

Query Match 80.6%; Score 1059.5; DB 4; Length 639;
Best Local Similarity 79.1%; Pred. No. 2.1e-89;
Matches 204; Conservative 24; Mismatches 25; Indels 5; Gaps 1;
QY 1 KSENVQDLLLLDVAPLSGLGLETAGVMTALIKRNTTPTKQTQITFTYSDNQPGVLIQVY 60
Db 387 KSENVQDLLLLDVTPSLGLETAGVMTPLIKRNTTPTKQTQITFTYSDNQSSVLVQVY 446
QY 61 EGERAMTKDNNLLGRFELSGIPAPRGVPOIEVTFDIDANGILNVATDKSTGKANKITI 120
Db 447 EGERAMTKDNNLLGKFLGTGIPAPRGVPOIEVTFDIDANGILNVATDKSTGKANKITI 506
QY 121 TNDKGRLSKEIEIRWVQAEAKYKAEDVQREVRSKNALESYAFNMKSAVEDGLGKGIS 180
Db 507 TNDKGRLSKEDIERWVQAEAKYKAEDQKRDQVSSKNSLESYAFNMKATVEDEKJQCKIN 566
QY 181 EADKKVKLDKQCEVISWLDANTLAEDFEHKKRKELEQVNCNPIISGLYQAGGPGGPG 240
Db 567 EQDKNKILDKQCEVISWLDANTLAEDFEHKKRKELEQVNCNPIISGLYQAGGPGGPG 240
QY 241 AQGPKGGSGGPTIEVD 258
Db 627 S-----GASGPTIEVD 639

RESULT 9
US-09-949-016-8177
; Sequence 8177, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8177
; LENGTH: 664
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-8177

Query Match 80.6%; Score 1059.5; DB 4; Length 664;
Best Local Similarity 79.1%; Pred. No. 2.2e-89;
Matches 204; Conservative 24; Mismatches 25; Indels 5; Gaps 1;

Qy	1	KSENVQDILLDDVAPLSIGLGTAGVMTALIKRSTIPTKQTOIFTTYSNDQPGVLQVY	60
Db	412	KSENVQDILLDDVPLSIGIETAGVMTPLIKRNTIPTKQTOFTTYSNDQSSVLQVY	471
Qy	61	EGERAMTKDNNLLGRFELSGIPPPAPRGVPQI EVTFDIDANGILNVMTATDKSTGKANKITI	120
Db	472	EGERAMTKDNNLLGCKFDLTGIPAPRGVPQI EVTFDIDANGILNVMTAADKSTGKENKITI	531
Qy	121	TNDKGRLSKBEIERWQVEAEKKADEVORERVSAKNALESYAFNMKSAVEDEGLKGKIS	180
Db	532	TNDKGRLSKDDIDRWQVEAEYKSEDEANRDRVAAKNALESYTYNIKQTVEDEKLRGKIS	591
Qy	181	EADKKKVLDKCQEVISWLDANTLAEKDBEFHKKRKELEQVCNPIISGLYQAGGPGPGGFG	240
Db	592	EODRKNILDKCQEVINLDRNQMAEKDEYEHKQELERVCPNPIISKLYQGGPGGSGGGG	651
Qy	241	AQGPKGSGSGPTTIEEVD	258
Db	652	S-----GASGGPTTIEEVD	664

RESULT 10
 US-09-919-039-204
 ; Sequence 204, Application US/09919039
 ; Patent No. 6727066
 ; GENERAL INFORMATION:
 ; APPLICANT: Kaser, Matthew R.
 ; TITLE OF INVENTION: GENES EXPRESSED IN TREATED HUMAN C3A LIVER CELL CULTURES
 ; FILE REFERENCE: PA-0035 US
 ; CURRENT APPLICATION NUMBER: US/09/919,039
 ; CURRENT FILING DATE: 2002-09-03
 ; PRIOR APPLICATION NUMBER: 60/222,113
 ; PRIOR FILING DATE: 2000-07-28
 ; NUMBER OF SEQ ID NOS: 401
 ; SOFTWARE: PERL Program
 ; SEQ ID NO 204
 ; LENGTH: 643
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; NAME/KEY: misc.feature
 ; OTHER INFORMATION: Incyte ID No. 6727066 1440032CD1
 US-09-919-039-204

```

: Patent No. 6268478
: GENERAL INFORMATION:
: APPLICANT: Adams, John
: TITLE OF INVENTION: INTRACELLULAR VITAMIN D BINDING PROTEIN
: NUMBER OF SEQUENCES: 9
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Campbell & Flores LLP
: STREET: 4370 La Jolla Village Drive, Suite 700
: CITY: San Diego
: STATE: California
: COUNTRY: United States
: ZIP: 92122
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: PatentIn Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/797,358B
: FILING DATE: 11-Feb-1997
: CLASSIFICATION: <Unknown>
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 60/011,491
: FILING DATE: 12-FEB-1996
: ATTORNEY/AGENT INFORMATION:
: NAME: Campbell, Cathryn A.
: REGISTRATION NUMBER: 31,815
: REFERENCE/DOCKET NUMBER: P-CE 3165
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (619) 535-9001
: TELEFAX: (619) 535-8949
: INFORMATION FOR SEQ ID NO: 3:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 643 amino acids
: TYPE: amino acid
: STRANDEDNESS: unknown
: TOPOLOGY: unknown
: MOLECULE TYPE: protein
: SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-08-797-358B-3

Query Match 76.8%; Score 1009; DB 3; Length 643;
Best Local Similarity 74.4%; Pred. No. 9.8e-85;
Matches 192; Conservative 34; Mismatches 32; Indels 0;

Qy 1 KSNVDDLLLDVAPLSGLGTAGGVWTLIKRNSTPTKQTQIFTTYSNDQPG
Db 386 KCEVDRDLDLDVAPLSGLGTAGGVWTLIQBNATPTKQTQFTTYSNDQPG
Qy 61 EGERAMTKDNLGLRPELSGIPAPRGVPOIEVTFDIDANGILNVTATDKSTGK
Db 446 EGERAMTKDNLGLRPELSGIPAPRGVPOIEVTFDIDANGILSVTATDRSTGK
Qy 121 TNDKGLSKEETRMVQEAKEYKAEDVQERVSQAKNALESYAFNMKSAVEDEG
Db 506 TNDKGLSKEEYRMVREAEQYKAEDQDRVAAKNLSLETHVFHVKGLSQEES
Qy 181 EADKKVLDKCEVISWLDANTLAERKDEPHKRKELEQVCNPISGLYQAGGPG
Db 566 KEDRHVQDKQCEVLAWLHQNLAQDEEYHOKRLEQICRFIFSLRYLGGFGVPG
Qy 241 AQGPKGGSGSGPTIEVD 258
Db 626 AQARQGRSTGPTIEVD 643

RESULT 12
US-08-257-073-7
: Sequence 7, Application US/08257073
: Patent No. 5766597
: GENERAL INFORMATION:
: APPLICANT: Paoletti, Enzo
: APPLICANT: de Taisne, Charles

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Db 179 KNDKRLSQADIDBMLSEAKYAEEDRHRQRTAARNQLETYLFGVKEAENG--DRIS 236
Qy 181 EADKKVLDKQCEVISWLDANTLAEDKDFEHRKRLKLEQVNCNPIISGLYQAGGPGGFG 240
Db 237 AADKSSIVCSAMKWLNTTAAKEEYEVKLKELQFCSPIMTKMHG-----GGDG 290
Qy 241 AQGP-----KGSQSGPTIEVD 258
Db 291 QQAPNFGQDGYKGTVEVD 312

RESULT 15
US-09-632-538C-36
; Sequence 36, Application US/09632538C
; Patent No. 6440674
; GENERAL INFORMATION:
; APPLICANT: Misra, Santosh et al.
; TITLE OF INVENTION: PLANT PROMOTER DERIVED FROM LUMINAL BINDING PROTEIN GENE AND METH
; TITLE OF INVENTION: ITS USE
; FILE REFERENCE: 54359
; CURRENT APPLICATION NUMBER: US/09/632,538C
; CURRENT FILING DATE: 2000-08-04
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 36
; LENGTH: 655
; TYPE: PRT
; ORGANISM: Pseudotsuga menziesii
US-09-632-538C-36

Query Match 56.5%; Score 742.5; DB 4; Length 655;
Best Local Similarity 60.3%; Pred. No. 4.4e-60;
Matches 143; Conservative 39; Mismatches 54; Indels 1; Gaps 1;

Qy 3 ENVQDILLDVLAPLSIGLETAGVMTALIKRNSIPTKQFIPTTYSNDQPGVLIQVYEG 62
Db 408 DETKDILLDVLAPLSIGLETAGVMTALIKRNSIPTKQFIPTTYSNDQPGVLIQVYEG 62
Qy 63 ERAMTKDNLLGRFELSGIPPPAPRGVQPIEVTFDIDANGILNVTATDKSTGKANKITIN 122
Db 468 ERSITKDCRELKGFSLSGIPPPAPRGVQPIEVTFDIDANGILNVTATDKSTGKANKITIN 122
Qy 123 DKRLSKERIEMVQAEKKAEDVQRRVSKNALESYAFNMKSAV--BDEGLKGKISE 181
Db 528 DKRLSQEIERMVKAEAEFEEDKKVKDKIDARNNLTYYNMKSTINEKDLADKIDS 587
Qy 182 ADKKKVLDCQEVISWLDANTLAEDKDFEHRKRLKLEQVNCNPIISGLYQAGGPGG 238
Db 588 EDKEKIETAKLEWLDNQSAEKEDFEKRLKEVEAVCSPIIKQVTEKGGSSGG 644

RESULT 16
US-08-441-139-16
; Sequence 16, Application US/08441139
; Patent No. 5773245
; GENERAL INFORMATION:
; APPLICANT: Wittrup, Dr. Karl D.
; APPLICANT: Robinson, Anne S.
; TITLE OF INVENTION: METHODS FOR INCREASING SECRETION OF
; TITLE OF INVENTION: RECOMBINANTLY EXPRESSED PROTEINS
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SCULLY, SCOTT, MURPHY & PRESSER
; STREET: 400 Garden City Plaza
; CITY: Garden City
; STATE: NY
; COUNTRY: USA
; ZIP: 11530
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: PatentIn Release #1.0, Version #1.25

Db 179 KNDKRLSQADIDBMLSEAKYAEEDRHRQRTAARNQLETYLFGVKEAENG--DRIS 236
Qy 181 EADKKVLDKQCEVISWLDANTLAEDKDFEHRKRLKLEQVNCNPIISGLYQAGGPGGFG 240
Db 237 AADKSSIVCSAMKWLNTTAAKEEYEVKLKELQFCSPIMTKMHG-----GGDG 290
Qy 241 AQGP-----KGSQSGPTIEVD 258
Db 291 QQAPNFGQDGYKGTVEVD 312

RESULT 15
US-09-632-538C-36
; Sequence 36, Application US/09632538C
; Patent No. 6440674
; GENERAL INFORMATION:
; APPLICANT: Misra, Santosh et al.
; TITLE OF INVENTION: PLANT PROMOTER DERIVED FROM LUMINAL BINDING PROTEIN GENE AND METH
; TITLE OF INVENTION: ITS USE
; FILE REFERENCE: 54359
; CURRENT APPLICATION NUMBER: US/09/632,538C
; CURRENT FILING DATE: 2000-08-04
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 36
; LENGTH: 655
; TYPE: PRT
; ORGANISM: Pseudotsuga menziesii
US-09-632-538C-36

Query Match 56.5%; Score 742.5; DB 4; Length 655;
Best Local Similarity 60.3%; Pred. No. 4.4e-60;
Matches 143; Conservative 39; Mismatches 54; Indels 1; Gaps 1;

Qy 3 ENVQDILLDVLAPLSIGLETAGVMTALIKRNSIPTKQFIPTTYSNDQPGVLIQVYEG 62
Db 408 DETKDILLDVLAPLSIGLETAGVMTALIKRNSIPTKQFIPTTYSNDQPGVLIQVYEG 62
Qy 63 ERAMTKDNLLGRFELSGIPPPAPRGVQPIEVTFDIDANGILNVTATDKSTGKANKITIN 122
Db 468 ERSITKDCRELKGFSLSGIPPPAPRGVQPIEVTFDIDANGILNVTATDKSTGKANKITIN 122
Qy 123 DKRLSKERIEMVQAEKKAEDVQRRVSKNALESYAFNMKSAV--BDEGLKGKISE 181
Db 528 DKRLSQEIERMVKAEAEFEEDKKVKDKIDARNNLTYYNMKSTINEKDLADKIDS 587
Qy 182 ADKKKVLDCQEVISWLDANTLAEDKDFEHRKRLKLEQVNCNPIISGLYQAGGPGG 238
Db 588 EDKEKIETAKLEWLDNQSAEKEDFEKRLKEVEAVCSPIIKQVTEKGGSSGG 644

RESULT 16
US-08-441-139-16
; Sequence 16, Application US/08441139
; Patent No. 5773245
; GENERAL INFORMATION:
; APPLICANT: Wittrup, Dr. Karl D.
; APPLICANT: Robinson, Anne S.
; TITLE OF INVENTION: METHODS FOR INCREASING SECRETION OF
; TITLE OF INVENTION: RECOMBINANTLY EXPRESSED PROTEINS
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SCULLY, SCOTT, MURPHY & PRESSER
; STREET: 400 Garden City Plaza
; CITY: Garden City
; STATE: NY
; COUNTRY: USA
; ZIP: 11530
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: PatentIn Release #1.0, Version #1.25

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; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/441,139
; FILING DATE: 15-MAY-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/089,997
; FILING DATE: 06-JUL-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Digiglio, Frank S.
; REGISTRATION NUMBER: 31,346
; REFERENCE/DOCKET NUMBER: 8646
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 516-742-4343
; TELEFAX: 516-742-4366
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 666 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-441-139-16

Query Match 55.1%; Score 724; DB 1; Length 666;
Best Local Similarity 59.5%; Pred. No. 2.3e-58;
Matches 141; Conservative 44; Mismatches 50; Indels 2; Gaps 2;

Qy 3 ENVQDILLDVLAPLSIGLETAGVMTALIKRNSIPTKQFIPTTYSNDQPGVLIQVYEG 62
Db 421 QDTGDLVLDVCPILGIEITVGWMTKLIPRNTVPTKKSQIFSTASDNOPTTIKVEG 480
Qy 63 ERAMTKDNLLGRFELSGIPPPAPRGVQPIEVTFDIDANGILNVTATDKSTGKANKITIN 122
Db 481 ERPLTKDNHLGTFDLTGIPPPAPRGVQPIEVTFEIDVNGILRVTAEDKGTGNKNTITN 540
Qy 123 DKRLSKERIEMVQAEKKAEDVQRRVSKNALESYAFNMKSAVED--EGLKGKISE 181
Db 541 DQNLTPTEIERMVNDAEKFAEEDKKLKERIDARNELESYASLKNQIGDKELGKLS 600
Qy 182 ADKKKVLDCQEVISWLDANTLAEDKDFEHRKRLKLEQVNCNPIISGLYQAGGPGG 238
Db 601 EDKETEKAVEEKLEWLESHQDADIEDFKSKKKELEEVQPIVSKLY--GSAGPPPTG 656

RESULT 17
US-08-441-139-11
; Sequence 11, Application US/08441139
; Patent No. 5773245
; GENERAL INFORMATION:
; APPLICANT: Wittrup, Dr. Karl D.
; APPLICANT: Robinson, Anne S.
; TITLE OF INVENTION: METHODS FOR INCREASING SECRETION OF
; TITLE OF INVENTION: RECOMBINANTLY EXPRESSED PROTEINS
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SCULLY, SCOTT, MURPHY & PRESSER
; STREET: 400 Garden City Plaza
; CITY: Garden City
; STATE: NY
; COUNTRY: USA
; ZIP: 11530
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/441,139
; FILING DATE: 15-MAY-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/089,997

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Db 469 ERPLTKDNHLLGTFDLTGTPPAPRGVQPIEVTFEIDVNGILRVTAEDKGTGNKNKITITN 528
 Qy 123 DKGRLSKEEIERMVQAEKVKAEDEVQRERVSAKNALESYAFNMKSAVED-EGLGKGIKE 181
 Db 529 DQNRLTPEEIERMVNDAEKFAEEDKKLERIDITRNELESYAIKLKQIGDKELGGKLS 588
 Qy 182 ADKKKVLDKQOEIVSWLDANTLAEKDFEHKKELEQVNCNPIISGLYQAGGPGPG 238
 Db 589 EDKETMEKAVEKIEWLESHQDADIEDFKAKKELEIEVQPIISKLY-GSAGPPPTG 644
 RESULT 19
 US-09-919-039-260
 ; Sequence 260, Application US/09919039
 ; Patent No. 6727066
 ; GENERAL INFORMATION:
 ; APPLICANT: Kaser, Matthew R.
 ; TITLE OF INVENTION: GENES EXPRESSED IN TREATED HUMAN C3A LIVER CELL CULTURES
 ; FILE REFERENCE: PA-0035 US
 ; CURRENT APPLICATION NUMBER: US/09/919,039
 ; CURRENT FILING DATE: 2002-09-09
 ; PRIOR APPLICATION NUMBER: 60/222,113
 ; PRIOR FILING DATE: 2000-07-28
 ; NUMBER OF SEQ ID NOS: 401
 ; SOFTWARE: PERL Program
 ; SEQ ID NO 260
 ; LENGTH: 654
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; NAME/KEY: misc feature
 ; OTHER INFORMATION: Incyte ID No. 6727066 2993696CD1
 US-09-919-039-260
 Query March 54.6%; Score 717; DB 4; Length 654;
 Best Local Similarity 53.1%; Pred. No. 1e-57; Indels 2; Gaps 2;
 Matches 140; Conservative 44; Mismatches 51;
 Qy 3 ENVQDLLLDVAPLSGLGLETAGGVMTALIKRNSTIPTKTQTQIFTYSDNQGVLIQVYEG 62
 Db 409 QDTGDLVLLDVCPLTGLIEVTGGVMTKLI PRNTVVPPTKKSQIFSTASDNQPTVTIKVYEG 468
 Qy 63 BRAMTKONLLGRFELSGIPPPAPRGVQPIEVTFEIDANGILNVTAETKSTGKANKKITITN 122
 Db 469 ERPLTKDNHLLGTFDLTGTPPAPRGVQPIEVTFEIDVNGILRVTAEDKGTGNKNKITITN 528
 Qy 123 DKGRLSKEEIERMVQAEKVKAEDEVQRERVSAKNALESYAFNMKSAVED-EGLGKGIKE 181
 Db 529 DQNRLTPEEIERMVNDAEKFAEEDKKLERIDITRNELESYAIKLKQIGDKELGGKLS 588
 Qy 182 ADKKKVLDKQOEIVSWLDANTLAEKDFEHKKELEQVNCNPIISGLYQAGGPGPG 238
 Db 589 EDKETMEKAVEKIEWLESHQDADIEDFKAKKELEIEVQPIISKLY-GSAGPPPTG 644
 RESULT 20
 US-09-248-796A-19789
 ; Sequence 19789, Application US/09248796A
 ; Patent No. 6747137
 ; GENERAL INFORMATION:
 ; APPLICANT: Keith Weinstock et al
 ; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDATE
 ; AND SURFACE PEPTIDES

```

, FILE REFERENCE: 107196.132
, CURRENT APPLICATION NUMBER: US/09/248,796A
, CURRENT FILING DATE: 1999-02-12
, PRIOR APPLICATION NUMBER: US 60/074,725
, PRIOR FILING DATE: 1998-02-13
, PRIOR APPLICATION NUMBER: US 60/096,409
, PRIOR FILING DATE: 1998-08-13
, NUMBER OF SEQ ID NOS: 28208
, SEQ ID NO 19789
, LENGTH: 692

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; TYPE: PRT
; ORGANISM: Candida albicans
US-09-248-796A-19789

Query Match      54.5%; Score 716; DB 4; Length 692;
Best Local Similarity 57.9%; Pred. No. 1.3e-57;
Matches 140; Conservative 44; Mismatches 54; Indels 4; Gaps 2;

Qy 3 ENVQDLLLLDVAPLSLGLTAGGVTALIKRNSIPTKTQIIFTTYSNDQPGVLIQYEG 62
Db 433 EGVDDVLLDWNPLTGLIETSGVMTTLIKRNTAIPTKKSQIFSTAADNQPTVLIQYEG 492

Qy 63 ERAMTKONNLLGRPELSGIPPPAPRGVQIEVTPDIDANGILNVATDKSTGKANKITITN 122
Db 493 ERTMAKDNRLGKPELTGIPPPAPRGVQIEVTPFSLDANGILKVEAADKGTGKSESITITN 552

Qy 123 DKGRLSKEETERMVQEAKEYKAEDVQRRVSAKNALESYAFNMKSAVED---EGLKGKI 179
Db 553 EKGRLSKDEIDRMVEEAKEYAQDQELKEIKRNSLENVAHVLRGQSLDTSETGLGSKL 612

Qy 180 SEADKKKVLDKCOEVLISWLDAN-TLAEKDBFEHKKRKELEQVNCNPIISGLYQGAGGPGPG 238
Db 613 DDDDKETLDDAIKETLFEIDNPTATAEFEEQKQLIDVANPITAKLYGGAGGAGG 672

Qy 239 FG 240
Db 673 AG 674

RESULT 21
US-08-441-139-2
; Sequence 2, Application US/08441139
; Patent No. 5773245
; GENERAL INFORMATION:
; APPLICANT: Wittrup, Dr. Karl D.
; APPLICANT: Robinson, Anne S.
; TITLE OF INVENTION: METHODS FOR INCREASING SECRETION OF
; TITLE OF INVENTION: RECOMBINANTLY EXPRESSED PROTEINS
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SCULLY, SCOTT, MURPHY & PRESSER
; STREET: 400 Garden City Plaza
; CITY: Garden City
; STATE: NY
; COUNTRY: USA
; ZIP: 11530
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/441,139
; FILING DATE: 15-MAY-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/089,997
; FILING DATE: 06-JUL-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: DiGiglio, Frank S.
; REGISTRATION NUMBER: 31,346
; REFERENCE/DOCKET NUMBER: 8646
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 516-742-4343
; TELEFAX: 516-742-4366
; TELEX: 230 901 SANS UR
; INFORMATION FOR SEQ ID NO: 2:
; LENGTH: 682 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-441-139-2

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Query Match      53.7%; Score 705; DB 1; Length 682;
Best Local Similarity 58.8%; Pred. No. 1.4e-56;
Matches 140; Conservative 43; Mismatches 53; Indels 2; Gaps 2;

Qy 3 ENVQDLLLLDVAPLSLGLTAGGVTALIKRNSIPTKTQIIFTTYSNDQPGVLIQYEG 62
Db 429 EGYEDVLLDWNALTLGIETTGGVMTPLIKRNTAIPTKKSQIFSTAVDNQPTVMIKYEG 488

Qy 63 ERAMTKONNLLGRPELSGIPPPAPRGVQIEVTPDIDANGILNVATDKSTGKANKITITN 122
Db 489 ERAMSKONNLLGKFEITGIPPPAPRGVQIEVTPFDANGILKVSATDKGTGKSESITITN 548

Qy 123 DKGRLSKEETERMVQEAKEYKAEDVQRRVSAKNALESYAFNMKSAVEDEGLKGKISEA 182
Db 549 DKGRLTQERIDRMVEEAKEYFASSEDASIKAKVESRNKLENYAHSLKNQVNGD-LGEKLEEE 607

Qy 183 DKKKVLDDKCOEVLISWLDAN-TLAEKDBFEHKKRKELEQVNCNPIISGLYQGAGGPGPG 239
Db 608 DKETLLDAANDVLEWLDNDFETAIEDDFEFESLSKVAYPIITSKLYGGADGSGAAYD 665

RESULT 22
US-09-581-001B-8
; Sequence 8, Application US/09581001B
; Patent No. 6472142
; GENERAL INFORMATION:
; APPLICANT: Danan-Van Oorschot, Mathieu
; APPLICANT:
; TITLE OF INVENTION: METHODS AND MEANS FOR INDUCING APOPTOSIS BY INTERFERING WITH
; TITLE OF INVENTION: BIP-LIKE PROTEINS
; FILE REFERENCE: 2906-4940US
; CURRENT APPLICATION NUMBER: US/09/581,001B
; CURRENT FILING DATE: 2000-07-24
; PRIOR APPLICATION NUMBER: PCT/NL98/00688
; PRIOR FILING DATE: 1998-12-03
; PRIOR APPLICATION NUMBER: EP 97203783.2
; PRIOR FILING DATE: 1997-12-03
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 8
; LENGTH: 253
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-581-001B-8

Query Match      53.5%; Score 703; DB 4; Length 253;
Best Local Similarity 58.2%; Pred. No. 5.2e-57;
Matches 138; Conservative 43; Mismatches 54; Indels 2; Gaps 2;

Qy 3 ENVQDLLLLDVAPLSLGLTAGGVTALIKRNSIPTKTQIIFTTYSNDQPGVLIQYEG 62
Db 8 QDTGDLVLLHVCPPLTGLIETVGGVMTKLIPSNVTVTKNSQIFSTASDNQPTVTIKYEG 67

Qy 63 ERAMTKONNLLGRPELSGIPPPAPRGVQIEVTPDIDANGILNVATDKSTGKANKITITN 122
Db 68 ERPLTKONHLLGTDLTGIPPPAPRGVQIEVTPDIDANGILRVTAEDKGTGNKNKITITN 127

Qy 123 DKGRLSKEETERMVQEAKEYKAEDVQRRVSAKNALESYAFNMKSAVED-EGLKGKISE 181
Db 128 DQNRLLTPEETERMVNDAAKFAEDKGLKERIDTRNELESYAVSLKQIIGDKELGKGLSS 187

Qy 182 ADKKKVLDDKCOEVLISWLDANTLAEKDBFEHKKRKELEQVNCNPIISGLYQGAGGPGPG 238
Db 188 EDKETWEKAVEEKIEWLESHQDADIEDFKAKKKELEIVQPIISKLY-GSAGPPPTG 243

RESULT 23
US-08-441-139-7
; Sequence 7, Application US/08441139
; Patent No. 5773245
; GENERAL INFORMATION:
; APPLICANT: Wittrup, Dr. Karl D.

```

```

; APPLICANT: Robinson, Anne S.
; TITLE OF INVENTION: METHODS FOR INCREASING SECRETION OF,
; TITLE OF INVENTION: RECOMBINANTLY EXPRESSED PROTEINS
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SCULLY, SCOTT, MURPHY & PRESSER
; STREET: 400 Garden City Plaza
; CITY: Garden City
; STATE: NY
; COUNTRY: USA
; ZIP: 11530
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/441,139
; FILING DATE: 15-MAY-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/089,997
; FILING DATE: 06-JUL-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Digiglio, Frank S.
; REGISTRATION NUMBER: 31,346
; REFERENCE/DOCKET NUMBER: 8646
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 516-742-4343
; TELEFAX: 516-742-4366
; TELEX: 230 901 SANS UR
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 663 amino acids
; TYPE: amino acid
; TOPOLOGY: : linear
; MOLECULE TYPE: protein
; US-08-441-139-7

Query Watch 51.6%; Score 678; DB 1; Length 6
Best Local Similarity 57.7%; Pred. No. 4.1e-54; Indels
Matches 135; Conservative 46; Mismatches 49;

QY 3 ENVQDLLLDVAPISLGLSETAGGVWYALIKRNSTIPTKQIQIPTTVS
DB 413 EGSDNVLDDVLIPTLGLIETTTGGVWYKLIGNTPIPTKRSQIFSTAV
QY 63 ERAMTKDNLLGRPELSGIPAPRGVQIEVTFDIDANGILNVTATD
DB 473 ERTLTKNNLLLGKFDLGRGIPAPRGVQIEVTFEVDANGVLTVSADV
QY 122 NDKGRLSKEEIERMWQEAETKAEDEVORERSVAKNALESYAFNMKMS
DB 533 NDKGRLSEEDIERMWKEAEFEAEEDKILKERIEARNTLENYASLKGK
QY 181 EADKKVLDKCOEVLISWLDAN-TLAKDQEFPHKKELEQV/CNLISS
DB 593 PEDKQAVLDAVEDVAEWLEIHGEDASKEEFEDQKLDVAVHPHTOKK

RESULT 24
US-08-441-139-5
; Sequence 5, Application US/08441139
; Patent No. 5773245
; GENERAL INFORMATION:
; APPLICANT: Wittrup, Dr. Karl D.
; APPLICANT: Robinson, Anne S.
; TITLE OF INVENTION: METHODS FOR INCREASING SECRETION OF
; TITLE OF INVENTION: RECOMBINANTLY EXPRESSED PROTEINS
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SCULLY, SCOTT, MURPHY & PRESSER
; STREET: 400 Garden City Plaza

```

[illegible]

Db 459 VKDVLDDVTPLSLGIETKGGVMTLRIERTTPTKRSEFTTTADNDQNPVSQVQVYQGER 518
QY 65 AMTKNNLLGRFELSGIPAPRGVQIETVTFDIDANGILNVATDSTGKANKITITNDK 124
Db 519 EIAAHNKLKLSFELTGIPAPRGVQIETVTFDIDANGIVHVTAKDGTGKENTIRIQEGS 578
QY 125 GRLSKEIEIRMVQAEKYKAEDVQERVSAAKNALESYAFN----MKSAAVEDGLKGKIS 180
Db 579 G-LSKEDIDRMIDKAEAAHEDKRREADVNRQAETLVYQTEKFVKEQREAG- GSKVP 636
QY 181 EADKKVKLDKQCVISWLDANTL-AEKDEFEHKKRKE---LEQVCPNPIISGLYQAGGPGP 236
Db 637 EDTLNKVDAAVAEAKAALGSDISAISAMEKLQESQALGOAIYEAQAASQATGAHP 696
QY 237 GGFGAQPKGSGSGPTIEVD 258
Db 697 G-----GEPGGAHPGSADDDVD 713
RESULT 29
US-10-267-311-45
; Sequence 45, Application US/10267311
; Patent No. 6657055
; GENERAL INFORMATION:
; APPLICANT: Siegel, Marvin
; APPLICANT: Chu, N. Randall
; APPLICANT: Mizzen, Lee A.
; TITLE OF INVENTION: INDUCTION OF A TH1-LIKE RESPONSE IN VITRO
; FILE REFERENCE: 12071/002001
; CURRENT APPLICATION NUMBER: US/10/267,311
; CURRENT FILING DATE: 2002-10-09
; PRIOR APPLICATION NUMBER: US/09/613,303
; PRIOR FILING DATE: 2000-07-10
; PRIOR APPLICATION NUMBER: US 60/143,757
; PRIOR FILING DATE: 1999-07-08
; NUMBER OF SEQ ID NOS: 55
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 45
; LENGTH: 724
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: fusion sequence
US-10-267-311-45
Query Match 40.4%; Score 531.5; DB 4; Length 724;
Best Local Similarity 47.7%; Pred. No. 1.6e-40;
Matches 125; Conservative 32; Mismatches 90; Indels 15; Gaps 6;
QY 5 VQDILLDVPAPLSGLGLETAGGVMTALIKRSTIPTKQTIPTTYSNQPGLIQVYQGER 64
Db 459 VKDVLDDVTPLSLGIETKGGVMTLRIERTTPTKRSEFTTTADNDQNPVSQVQVYQGER 518
QY 65 AMTKNNLLGRFELSGIPAPRGVQIETVTFDIDANGILNVATDSTGKANKITITNDK 124
Db 519 EIAAHNKLKLSFELTGIPAPRGVQIETVTFDIDANGIVHVTAKDGTGKENTIRIQEGS 578
QY 125 GRLSKEIEIRMVQAEKYKAEDVQERVSAAKNALESYAFN----MKSAAVEDGLKGKIS 180
Db 579 G-LSKEDIDRMIDKAEAAHEDKRREADVNRQAETLVYQTEKFVKEQREAG- GSKVP 636
QY 181 EADKKVKLDKQCVISWLDANTL-AEKDEFEHKKRKE---LEQVCPNPIISGLYQAGGPGP 236
Db 637 EDTLNKVDAAVAEAKAALGSDISAISAMEKLQESQALGOAIYEAQAASQATGAHP 696
QY 237 GGFGAQPKGSGSGPTIEVD 258
Db 697 G-----GEPGGAHPGSADDDVD 713

RESULT 30
US-09-603-208A-32
; Sequence 32, Application US/09603208A

; Patent No. 6822084
; GENERAL INFORMATION:
; APPLICANT: Pompejus, Markus
; APPLICANT: Kroger, Burkhard
; APPLICANT: Schroder, Hartwig
; APPLICANT: Zelder, Oskar
; APPLICANT: Haberhauer, Gregor
; APPLICANT: Lee, Heung-Shick
; APPLICANT: Kim, Hyung-Joon
; TITLE OF INVENTION: CORYNEBACTERIUM GLUTAMICUM GENES ENCODING STRESS,
; TITLE OF INVENTION: RESISTANCE AND TOLERANCE PROTEINS
; FILE REFERENCE: BGI-124CP
; CURRENT APPLICATION NUMBER: US/09/603,208A
; CURRENT FILING DATE: 2000-06-23
; PRIOR APPLICATION NUMBER: 60/141031
; PRIOR FILING DATE: 1999-06-25
; PRIOR APPLICATION NUMBER: 60/142692
; PRIOR FILING DATE: 1999-07-01
; PRIOR APPLICATION NUMBER: 60/151214
; PRIOR FILING DATE: 1999-08-27
; PRIOR APPLICATION NUMBER: DE 19930429.7
; PRIOR FILING DATE: 1999-07-01
; PRIOR APPLICATION NUMBER: DE 19931413.6
; PRIOR FILING DATE: 1999-07-08
; PRIOR APPLICATION NUMBER: DE 19931457.8
; PRIOR FILING DATE: 1999-07-08
; PRIOR APPLICATION NUMBER: DE 19931541.8
; PRIOR FILING DATE: 1999-07-08
; PRIOR APPLICATION NUMBER: DE 19932209.0
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: DE 19932230.9
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: DE 19932914.1
; PRIOR FILING DATE: 1999-07-14
; PRIOR APPLICATION NUMBER: DE 19940764.9
; PRIOR FILING DATE: 1999-08-27
; PRIOR APPLICATION NUMBER: DE 19941382.7
; PRIOR FILING DATE: 1999-08-31
; NUMBER OF SEQ ID NOS: 306
; SEQ ID NO 32
; LENGTH: 618
; TYPE: PRT
; ORGANISM: Corynebacterium glutamicum
US-09-603-208A-32
Query Match 40.3%; Score 530; DB 4; Length 618;
Best Local Similarity 48.6%; Pred. No. 1.8e-40;
Matches 119; Conservative 35; Mismatches 75; Indels 16; Gaps 5;
QY 5 VQDILLDVPAPLSGLGLETAGGVMTALIKRSTIPTKQTIPTTYSNQPGLIQVYQGER 64
Db 360 VKDVLDDVTPLSLGIETKGGVMTLRIERTTPTKRSEFTTTADNDQNPVSQVQVYQGER 419
QY 65 AMTKNNLLGRFELSGIPAPRGVQIETVTFDIDANGILNVATDSTGKANKITITNDK 124
Db 420 EIAAHNKLKLSFELTGIPAPRGVQIETVTFDIDANGIVHVTAKDGTGKENTIRIQEGS 479
QY 125 GRLSKEIEIRMVQAEKYKAEDVQERVSAAKNALESYAFNPKSAVED-----EGLKGK 178
Db 480 G-LSQDEIDRMIDKAEAAHEDKRREADVNRQAETLVYQTEKFVKEQREAG- GSKVP 538
QY 179 ISEADKKVKLDKQCVISWLDANTL-AEKDEFEHKKRKELEQVCPNPIISGLYQAGGPGP 238
Db 539 VEEAAK-----GVVEALKGEDLEAI--KAAVEKLNTSEQEMGKAIYEA--DAAAGATQAD 589
QY 239 FGAGQ 243
Db 590 AGAEG 594
RESULT 31
US-09-603-208A-34
; Sequence 34, Application US/09603208A

```
; Patent No. 6822084
; GENERAL INFORMATION:
; APPLICANT: Pompejus, Markus
; APPLICANT: Kroger, Burkhard
; APPLICANT: Schroder, Hartwig
; APPLICANT: Zelder, Oskar
; APPLICANT: Haberhauer, Gregor
; APPLICANT: Lee, Heung-Shick
; APPLICANT: Kim, Hyung-Joon
; TITLE OF INVENTION: CORYNEBACTERIUM GLUTAMICUM GENES ENCODING STRESS,
; RESISTANCE AND TOLERANCE PROTEINS
; FILE REFERENCE: BGI-124CP
; CURRENT APPLICATION NUMBER: US/09/603,208A
; CURRENT FILING DATE: 2000-06-23
; PRIOR APPLICATION NUMBER: 60/141031
; PRIOR FILING DATE: 1999-06-25
; PRIOR APPLICATION NUMBER: 60/142692
; PRIOR FILING DATE: 1999-07-01
; PRIOR APPLICATION NUMBER: 60/151214
; PRIOR FILING DATE: 1999-08-27
; PRIOR APPLICATION NUMBER: DE 19930429.7
; PRIOR FILING DATE: 1999-07-01
; PRIOR APPLICATION NUMBER: DE 19931413.6
; PRIOR FILING DATE: 1999-07-08
; PRIOR APPLICATION NUMBER: DE 19931457.8
; PRIOR FILING DATE: 1999-07-08
; PRIOR APPLICATION NUMBER: DE 19931541.8
; PRIOR FILING DATE: 1999-07-08
; PRIOR APPLICATION NUMBER: DE 19932209.0
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: DE 19932230.9
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: DE 19932914.1
; PRIOR FILING DATE: 1999-07-14
; PRIOR APPLICATION NUMBER: DE 19940764.9
; PRIOR FILING DATE: 1999-08-27
; PRIOR APPLICATION NUMBER: DE 19941382.7
; PRIOR FILING DATE: 1999-08-31
; NUMBER OF SEQ ID NOS: 306
; SEQ ID NO 34
; LENGTH: 618
; TYPE: PRT
; ORGANISM: Corynebacterium glutamicum
; FEATURE:
; OTHER INFORMATION: All occurrences of xaa indicate any amino acid
US-09-603-208A-34

Query Match          40.1%; Score 526.5; DB 4; Length 618;
Best Local Similarity 58.1%; Pred. No. 3.8e-40;
Matches 108; Conservative 28; Mismatches 43; Indels 7; Gaps 2;

QY      5 VQDLLLDVAPLSLGLETAGGVTALIKRNSTIPTKTQIFTTYSNQPQVLIQVYQGER 64
Db      360 VKDVLDDVTPLSLGLETGKGVMTKLIERNTTPTKRSEFTTTAEDNQPSVQIQVQGER 419

QY      65 AMTKNNLLGRFELSGIPAPRGVPOIEVTFDIDANGILNVTATDKSTGKANKITITNDK 124
Db      420 EIATANKLLGSFELGGIAPAPRGVPOIEVTFDIDANGIVHTAKDKGTGKENTITIDQS 479

QY      125 GRLSKEEIERMVQAEKYKAEDVQRRVSAKVALESYAFN-----EGLKKGK 178
Db      480 G-LSQDEIDRMKDAEAHADEKRRREQEVRNNAESLVQTRKFVEENSEKVSDELKAK 538

QY      179 ISEADK 184
Db      539 VEEAAK 544

RESULT 32
US-09-613-303-41
; Sequence 41, Application US/09613303
; Patent No. 6495347
; GENERAL INFORMATION:
; APPLICANT: Chu, N. Randall
; APPLICANT: Mizzen, Lee A.
; TITLE OF INVENTION: INDUCTION OF A TH1-LIKE RESPONSE IN VITRO
; FILE REFERENCE: 12071/002001
; CURRENT APPLICATION NUMBER: US/10/267,311
; CURRENT FILING DATE: 2002-10-09
; PRIOR APPLICATION NUMBER: US/09/613,303
; PRIOR FILING DATE: 2000-07-10
; PRIOR APPLICATION NUMBER: US 60/143,757
; PRIOR FILING DATE: 1999-07-08
; NUMBER OF SEQ ID NOS: 55
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 41
; LENGTH: 711
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: fusion sequence
US-10-267-311-41

Query Match          40.0%; Score 525.5; DB 4; Length 711;
Best Local Similarity 48.2%; Pred. No. 5.7e-40;
Matches 123; Conservative 31; Mismatches 86; Indels 15; Gaps 6;
```

```
; APPLICANT: Siegel, Marvin
; APPLICANT: Chu, N. Randall
; APPLICANT: Mizzen, Lee A.
; TITLE OF INVENTION: INDUCTION OF A TH1-LIKE RESPONSE IN VITRO
; FILE REFERENCE: 12071/002001
; CURRENT APPLICATION NUMBER: US/09/613,303
; CURRENT FILING DATE: 2000-07-10
; PRIOR APPLICATION NUMBER: US 60/143,757
; PRIOR FILING DATE: 1999-07-08
; NUMBER OF SEQ ID NOS: 55
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 41
; LENGTH: 711
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: fusion sequence
US-09-613-303-41

Query Match          40.0%; Score 525.5; DB 4; Length 711;
Best Local Similarity 48.2%; Pred. No. 5.7e-40;
Matches 123; Conservative 31; Mismatches 86; Indels 15; Gaps 6;

QY      5 VQDLLLDVAPLSLGLETAGGVTALIKRNSTIPTKTQIFTTYSNQPQVLIQVYQGER 64
Db      459 VKDVLDDVTPLSLGLETGKGVMTKLIERNTTPTKRSEFTTTTADDNQPSVQIQVQGER 518

QY      65 AMTKNNLLGRFELSGIPAPRGVPOIEVTFDIDANGILNVTATDKSTGKANKITITNDK 124
Db      519 EIAHNKLLGSFELTGIIPAPRGVPOIEVTFDIDANGIVHTAKDKGTGKENTIRQEGS 578

QY      125 GRLSKEEIERMVQAEKYKAEDVQRRVSAKVALESYAFN-----MKS AVEDEGLKGIS 180
Db      579 G-LSKEDIDRMKDAEAHADEKRRREQEVRNNAESTLVQTEKFVKEQREASG-GSKVP 636

QY      181 EADKKVLDKQCEVISWLDANTL-AEKDEFHKRKE---LEQVCNFIISGLYQAGGPGP 236
Db      637 EDTLANKVDAVAEAKAALGGSDISAITSAMEKLGQESQALGQAIYBAQAASQATGAHP 696

QY      237 GGFGAQQPKGGSGG 251
Db      697 G-----GEFGGAHPG 706

RESULT 33
US-10-267-311-41
; Sequence 41, Application US/10267311
; Patent No. 6657055
; GENERAL INFORMATION:
; APPLICANT: Siegel, Marvin
; APPLICANT: Chu, N. Randall
; APPLICANT: Mizzen, Lee A.
; TITLE OF INVENTION: INDUCTION OF A TH1-LIKE RESPONSE IN VITRO
; FILE REFERENCE: 12071/002001
; CURRENT APPLICATION NUMBER: US/10/267,311
; CURRENT FILING DATE: 2002-10-09
; PRIOR APPLICATION NUMBER: US/09/613,303
; PRIOR FILING DATE: 2000-07-10
; PRIOR APPLICATION NUMBER: US 60/143,757
; PRIOR FILING DATE: 1999-07-08
; NUMBER OF SEQ ID NOS: 55
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 41
; LENGTH: 711
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: fusion sequence
US-10-267-311-41

Query Match          40.0%; Score 525.5; DB 4; Length 711;
Best Local Similarity 48.2%; Pred. No. 5.7e-40;
Matches 123; Conservative 31; Mismatches 86; Indels 15; Gaps 6;
```


Db 61 NDQNLTPBIEIRWVNDKFAEDKKLKERIDTRNELESYAYSLKNQIGDKKLGKLS 120
 QY 181 EADKKVLDKQEVISWLDANTLAEDKDEFEHKKKELEQVNCNPIISGLYQAGGPGG 238
 Db 121 SEDKETMEKAVEKIEWLESHQDADIEDFKAKKKELEIIVQPIISKLY-GSAGPPPTG 177

RESULT 37
 5196523-13
 ; PATENT NO. 5196523
 ; APPLICANT: LEE, AMY S.
 ; TITLE OF INVENTION: CONTROL OF GENE EXPRESSION BY GLUCOSE,
 ; CALCIUM AND TEMPERATURE
 ; NUMBER OF SEQUENCES: 28
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/07/354,988
 ; FILING DATE: 19-MAY-1989
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 282,880
 ; FILING DATE: 05-DEC-1988
 ; APPLICATION NUMBER: 690,951
 ; FILING DATE: 01-JAN-1985
 ; SEQ ID NO:13:
 ; LENGTH: 187
 5196523-13

Query Match 39.4%; Score 518; DB 6; Length 187;
 Best Local Similarity 57.3%; Pred. No. 4.4e-40;
 Matches 102; Conservative 33; Mismatches 41; Indels 2; Gaps 2;

QY 62 GERAMTKNNLLGRFELSGIPAPRGVPOIEVTFDIDANGILNVATDSTGKANKITIT 121
 Db 1 GERPLTKDNLHLLGTFDLTGIPAPRGVPOIEVTFDIDANGILNVATDSTGKANKITIT 60

QY 122 NDKGRLSKEIERMVOEAKYKAEDEVORERSAKNALESYAFNMKSAVED-EGLKGIS 180
 Db 61 NDQNLTPBIEIRWVNDKFAEDKKLKERIDTRNELESYAYSLKNQIGDKKLGKLS 120

QY 181 EADKKVLDKQEVISWLDANTLAEDKDEFEHKKKELEQVNCNPIISGLYQAGGPGG 238
 Db 121 SEDKETMEKAVEKIEWLESHQDADIEDFKAKKKELEIIVQPIISKLY-GSAGPPPTG 177

RESULT 38
 US-09-438-185A-505
 ; Sequence 505, Application US/09438185A
 ; Patent No. 6822071
 ; GENERAL INFORMATION:
 ; APPLICANT: Stephens, Richard
 ; APPLICANT: Mitchell, Wayne
 ; APPLICANT: Kalman, Sue
 ; APPLICANT: Davis, Ronald
 ; APPLICANT: The Regents of the University of California
 ; TITLE OF INVENTION: Chlamydia Pneumoniae Genome Sequence
 ; FILE REFERENCE: 018941-000411US
 ; CURRENT APPLICATION NUMBER: US/09/438,185A
 ; PRIOR FILING DATE: 2002-03-13
 ; PRIOR APPLICATION NUMBER: US 60/108,279
 ; PRIOR FILING DATE: 1998-11-12
 ; PRIOR APPLICATION NUMBER: US 60/128,606
 ; PRIOR FILING DATE: 1999-04-08
 ; NUMBER OF SEQ ID NOS: 1074
 ; SOFTWARE: Fast-Seq for Windows Version 3.0
 ; SEQ ID NO 505
 ; LENGTH: 663
 ; TYPE: PRT
 ; ORGANISM: Chlamydia pneumoniae
 ; FEATURE:
 ; OTHER INFORMATION: CPn0503
 US-09-438-185A-505

Query Match 39.3%; Score 517; DB 4; Length 663;
 Best Local Similarity 44.6%; Pred. No. 3.2e-39;

Matches 121; Conservative 42; Mismatches 88; Indels 20; Gaps 5;
 QY 5 VODLLLDVAPISLGLTAGVMTALIKKNSITPTKQTIQFTTYSNQGVLIQVTEGER 64
 Db 387 VKDVLDDVPLSLGLIETLGGVMTLVVNTTIPTQKKQIFSTADNQPAVTIVLQGER 446
 QY 65 AMTKONNLLGRFELSGIPAPRGVPOIEVTFDIDANGILNVATDSTGKANKITITNDK 124
 Db 447 PMAKDNKEIGRDLTDIPAPRGVPOIEVTFDIDANGILNVATDSTGKANKITITNDK 506
 QY 125 GLSKKEIERMVOEAKYKAEDEVORERSAKNALESYAFNMKSAVEDGLKGISEADK 184
 Db 507 G-LQDEIQRMVDAEINKEDKKREASDANKREASDMIFRAEKAID--YKQIPETLV 553
 QY 185 KKVLDKQEVISWLDANTLAEK-----DEFEHKKKELE-----QVCNPIISGLYQAGG 234
 Db 564 KEIEERINVRNALKDDAPIEKIKEVTEDLSKHMQKIGESMQSQSASASAAANAKGGP 623
 QY 235 G-----PGFGAQGPKGSGSGGPTIEVD 258
 Db 624 NINTEDLKKHSFSTKPPSNNGSSSEHIEAD 654

RESULT 39
 US-09-066-047-5
 ; Sequence 5, Application US/09066047A
 ; Patent No. 6306394
 ; GENERAL INFORMATION:
 ; APPLICANT: MURPHY, Cheryl
 ; STOREY, James
 ; BELTZ, Gerald A.
 ; COUGHLIN, Richard T.
 ; TITLE OF INVENTION: NUCLEIC ACIDS, PROTEINS, AND METHODS OF
 ; USE OF GRANULOCYTIC ERLHICHA
 ; NUMBER OF SEQUENCES: 41
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: HALE AND DORR LLP
 ; STREET: 60 State Street
 ; CITY: Boston
 ; STATE: Massachusetts
 ; COUNTRY: United States
 ; ZIP: 02109
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/066,047A
 ; FILING DATE: 24-Apr-1998
 ; CLASSIFICATION: <Unknown>
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 60/044,869
 ; FILING DATE: 25-APR-1997
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Superko, Colleen
 ; REGISTRATION NUMBER: 39,850
 ; REFERENCE/DOCKET NUMBER: 106.941.156
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (617) 526-6000
 ; TELEFAX: (617) 526-5000
 ; INFORMATION FOR SEQ ID NO: 5:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 649 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: <Unknown>
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; SEQUENCE DESCRIPTION: SEQ ID NO: 5:
 US-09-066-047-5

Query Match 38.8%; Score 509.5; DB 3; Length 649;
 Best Local Similarity 44.7%; Pred. No. 1.5e-38;

Matches 115; Conservative 44; Mismatches 91; Indels 7; Gaps 5;

QY 4 NVQDILLDVAPLSGLTAGGVTALIKRNSIPTKQIQTFTYSDNQPGVLIQVYGE 63
 Db 383 DVRDVLDDVAPLSGLTGLGVTPLIERNTTPTKQSVFSTAEDGGTAVTIKYQGE 442

QY 64 RAMTKNNLLGRFELSGLPAPRGVQIEVTFDIDANGILNVATDKSTGKANKITIND 123
 Db 443 RKMAINDKLGQSLGEPHAPRGVQIEVTFDIDANGIVHVSADKASGKEQTIKI-QS 501

QY 124 KGRLSKEEIERMVQAEKKADEQVRVSAKNALESYAFNMKSAAVEDEGLKGISEAD 183
 Db 502 SGLSDEEIKKWKDAQDRAEDDEKRRKVKELKNSSEGLIHSVEKSLKQVY--DKVAGAD 559

QY 184 KKVLDKQCVISWL--DANTLAEKDEPHEKKELEQVNCNPIISGLYQAGGPGGFGAQ 242
 Db 560 KSNIESAIKDLRECLDNDN--CSTDTLQKYDALMNLMLKGEAAYAAANKNDGAGSADOS 617

QY 243 G-PKGGSGSPTIEVD 258
 Db 618 GSSSGSDGNGPERVVD 634

RESULT 40
 US-09-540-236-2873
 ; Sequence 2873, Application US/09540236
 ; Patent No. 6671910
 ; GENERAL INFORMATION:
 ; APPLICANT: Gary L. Breton et al.
 ; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO MORAXELLA CATAR
 ; TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
 ; FILE REFERENCE: 2709.2005-001
 ; CURRENT APPLICATION NUMBER: US/09/540.236
 ; CURRENT FILING DATE: 2000-04-04
 ; NUMBER OF SEQ ID NOS: 3840
 ; SEQ ID NO 2873
 ; LENGTH: 636
 ; TYPE: PRT
 ; ORGANISM: M.catarrhalis
 US-09-540-236-2873

Query Match 38.1%; Score 500; DB 4; Length 636;
 Best Local Similarity 46.0%; Pred. No. 1.1e-37;
 Matches 109; Conservative 48; Mismatches 68; Indels 12; Gaps 5;

QY 2 SENVDILLDVAPLSGLTAGGVTALIKRNSIPTKQIQTFTYSDNQPGVLIQVY 61
 Db 383 SGDKKVLDDVPTLGLTGLTGGVTPLIERNTTPTKQSVFSTAEDGGTAVTIKYQ 442

QY 62 GERAMTKNNLLGRFELSGLPAPRGVQIEVTFDIDANGILNVATDKSTGKANKITIT 121
 Db 443 GERKIANQNLGNFDTLDPAPRGVQIEVTFDIDANGILNVATDKSTGKANKITIT 502

QY 122 NDKGRLSKEEIERMVQAEKKADEQVRVSAKNALESYAFNMKSAAVEDEGLKGISE 181
 Db 503 ADSG-LSESEITEEMIRTAENAADEDEKRRKVKELKNSSEGLIHSVEKSLKQVY--DKVTT 559

QY 182 ADKKVLDDKQCVISWL--DANTLAEKDEPHEKKELEQVNCN--PIISGLYQAGGPG 235
 Db 560 EETAV-----ESAISTLEA--AAKEDDADIKAKLEALDNLAFIPISQKIYADAGAQ 610

RESULT 41
 US-08-214-583-2
 ; Sequence 2, Application US/08214583
 ; Patent No. 5627039
 ; GENERAL INFORMATION:
 ; APPLICANT: Pereira-Smith, Olivia
 ; APPLICANT: Washwa, Renu
 ; TITLE OF INVENTION: MORTALIN AND METHODS FOR DETERMINING
 ; TITLE OF INVENTION: COMPLEMENTATION GROUP ASSIGNMENT OF CANCER CELLS
 ; NUMBER OF SEQUENCES: 2
 ; CORRESPONDENCE ADDRESS:

ADDRESSER: Howrey & Simon
 STREET: 1299 Pennsylvania Ave, NW
 CITY: Washington
 STATE: DC
 COUNTRY: US
 ZIP: 20004

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent In Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/214.583
 FILING DATE:
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: Auerbach, Jeffrey I.
 REGISTRATION NUMBER: 32.680
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 202-383-7451
 TELEFAX: 202-383-6610
 INFORMATION FOR SEQ ID NO: 2:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 679 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 HYPOTHETICAL: NO
 ORIGINAL SOURCE:
 ORGANISM: Murine
 IMMEDIATE SOURCE:
 CLONE: mortalin
 US-08-214-583-2

Query Match 37.8%; Score 497; DB 1; Length 679;
 Best Local Similarity 45.9%; Pred. No. 2.3e-37;
 Matches 111; Conservative 41; Mismatches 78; Indels 12; Gaps 4;

QY 4 NVQDILLDVAPLSGLTAGGVTALIKRNSIPTKQIQTFTYSDNQPGVLIQVYGE 63
 Db 431 DVTVDLLDDVPTLGLTGLTGGVTPLIERNTTPTKQSVFSTAEDGGTAVTIKYQGE 490

QY 64 RAMTKNNLLGRFELSGLPAPRGVQIEVTFDIDANGILNVATDKSTGKANKITIND 123
 Db 491 REMAGNKLGLGFTLIGIPAPRGVQIEVTFDIDANGIVHVSADKGTGREQQIIV-QS 549

QY 124 KGRLSKEEIERMVQAEKKADEQVRVSAKNALESYAFNMKSAAVEDEGLKGISEAD 183
 Db 550 SGLSKDDIDENVMVKNKAEEDRRKKEVEAVNMAEGIIHDTETWEEFKDQLPADECN 609

QY 184 K-KKVLDKQCVISWL--DANTLAEKDEPHEKKELEQVNCNPIISGLY-----QGAGGPG 235
 Db 610 KLKKEISKVALLARKDSET---GENIRQAASSLQOASLKLPEMAYKKMASREGSGSSG 666

QY 236 PG 237
 Db 667 TG 668

RESULT 42
 US-09-248-796A-17736
 ; Sequence 17736, Application US/09248796A
 ; Patent No. 6747137
 ; GENERAL INFORMATION:
 ; APPLICANT: Keith Weinstein et al
 ; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN
 ; TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
 ; FILE REFERENCE: 107196.132
 ; CURRENT APPLICATION NUMBER: US/09/248.796A
 ; CURRENT FILING DATE: 1999-02-12
 ; PRIOR APPLICATION NUMBER: US 60/074,725
 ; PRIOR FILING DATE: 1998-02-13

Db 516 ANSG-LSDAIEAMIXDAEANAEDRKFELAKARNEADALISSNKA VKDLG--DKVTE 572

Qy 182 ADKKVLDKQEVISWLDANTLAEKDE-FEHKKELEQVCNPIISGLYQ-----CAGGP 234

Db 573 DEKTAV-----NTAVSELEAAKENDVEVIKAKTEALQNILMPITQRAYBOAQAGGAE 628

Qy 235 GPGGFGAQQGPKGG 247

Db 629 DPNAF--QGGDAG 639

RESULT 46

US-09-440-967-3

; Sequence 3, Application US/09440967

; Patent No. 6730302

; GENERAL INFORMATION:

; APPLICANT: Bristol-Myers Squibb Company

; TITLE OF INVENTION: INTRACELLULAR TARGETED DELIVERY OF COMPOUNDS BY 70 KD HEAT SHOCK

; FILE REFERENCE: DB8

; CURRENT APPLICATION NUMBER: US/09/440,967

; CURRENT FILING DATE: 1999-11-16

; PRIOR FILING DATE: 60/109,872

; NUMBER OF SEQ ID NOS: 5

; SOFTWARE: PatentIn version 3.0

; SEQ ID NO 3

; LENGTH: 92

; TYPE: PRT

; ORGANISM: Homo Sapien

US-09-440-967-3

Query Match 37.0%; Score 486; DB 4; Length 92;

Best Local Similarity 100.0%; Pred. No. 1.5e-37;

Matches 92; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 167 KSAVEDGLKGIKSEADKKVLDKQEVISWLDANTLAEKDEFEHKKKELEQVCNPIISG 226

Db 1 KSAVEDGLKGIKSEADKKVLDKQEVISWLDANTLAEKDEFEHKKKELEQVCNPIISG 60

Qy 227 LYQAGGPGPGGGAQGPKGSGSGPTIEVD 258

Db 61 LYQAGGPGPGGGAQGPKGSGSGPTIEVD 92

RESULT 47

US-09-207-388-14

; Sequence 14, Application US/09207388

; Patent No. 6497880

; GENERAL INFORMATION:

; APPLICANT: Wisniewski, Jan

; TITLE OF INVENTION: HEAT SHOCK GENES AND PROTEINS FROM

; TITLE OF INVENTION: NEISSERIA MENINGITIDIS, CANDIDA GLABRATA AND ASPERGILLUS

; FILE REFERENCE: 870109.411

; CURRENT APPLICATION NUMBER: US/09/207,388

; CURRENT FILING DATE: 1998-12-08

; NUMBER OF SEQ ID NOS: 102

; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 14

; LENGTH: 562

; TYPE: PRT

; ORGANISM: Neisseria meningitidis

US-09-207-388-14

Query Match 36.8%; Score 484; DB 4; Length 562;

Best Local Similarity 51.2%; Pred. No. 2.8e-36;

Matches 105; Conservative 33; Mismatches 61; Indels 6; Gaps 3;

Qy 7 DLLLLDVAPLSGLGTAGVWMTALKRNSTIPTKQTIPTTSDNQPGLVIOVYGERAM 66

Db 309 DVLLLDVTPLSGLGTAGVWMTALKRNSTIPTKQTIPTTSDNQPGLVIOVYGERAM 368

Qy 67 TKONNLLGRFELSGIPAPRGVPQIEVTFDIDANGILNVATDKSTGKANKITITNDKGR 126

Db 369 ASANKSLQGFNLGDIAPAPRGMPQIEVTFDIDANGILHVSADKGTGKAANITIQSSG- 427

Qy 127 LSKEEIERMVQAEKYKAEDVQREVSANAKNALESYAFNMKSAVEDGLKGIKSEADKKK 186

Db 428 LSEEEIERMVQDAEANAEDKKLTVELVASRNOAEALIHVSVKSLADYG--DKLDAAEKEK 485

Qy 187 V---LDKQCEVISWLDANTLAEKDE 208

Db 486 IEAALKEAEAEAVKGGDKAAIDAKTE 510

RESULT 48

US-09-207-388-15

; Sequence 15, Application US/09207388

; Patent No. 6497880

; GENERAL INFORMATION:

; APPLICANT: Wisniewski, Jan

; TITLE OF INVENTION: HEAT SHOCK GENES AND PROTEINS FROM

; TITLE OF INVENTION: NEISSERIA MENINGITIDIS, CANDIDA GLABRATA AND ASPERGILLUS

; FILE REFERENCE: 870109.411

; CURRENT APPLICATION NUMBER: US/09/207,388

; CURRENT FILING DATE: 1998-12-08

; NUMBER OF SEQ ID NOS: 102

; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 15

; LENGTH: 642

; TYPE: PRT

; ORGANISM: Neisseria meningitidis

US-09-207-388-15

Query Match 36.8%; Score 484; DB 4; Length 642;

Best Local Similarity 51.2%; Pred. No. 3.4e-36;

Matches 105; Conservative 33; Mismatches 61; Indels 6; Gaps 3;

Qy 7 DLLLLDVAPLSGLGTAGVWMTALKRNSTIPTKQTIPTTSDNQPGLVIOVYGERAM 66

Db 389 DVLLLDVTPLSGLGTAGVWMTALKRNSTIPTKQTIPTTSDNQPGLVIOVYGERAM 448

Qy 67 TKONNLLGRFELSGIPAPRGVPQIEVTFDIDANGILNVATDKSTGKANKITITNDKGR 126

Db 449 ASANKSLQGFNLGDIAPAPRGMPQIEVTFDIDANGILHVSADKGTGKAANITIQSSG- 507

Qy 127 LSKEEIERMVQAEKYKAEDVQREVSANAKNALESYAFNMKSAVEDGLKGIKSEADKKK 186

Db 508 LSEEEIERMVQDAEANAEDKKLTVELVASRNOAEALIHVSVKSLADYG--DKLDAAEKEK 565

Qy 187 V---LDKQCEVISWLDANTLAEKDE 208

Db 566 IEAALKEAEAEAVKGGDKAAIDAKTE 590

RESULT 49

US-09-207-388-16

; Sequence 16, Application US/09207388

; Patent No. 6497880

; GENERAL INFORMATION:

; APPLICANT: Wisniewski, Jan

; TITLE OF INVENTION: HEAT SHOCK GENES AND PROTEINS FROM

; TITLE OF INVENTION: NEISSERIA MENINGITIDIS, CANDIDA GLABRATA AND ASPERGILLUS

; FILE REFERENCE: 870109.411

; CURRENT APPLICATION NUMBER: US/09/207,388

; CURRENT FILING DATE: 1998-12-08

; NUMBER OF SEQ ID NOS: 102

; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 16

; LENGTH: 662

; TYPE: PRT

; ORGANISM: Neisseria meningitidis

US-09-207-388-16

Query Match 36.8%; Score 484; DB 4; Length 662;
 Best Local Similarity 51.2%; Pred. No. 3.6e-36;
 Matches 105; Conservative 33; Mismatches 61; Indels 6; Gaps 3;
 QY 7 DILLDDVAPLSGLGTAGGVTALIKRSTPTKOTQIFTYSDNQGVLIQVYGERAM 66
 Db 409 DVLLDDVTPSLGIEGTGGVTMLIKRSTPTKASQVFTADNQSAVTHVLQGER 468
 QY 67 TKDNNLLGRFELSGIPAPRGVQIEVTFDIDANGILNVTTATDKSTGKANKITITNDKGR 126
 Db 469 ASANKSLGQPNLGDIAAPAPRGVQIEVTFDIDANGILNVTTATDKSTGKANKITITNDKGR 527
 QY 127 LSKEEIERMVOEAKYKADEVORERSAKNALESYAFNMKSAVEDGLKGIKSEADKK 186
 Db 528 LSEETIERMVKDAEAEEDKLTIVASRQAEALHSHVKKSLADYG--DKLDAAEK 585
 QY 187 V--LDKQCVISWLDANTLAEKDE 208
 Db 586 IEAALKEAEAEAVKGDGDKAAIDAKTE 610

RESULT 50
 US-08-441-139-4
 ; Sequence 4, Application US/08441139
 ; Patent No. 5773245
 ; GENERAL INFORMATION:
 ; APPLICANT: Wittrop, Dr. Karl D.
 ; APPLICANT: Robinson, Anne S.
 ; TITLE OF INVENTION: METHODS FOR INCREASING SECRETION OF
 ; TITLE OF INVENTION: RECOMBINANTLY EXPRESSED PROTEINS
 ; NUMBER OF SEQUENCES: 20
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: SCULLY, SCOTT, MURPHY & PRESSER
 ; STREET: 400 Garden City Plaza
 ; CITY: Garden City
 ; STATE: NY
 ; COUNTRY: USA
 ; ZIP: 11530
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patencin Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/441,139
 ; FILING DATE: 15-MAY-1995
 ; CLASSIFICATION: 435
 ; PRIORITY APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/089,997
 ; FILING DATE: 06-JUL-1993
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Digiglio, Frank S.
 ; REGISTRATION NUMBER: 31,346
 ; REFERENCE/DOCKET NUMBER: 8646
 ; TELEPHONE: 516-742-4343
 ; TELEFAX: 516-742-4366
 ; TELEX: 230 901 SANS UR
 ; INFORMATION FOR SEQ ID NO: 4:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 641 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; US-08-441-139-4

Query Match 36.7%; Score 482.5; DB 1; Length 641;
 Best Local Similarity 41.2%; Pred. No. 4.7e-36;
 Matches 107; Conservative 54; Mismatches 70; Indels 29; Gaps 7;
 QY 2 SENVDLLLDVAPLSGLGTAGGVTALIKRSTPTKOTQIFTYSDNQGVLIQVYE 61
 Db 393 SGHVKLVLLDVTPSLGIEGTGGVTMLIKRSTPTKASQVFTADNQSAVTHVLQ 452

QY 62 GERAMTKDNNLLGRFELSGIPAPRGVQIEVTFDIDANGILNVTTATDKSTGKANKITIT 121
 Db 453 GERELVRDNNKLGIFQLTGIAPAPKQPOIEVDFDADGIIINVARDKATNKDSSITVA 512
 QY 122 NDKGRLSKEEIERMVOEAKYKADEVORERSAKNALESYAFNMKS-----A 169
 Db 513 GSSG-LTDSIEIAMVADAEKYRASDMARKAEIENGRAESVCTDIENLDIHKDKLDDQA 571
 QY 170 VEDEGLKGIKSEADKKVLDKQEVISWLDANTLA-EKDEFEHKKRKELEQVCNPIISGLY 228
 Db 572 VED--LRSKITD-----LRFTVAKVYAGDEGITSDDMKKIDIEIQLSLKVPEVY 620
 QY 229 --QGAGGPGPGGGAQCPKG 246
 Db 621 KNQNGNESSGDNDA--PEG 638

RESULT 51
 US-09-252-991A-27358
 ; Sequence 27358, Application US/09252991A
 ; Patent No. 6551795
 ; GENERAL INFORMATION:
 ; APPLICANT: Marc J. Rubenfield et al.
 ; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
 ; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
 ; FILE REFERENCE: 107196.136
 ; CURRENT APPLICATION NUMBER: US/09/252,991A
 ; CURRENT FILING DATE: 1999-02-18
 ; PRIOR APPLICATION NUMBER: US 60/074,788
 ; PRIOR FILING DATE: 1998-02-18
 ; PRIOR APPLICATION NUMBER: US 60/094,190
 ; PRIOR FILING DATE: 1998-07-27
 ; NUMBER OF SEQ ID NOS: 33142
 ; SEQ ID NO 27358
 ; LENGTH: 657
 ; TYPE: PRT
 ; ORGANISM: Pseudomonas aeruginosa
 ; US-09-252-991A-27358
 Query Match 36.6%; Score 480.5; DB 4; Length 657;
 Best Local Similarity 45.1%; Pred. No. 7.4e-36;
 Matches 107; Conservative 41; Mismatches 76; Indels 13; Gaps 5;
 QY 4 NVQDILLDDVAPLSGLGTAGGVTALIKRSTPTKOTQIFTYSDNQGVLIQVYGE 63
 Db 405 DVKDVLLDDVTPSLGIEGTGGVTMLIKRSTPTKASQVFTADNQSAVTHVLQGE 464
 QY 64 RAMTKDNNLLGRFELSGIPAPRGVQIEVTFDIDANGILNVTTATDKSTGKANKITITND 123
 Db 465 RKQAAQNKSLGKFPDLADIPAPRGVQIEVTFDIDANGILNVTTATDKSTGKANKITITND 524
 QY 124 KGRLSKEEIERMVOEAKYKADEVORERSAKNALESYAFNMKSAVEDGLKGIKSEAD 183
 Db 525 SG--LSEDEITQMVVDAEAEEDKFEELAAAKNGDALLVHATKRMITEAGDK---ATAE 580
 QY 184 KKKVLDKQCVISWLDANTLA-EKDEFEHKKRKELEQVCNPIISGLY-----QGAGGP 234
 Db 581 DKATIEK---ALGELEAAVKGDDKAEIEMNALSQAETPLAQKMYAEQAQGGEDAP 634

RESULT 52
 US-09-902-540-12527
 ; Sequence 12527, Application US/09902540
 ; Patent No. 6833447
 ; GENERAL INFORMATION:
 ; APPLICANT: Goldman, Barry S.
 ; APPLICANT: Hinkle, Gregory J.
 ; APPLICANT: Slater, Steven C.
 ; APPLICANT: Wiegand, Roger C.
 ; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
 ; FILE REFERENCE: 38-10(15849)B
 ; CURRENT APPLICATION NUMBER: US/09/902,540

```
US-08-472-534-5
; Sequence 5, Application US/08472534
; Patent No. 5919620
; GENERAL INFORMATION:
; APPLICANT: Hamel, Josee
; APPLICANT: Brodeur, Bernard R
; APPLICANT: Martin, Denis
; TITLE OF INVENTION: HEAT SHOCK PROTEIN HSP72 FROM
; TITLE OF INVENTION: STREPTOCOCCUS PNEUMONIAE
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Neave
; STREET: 1251 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: United States of America
; ZIP: 10020
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/472,534
; FILING DATE:
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Haley Jr. James F
; REGISTRATION NUMBER: 27,794
; REFERENCE/DOCKET NUMBER: Biovac-2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-596-9000
; TELEFAX: 212-596-9090
; TELEX: 14-8367
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 607 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-472-534-5

Query Match 35.9%; Score 472; DB 2; Length 607;
Best Local Similarity 41.6%; Pred. No. 4.1e-35;
Matches 106; Conservative 46; Mismatches 89; Indels 14; Gaps 4;

QY 4 NVQDILLDVAPLSGLTAGVMTALIKRNSTPTKQTQIFTYSNQPQVLIQVYEGE 63
DB 355 DVKDVLLDVTPLSGLIETWGGVFTKIDRNTIPTSKSVFTSTADNQPVDIHLQGE 414

QY 64 RAMTKDNNLLGRFELSGIPAPRGVQIEVTFDIDANGILNVTATDKSTGKANKITIND 123
DB 415 RPAADNKTGRFQLTIDPAAPRGIPQIEVTFDIDKNGIVSVKAKDLGTQKEQTVIQSN 474

QY 124 KGLSKKEIERMVQAEKYKAEDVQERVSNAKNALESYAFNMKSAVEDGLKGIKISEAD 183
DB 475 SG-LTDEEIDRMKDAEANAESDKKKEVDLRNEVDQAFATEKTIKTEGKGFPAERD 533

QY 184 KKXV----LDKQCEVISWLDANTLAEKDFEHRKELEQVCNPIISGLYQGAGGPGPGGF 239
DB 534 AAQAALDDLKQAE-----DNNL-----DDMKAKLEALNEKAQGLAVKLVEQAAAAQAAQE 584

QY 240 GAQPKGGSGSGPTI 254
DB 585 GAEGAQATGNAGDDV 599

RESULT 55
US-09-583-110-4651
; Sequence 4651, Application US/09583110
; Patent No. 6699703
; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al.
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US-09-646-835-1
; CURRENT FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 60/217,883
; PRIOR FILING DATE: 2000-07-10
; NUMBER OF SEQ ID NOS: 16825
; SEQ ID NO 12527
; LENGTH: 569
; TYPE: PRT
; ORGANISM: Myxococcus xanthus
US-09-902-540-12527

Query Match 36.5%; Score 480; DB 4; Length 569;
Best Local Similarity 43.1%; Pred. No. 6.8e-36;
Matches 97; Conservative 55; Mismatches 65; Indels 8; Gaps 4;

QY 5 VQDILLDVAPLSGLTAGVMTALIKRNSTPTKQTQIFTYSNQPQVLIQVYEGE 64
DB 347 VKDVLDDVTPLSGLVETAGVFTKIIDKNTTIPCKKSVFTAVDNPQLSVHVLQGER 406

QY 65 AMTKDNNLLGRFELSGIPAPRGVQIEVTFDIDANGILNVTATDKSTGKANKITINDK 124
DB 407 EMAADNKTGRFELSGIPAPRGVQIEVTFDIDANGILNVTATDKSTGKANKITINDK 466

QY 125 GRLSKEIERMVQAEKYKAEDVQERVSNAKNALESYAFNMKSAVEDGLKGIKISEADK 184
DB 467 G-LSEAEIQAMISDAQSHSDKKKELAE LRNNADGLIYVTEKSLEE--YASILLSEKDR 523

QY 185 KKV---LDKQCEVISWLDANTLAEKDFEHRKELEQVCNPIISG 226
DB 524 EEIKADLERLKEVLNTSDAVAL--KESFORLEGSAYRIADIIYTG 566

RESULT 53
US-09-207-388-13
; Sequence 13, Application US/09207388
; Patent No. 6497880
; GENERAL INFORMATION:
; APPLICANT: Wisniewski, Jan
; TITLE OF INVENTION: HEAT SHOCK GENES AND PROTEINS FROM
; TITLE OF INVENTION: NEISSERIA MENINGITIDIS, CANDIDA GLABRATA AND ASPERGILLUS
; TITLE OF INVENTION: FUMIGATUS
; FILE REFERENCE: 870109.411
; CURRENT APPLICATION NUMBER: US/09/207,388
; CURRENT FILING DATE: 1998-12-08
; NUMBER OF SEQ ID NOS: 102
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 13
; LENGTH: 642
; TYPE: PRT
; ORGANISM: Neisseria meningitidis
US-09-207-388-13

Query Match 36.5%; Score 480; DB 4; Length 642;
Best Local Similarity 50.7%; Pred. No. 8e-36;
Matches 104; Conservative 33; Mismatches 62; Indels 6; Gaps 3;

QY 7 DLLLDVAPLSGLTAGVMTALIKRNSTPTKQTQIFTYSNQPQVLIQVYEGE 66
DB 389 DVLLDDVTPLSGLIETWGGVMTKLIQKNTTPTKASQVFTAEADNQSAVTHVLQGER 448

QY 67 TKDNNLLGRFELSGIPAPRGVQIEVTFDIDANGILNVTATDKSTGKANKITINDKGR 126
DB 449 ASANKSLGQFNLDIAPAPRGVQIEVTFDIDANGILNVTATDKSTGKANKITINDKGR 507

QY 127 LSKEIERMVQAEKYKAEDVQERVSNAKNALESYAFNMKSAVEDGLKGIKISEADKKK 186
DB 508 LGEEIEIERMVQDAEANAESDKKLTAVASRQAELHLSVKSLADYG--DKLDAEKEK 565

QY 187 V---LDKQCEVISWLDANTLAEKDE 208
DB 566 IEAALKEAEAVKGDKAIDAkte 590

RESULT 54
```

;; TITLE OF INVENTION: Nucleic Acid and Amino Acid Sequences Relating to Streptococcus
;; FILE OF INVENTION: Pneumoniae for Diagnostics and Therapeutics
;; REFERENCE: PAT00-07A
;; CURRENT APPLICATION NUMBER: US/09/583,110
;; CURRENT FILING DATE: 2000-05-26
;; PRIOR APPLICATION NUMBER: US 09/107,433
;; PRIOR FILING DATE: 1998-06-30
;; PRIOR APPLICATION NUMBER: US 60/085,131
;; PRIOR FILING DATE: 1998-05-12
;; PRIOR APPLICATION NUMBER: US 60/051,553
;; PRIOR FILING DATE: 1997-07-02
;; NUMBER OF SEQ ID NOS: 5322
;; SEQ ID NO 4651
;; LENGTH: 607
;; TYPE: PRT
;; ORGANISM: Streptococcus pneumoniae
US-09-583-110-4651

Query Match 35.9%; Score 472; DB 4; Length 607;
Best Local Similarity 41.6%; Pred. No. 4.1e-35;
Matches 106; Conservative 46; Mismatches 89; Indels 14; Gaps 4;

QY 4 NVODLLLDVAPLSGLGLETAGGVMTALIKRNTIPTKTQTQFTTYSNQRGVLIQVYGE 63
Db 355 DVKDVLLDVTPLSLGIETMGVFTKLIDRNTIPTSKSVFSTAADNQPAVDLHVLOQE 414
QY 64 RAMTKNNLLGRFELSGIPPAQGVPOIEVTFDIDANGILNVTATDKSTGKANKITIND 123
Db 415 RPAADNKTILGRFQLTIDPAAPRGIPQIEVTFDIDKNGIVSVKAKDLGTQKEQTIVIQSN 474
QY 124 KGRLSKEIERMVOEAKYKAEDVQREVRSNAKNALESYAFNMKSAVEDGLKGIKISEAD 183
Db 475 SG-LTDEEIDRMMDAANAESDKRKEEVDLRNEVDQAIFATEKTIKETEGKGFDAERD 533
QY 184 KKKV----LDKCEVTSWLDANTLAEKDEPEHKKLEQVNCNPIISGLYQAGGPGPGGF 239
Db 534 AAQAALDDLKKAQE-----DNNL----DDMKAKLEALNEKAQGLAVKLVEQAAAAQAAQAE 584
QY 240 GAQPKGGSGSGPTI 254
Db 585 GAEGAQATGNAGDDV 599

RESULT 56
US-09-107-433-3621
; Sequence 3621, Application US/09107433
; Patent No. 6800744
; GENERAL INFORMATION:
; APPLICANT: Lynn A Doucette-Stamm and David Bush
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID
; SEQUENCES RELATING TO STREPTOCOCCUS PNEUMONIAE FOR DIAGNOSTICS
; AND THERAPEUTICS
; NUMBER OF SEQUENCES: 5206
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: GENOME THERAPEUTICS CORPORATION
; STREET: 100 Beaver Street
; CITY: Waltham
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02354
; COMPUTER READABLE FORM:
; MEDIUM TYPE: CD-ROM ISO9660
; COMPUTER: <Unknown>
; OPERATING SYSTEM: <Unknown>
; SOFTWARE: <Unknown>
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/107,433
; FILING DATE: 30-Jun-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/ 085131
; FILING DATE: May 12, 1998
; APPLICATION NUMBER: 60/051553
; FILING DATE: July 2, 1997

;; TITLE OF INVENTION: Nucleic Acid and Amino Acid Sequences Relating to Streptococcus
;; FILE OF INVENTION: Pneumoniae for Diagnostics and Therapeutics
;; REFERENCE: PAT00-07A
;; CURRENT APPLICATION NUMBER: US/09/583,110
;; CURRENT FILING DATE: 2000-05-26
;; PRIOR APPLICATION NUMBER: US 09/107,433
;; PRIOR FILING DATE: 1998-06-30
;; PRIOR APPLICATION NUMBER: US 60/085,131
;; PRIOR FILING DATE: 1998-05-12
;; PRIOR APPLICATION NUMBER: US 60/051,553
;; PRIOR FILING DATE: 1997-07-02
;; NUMBER OF SEQ ID NOS: 5322
;; SEQ ID NO 4651
;; LENGTH: 607
;; TYPE: PRT
;; ORGANISM: Streptococcus pneumoniae
US-09-583-110-4651

Query Match 35.9%; Score 472; DB 4; Length 612;
Best Local Similarity 41.6%; Pred. No. 4.1e-35;
Matches 106; Conservative 46; Mismatches 89; Indels 14; Gaps 4;

QY 4 NVODLLLDVAPLSGLGLETAGGVMTALIKRNTIPTKTQTQFTTYSNQRGVLIQVYGE 63
Db 360 DVKDVLLDVTPLSLGIETMGVFTKLIDRNTIPTSKSVFSTAADNQPAVDLHVLOQE 419
QY 64 RAMTKNNLLGRFELSGIPPAQGVPOIEVTFDIDANGILNVTATDKSTGKANKITIND 123
Db 420 RPAADNKTILGRFQLTIDPAAPRGIPQIEVTFDIDKNGIVSVKAKDLGTQKEQTIVIQSN 479
QY 124 KGRLSKEIERMVOEAKYKAEDVQREVRSNAKNALESYAFNMKSAVEDGLKGIKISEAD 183
Db 480 SG-LTDEEIDRMMDAANAESDKRKEEVDLRNEVDQAIFATEKTIKETEGKGFDAERD 538
QY 184 KKKV----LDKCEVTSWLDANTLAEKDEPEHKKLEQVNCNPIISGLYQAGGPGPGGF 239
Db 539 AAQAALDDLKKAQE-----DNNL----DDMKAKLEALNEKAQGLAVKLVEQAAAAQAAQAE 589
QY 240 GAQPKGGSGSGPTI 254
Db 590 GAEGAQATGNAGDDV 604

RESULT 57
US-08-858-207A-481
; Sequence 481, Application US/08858207A
; Patent No. 6348328
; GENERAL INFORMATION:
; APPLICANT: Black, Michael
; APPLICANT: Hodgson, John
; APPLICANT: Knowles, David
; APPLICANT: Nicholas, Richard
; APPLICANT: Stodola, Robert
; TITLE OF INVENTION: No. 6348328el Compounds
; NUMBER OF SEQUENCES: 552
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SmithKline Beecham Corporation
; STREET: 709 Swedeland Road
; CITY: King of Prussia
; STATE: PA
; COUNTRY: USA
; ZIP: 19406-0939
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FASTSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/858,207A

;; PRIOR FILING DATE: 1998-12-03
;; PRIOR APPLICATION NUMBER: EP 97203783.2
;; PRIOR FILING DATE: 1997-12-03
;; NUMBER OF SEQ ID NOS: 23
;; SOFTWARE: PatentIn version 3.1
;; SEQ ID NO 9
;; LENGTH: 196
;; TYPE: PRT
;; ORGANISM: Homo sapiens
;; FEATURE:
;; NAME/KEY: MISC FEATURE
;; LOCATION: (124)..(124)
;; OTHER INFORMATION: The "Xaa" at position 124 may be any amino acid residue.
;; FEATURE:
;; NAME/KEY: MISC FEATURE
;; LOCATION: (143)..(144)
;; OTHER INFORMATION: The "Xaa" at positions 143-144 may be any amino acid residue.
;; FEATURE:
;; NAME/KEY: MISC FEATURE
;; LOCATION: (192)..(193)
;; OTHER INFORMATION: The "Xaa" at positions 192-193 may be any amino acid residue.
US-09-581-001B-9

Query Match 35.2%; Score 463; DB 4; Length 196;
Best Local Similarity 49.0%; Pred. No. 5.7e-35;
Matches 100; Conservative 32; Mismatches 46; Indels 26; Gaps 4;
QY 32 KRNSTPTKQTQFTTYSNQPGLIOYGERAMTKDNLLGRFELSGIPAPRGVPOI 91
DB 6 RRTVPTKKSQIFSTASDNQPTVIKVGEGPLTKDNHLLGTFDTGIPAPRGVPOI 65
QY 92 EVTFDIDANGILNVTATDKSTGKANKITITNDKRLSKKEIERMVQBAEKYKADEVORE 151
DB 66 EVTFEIDVNGILRTAEDKGTGNKNKITITNDQNRLTPEIERMVNDAEKFAEDKKLXE 125
QY 152 RVSAKNALESYAFNMKSAVEDEG----LKGISEADKKVL---DKQEVISWLDANTLA 204
DB 126 RIDTKGKL--CLFSKESDWWXXKAGRTFLRGDHGKSCRRKMDAGKPPCHRL----- 173
QY 205 EKDBEFHKKRLEQVNCNPIISGLY 228
DB 174 -----QBELEHIVQPIISKLY 190

RESULT 61
US-09-248-796A-19329
;; Sequence 19329, Application US/09248796A
;; Patent No. 6747137
;; GENERAL INFORMATION:
;; APPLICANT: Keith Weinstock et al
;; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN
;; TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
;; FILE REFERENCE: 107196.132
;; CURRENT APPLICATION NUMBER: US/09/248,796A
;; CURRENT FILING DATE: 1999-02-12
;; PRIOR APPLICATION NUMBER: US 60/074,725
;; PRIOR FILING DATE: 1998-02-13
;; PRIOR APPLICATION NUMBER: US 60/096,409
;; PRIOR FILING DATE: 1998-08-13
;; NUMBER OF SEQ ID NOS: 28208
;; SEQ ID NO 19329
;; LENGTH: 187
;; TYPE: PRT
;; ORGANISM: Candida albicans
US-09-248-796A-19329

Query Match 35.2%; Score 462.5; DB 4; Length 187;
Best Local Similarity 59.7%; Pred. No. 5.9e-35;
Matches 95; Conservative 17; Mismatches 46; Indels 1; Gaps 1;
QY 93 VTFDIDANGILNVTATDKSTGKANKITITNDKRLSKKEIERMVQBAEKYKADEVORE 152
DB 17 VSPFIDANGILNVALEKGTGKTQKITITNDKRLSKKEIERMDKMSAEKFKBEDEKEAAR 76

QY 153 VSAKNALESYAFNMKSAVEDEGLKGISEADKKKVLDKQEVISWLDANTLAERKDFEHK 212
DB 77 VQAKNQLESYAVPLKNTINDGEMKDKIGADDKEKLTAKAIDETISWLDASQAASTEVEDK 136
QY 213 RKELEQVNCNPIISGLYQAGGPGPGGFGAGGPKGSGSG 251
DB 137 RKELESVANPIISGAY-GAAGGAPGGAGGFPFRAGGPPGG 174

RESULT 62
US-09-107-532A-6930
;; Sequence 6930, Application US/09107532A
;; Patent No. 6583275
;; GENERAL INFORMATION:
;; APPLICANT: Lynn A Doucette-Stamm and David Bush
;; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
;; CORRESPONDENCE ADDRESS: ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS
;; NUMBER OF SEQUENCES: 7310
;; ADDRESS: 100 Beaver Street
;; CITY: Waltham
;; STATE: Massachusetts
;; COUNTRY: USA
;; ZIP: 02354
;; COMPUTER READABLE FORM: CD/ROM ISO9660
;; MEDIUM TYPE: PC
;; OPERATING SYSTEM: <Unknown>
;; SOFTWARE: ASCII
;; CURRENT APPLICATION DATA:
;; FILING DATE: 30-Jun-1998
;; APPLICATION NUMBER: US/09/107,532A
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: 60/085,598
;; FILING DATE: 14 May 1998
;; APPLICATION NUMBER: 60/051571
;; FILING DATE: July 2, 1997
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Ariniello, Pamela Deneke
;; REGISTRATION NUMBER: 40,489
;; REFERENCE/DOCKET NUMBER: GTC-012
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (781)893-5007
;; TELEFAX: (781)893-8277
;; INFORMATION FOR SEQ ID NO: 6930:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 536 amino acids
;; TYPE: amino acid
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
;; HYPOTHETICAL: YES
;; ORIGINAL SOURCE:
;; ORGANISM: Enterococcus faecium
;; FEATURE:
;; NAME/KEY: misc feature
;; LOCATION: (B) LOCATION 1...536
;; SEQUENCE DESCRIPTION: SEQ ID NO: 6930:
US-09-107-532A-6930

Query Match 35.0%; Score 460.5; DB 4; Length 536;
Best Local Similarity 53.8%; Pred. No. 4e-34;
Matches 91; Conservative 33; Mismatches 44; Indels 1; Gaps 1;
QY 4 NVODLLLDVAPLSGLGTAGGVMALIKRNSTIPTKQTIQFTTYSNQPGLIOYVEGE 63
DB 368 DVKDVLLDVTPLSGLGTAGGVMALIKRNSTIPTKQTIQFTTYSNQPGLIOYVEGE 427
QY 64 RAMTKDNLLGRPELSGIPAPRGVPOIETFDIDANGILNVTATDKSTGKANKITIND 123
DB 428 RPAADNKTGRFQLTDIPAPRGVPOIETFDIDKNGIVNVSAKOLGTQKEQKITIKSS 487

QY 124 KGLSKKEEIERMVQEAKEYAEDVQERVSARKNALESYAFNMKSAVED 172
DB 488 SG-LTDEEIERMVKDAEANAADKARKEEVDLRNDVDALLFSVDKTLKE 535

RESULT 63
US-09-134-000C-3432
; Sequence 3432, Application US/09134000C
; Patent No. 6617156
; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
; TITLE OF INVENTION: ENTEROCOCCUS FAECALIS FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 032796-032
; CURRENT APPLICATION NUMBER: US/09/134,000C
; CURRENT FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: US 60/055,778
; PRIOR FILING DATE: 1997-08-15
; NUMBER OF SEQ ID NOS: 6812
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 3432
; LENGTH: 281
; TYPE: PRT
; ORGANISM: Enterococcus faecalis
; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (54)..(54)
; OTHER INFORMATION: Amino acid 54 is Xaa wherein Xaa = any amino acid.
US-09-134-000C-3432

Query Match 34.5%; Score 453.5; DB 4; Length 281;
Best Local Similarity 53.8%; Pred. No. 7.1e-34;
Matches 91; Conservative 30; Mismatches 47; Indels 1; Gaps 1;

QY 4 NVODLLLDVAPLSGLGTAGGVTALIKNSTIPKQTOIFTYSNQGVLIQVVEGE 63
DB 109 DVKXDVLLDVTPLSLGLETWGGVFTKLIDRNTIPTTSKSQVFTAADNPVDIHVLQGE 168

QY 64 RAMTKNNILGRFELSGIPPAKRGVPOIEVTFDIDANGILNVTATDKSTGKANKITIND 123
DB 169 RPAANDKTLGRFQLTDIPAPKRGVPOIEVTFDIDKNGIWNVRADKLGTOKEQTIIKSS 228

QY 124 KGLSKKEEIERMVQEAKEYAEDVQERVSARKNALESYAFNMKSAVED 172
DB 229 SG-LSDDIEIERMVKDAEANAADKQKKEEVDLRNDADAFLETVDKTLDD 276

RESULT 64
US-09-248-796A-19897
; Sequence 19897, Application US/09248796A
; Patent No. 6747137
; GENERAL INFORMATION:
; APPLICANT: Keith Weinstock et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICANS
; TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.132
; CURRENT APPLICATION NUMBER: US/09/248,796A
; CURRENT FILING DATE: 1999-02-12
; PRIOR APPLICATION NUMBER: US 60/074,725
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: US 60/096,409
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 28208
; SEQ ID NO 19897
; LENGTH: 549
; TYPE: PRT
; ORGANISM: Candida albicans
US-09-248-796A-19897

Query Match 34.1%; Score 448.5; DB 4; Length 549;
Best Local Similarity 41.9%; Pred. No. 5.3e-33;
Matches 90; Conservative 46; Mismatches 76; Indels 3; Gaps 1;


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RESULT 70
US-09-248-796A-17735
; Sequence 17735, Application US/09248796A
; Patent No. 6747137
; GENERAL INFORMATION:
; APPLICANT: Keith Weinstock et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN
; FILE REFERENCE: 107196.132
; CURRENT APPLICATION NUMBER: US/09/248,796A
; PRIOR FILING DATE: 1999-02-12
; PRIOR APPLICATION NUMBER: US 60/074,725
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: US 60/096,409
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 28208
; SEQ ID NO 17735
; LENGTH: 654
; TYPE: PRT
; ORGANISM: Candida albicans
; FEATURE:
; NAME/KEY: UNSURE
; LOCATION: (66)
; OTHER INFORMATION: Identity of amino acid sequences at the above locations are unkno
US-09-248-796A-17735

Query Match 30.4%; Score 400; DB 4; Length 654;
Best Local Similarity 37.9%; Pred. No. 2.1e-28;
Matches 91; Conservative 47; Mismatches 70; Indels 32; Gaps 5;

QY 2 SENVODLLLDVAPLSGLTAGGVTALIKRNSTIPTKTQIFTTYSNQPGLVQVYE 61
DB 407 SQVKNVLLDVLPISGLIETGIGIFPLIPRISAVPIKKEQFSTAVDQGTGVEIGVQ 466
QY 62 GERAMTKDNLLGRFELSGIPAPRGVPOIEVTFDIDANGILNVTATDKST-----G 113
DB 467 GERTLVKDNKHIGQKLSNIPQGPKGTPQIAVSFEIDADGIINVSATDKTPPKDLEHYG 526
QY 114 KANKITINDKGRLSKEEIERMQEAKYKAEDEVOQRRVSANNALESYAFNMKSAAVEDE 173
DB 527 KPNITVAIQVTEVGLTDAVEKMIQESNRNKKKADEKRLYEHASRAEILCTDTETALIQ- 585
QY 174 GLKGISEADKKKVLDCQEVISWLDANTLAEK-DE-----FHKRKELEQVC 220
DB 586 --FGLMEDEKTKIKEY-----ANTIKEMIDEIRSGEKLHHPNILNQKYNEMQKTC 635

RESULT 71
US-09-902-540-15923
; Sequence 15923, Application US/09902540
; Patent No. 6833447
; GENERAL INFORMATION:
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Wiegand, Roger C.
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
; FILE REFERENCE: 38-10(15849)B
; CURRENT APPLICATION NUMBER: US/09/902,540
; CURRENT FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 60/217,883
; PRIOR FILING DATE: 2000-07-10
; NUMBER OF SEQ ID NOS: 16825
; SEQ ID NO 15923
; LENGTH: 298
; TYPE: PRT
; ORGANISM: Myxococcus xanthus
US-09-902-540-15923

Query Match 29.9%; Score 393; DB 4; Length 298;
Best Local Similarity 37.6%; Pred. No. 3e-28;

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Matches 94; Conservative 44; Mismatches 72; Indels 40; Gaps 6;

QY 2 SENVODLLLDVAPLSGLTAGGVTALIKRNSTIPTKTQIFTTYSNQPGLVQVYE 61
DB 62 ADRQDDVLLDVLPISGLIETGIGIFPLIPRISAVPIKKEQFSTAVDQGTGVEIGVQ 121
QY 62 GERAMTKDNLLGRFELSGIPAPRGVPOIEVTFDIDANGILNVTATDKSTKANKITIT 121
DB 122 GERELVEDNRSLARFTLSGIPPAAGMARVEVRFOVDADGILSVSAQEOSTGVSQITVK 181
QY 122 NDKGRLSKEEIERMQEAKYKAEDEVO-----RERVSANNALESYAFNMKSAAVEDEGLK 176
DB 182 PSHG-LTDEIEQMLLDSIDY-AEDDIQARVREQRVDAERVL-----AEADROLGSH 232
QY 177 GKISEADKKKVLDCQEVISWLDANTLAEKDEFEHKKRKELEQVC 220
DB 233 GSLIQEGERATIDSARVRELKMGEDHLKLEAVHALD-----EASRPPIERVM 282
QY 221 NPIISGLYQG 230
DB 283 NQAITQVAVG 292

RESULT 72
US-09-248-796A-17616
; Sequence 17616, Application US/09248796A
; Patent No. 6747137
; GENERAL INFORMATION:
; APPLICANT: Keith Weinstock et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN
; FILE REFERENCE: 107196.132
; CURRENT APPLICATION NUMBER: US/09/248,796A
; PRIOR FILING DATE: 1999-02-12
; PRIOR APPLICATION NUMBER: US 60/074,725
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: US 60/096,409
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 28208
; SEQ ID NO 17616
; LENGTH: 96
; TYPE: PRT
; ORGANISM: Candida albicans
US-09-248-796A-17616

Query Match 28.8%; Score 379; DB 4; Length 96;
Best Local Similarity 80.7%; Pred. No. 1.2e-27;
Matches 71; Conservative 11; Mismatches 6; Indels 0; Gaps 0;

QY 2 SENVODLLLDVAPLSGLTAGGVTALIKRNSTIPTKTQIFTTYSNQPGLVQVYE 61
DB 7 SSKIQELLLDVAPLSGLIETAGGIMTKLIPRNSTIPTKKTSETFTSYADNPQGLVQVFE 66
QY 62 GERAMTKDNLLGRFELSGIPAPRGVP 89
DB 67 GERAQTKDNLLGRFELSGIPAPRGVP 94

RESULT 73
US-09-581-001B-10
; Sequence 10, Application US/09581001B
; Patent No. 6472142
; GENERAL INFORMATION:
; APPLICANT: Danan-Van Oorschot, Mathieu
; APPLICANT: Danan-Van Oorschot, Astrid
; TITLE OF INVENTION: METHODS AND MEANS FOR INDUCING APOPTOSIS BY INTERFERING WITH
; FILE REFERENCE: 2906-4940US
; CURRENT APPLICATION NUMBER: US/09/581,001B
; CURRENT FILING DATE: 2000-07-24
; PRIOR APPLICATION NUMBER: PCT/NL98/00688
; PRIOR FILING DATE: 1998-12-03
; PRIOR APPLICATION NUMBER: EP 97203783.2

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; PRIOR FILING DATE: 1997-12-03
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 10
; LENGTH: 192
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (146)..(146)
; OTHER INFORMATION: The "Xaa" at position 146 may be any amino acid residue.
; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (153)..(153)
; OTHER INFORMATION: The "Xaa" at position 153 may be any amino acid residue.
; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (156)..(156)
; OTHER INFORMATION: The "Xaa" at position 156 may be any amino acid residue.
; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (158)..(158)
; OTHER INFORMATION: The "Xaa" at position 158 may be any amino acid residue.
; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (164)..(164)
; OTHER INFORMATION: The "Xaa" at position 164 may be any amino acid residue.
; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (187)..(189)
; OTHER INFORMATION: The "Xaa" at positions 187-189 may be any amino acid residue.
; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (192)..(192)
; OTHER INFORMATION: The "Xaa" at position 192 may be any amino acid residue.
; US-09-581-0018-10

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RESULT 74
US-09-252-991A-22906
; Sequence 22906, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 22906
; LENGTH: 623
; TYPE: prt
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-22906
Query Match 27.0%; Score 354.5; DB 4; Length 623;

Best Local Similarity 38.4%; Pred. No. 3.1e-24;
Matches 86; Conservative 43; Mismatches 70; Indels 25; Gaps 5;

QY 6 QDLLLLDVAPLSGLETAGGVNTALIKENSTIPTKQTQIFTTYSNQPQGLIQVVEGERA 65
DB :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
388 BEULLLDVIPLSGLETMGGLMEKVIPNTTIPVARAQEFTTYKDGTAMMIHVLQGERE 447
QY 66 MTXNNLLGRPELGGIPAPRGVPQIEVTFDIDANGILNVATDKSTGKANKITITNDKG 125
DB LVKDCRLARFELRGIPIPPWAGAARIKIRVTQVDADGLLGVSARELSSGVEASIQVKPSYG 507
QY 126 RLSKEETRMVQAEKYKAEDVOR---ERVSAKNALESYAFNMKSVADEGLKGKISE 181
DB |:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
508 -LTDGETARMLKOSDFVAGDDKAARLEQQVEAQRLLAEA-----VQSALDVDG----- 555
QY 182 ADKKLVLDKCOEVISWLDTANTLAE-----KDEFPHKRKELEV 219
DB ::|||:::|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
556 ---ERLLDEERLAIAQMDFLRELAGGSDTAAIENIKRLSQV 596

RESULT 75
US-09-540-236-3242
; Sequence 3242, Application US/09540236
; Patent No. 6673910
; GENERAL INFORMATION:
; APPLICANT: Gary L. Breton et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO MORAXELLA CATARRI
; TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 2709.2005-001
; CURRENT APPLICATION NUMBER: US/09/540,236
; PRIORITY FILING DATE: 2000-04-04
; NUMBER OF SEQ ID NOS: 3840
; SEQ ID NO 3242
; LENGTH: 622
; TYPE: PRT
; ORGANISM: M.catarrhalis
US-09-540-236-3242

Query Match 25.4%; Score 334; DB 4; Length 622;
Best Local Similarity 36.7%; Pred. No. 2.4e-22;
Matches 83; Conservative 48; Mismatches 73; Indels 22; Gaps 5;

QY 2 SENVDILLDLVAPLSGLETAGGVNTALIKENSTIPTKQTQIFTTYSNQPQGLIQVYE 61
DB :::|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
386 NQSNETLLLDVPLSLGIETMGLVEIIPRNPTRPVRQVFTTHQDGOTGMIIQVVQ 445
QY 62 GERAMTKDNLLGRFELSGIPPARGVPQIEVTPDIDANGILNVATDKSTGKANKITIT 121
DB |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
446 GERTVANCRLARFELHGIPMKAGLARIEVTVYDAIDANGQLTVSARETTDIISOIQVS 505
QY 122 NDKRLSKREETRMVQAEKYKAED-----EVQREVSARKNALESYAFNMKSVA 170
DB |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
506 PSYG-LSEEQEQLLAGFIHAEDKAARMLIETKVEAORELLALQSALDEFT-DLLSDE 563
QY 171 EDEGLKGKIS-----EADKKKVL D----KCOEVISWLDTANTLAEKD 207
DB |:|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
564 EQTNLRHHMQVADSNTLNTDDKAAIDEAIKALKVSHDFASFVIMDKN 609

RESULT 76
US-09-489-039A-11583
; Sequence 11583, Application US/09489039A
; Patent No. 6610836
; GENERAL INFORMATION:
; APPLICANT: Gary Breton et. al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLBBSIELLA
; TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 2709.2004001
; CURRENT APPLICATION NUMBER: US/09/489,039A
; PRIORITY FILING DATE: 2000-01-27
; PRIOR APPLICATION NUMBER: US 60/117,747
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 14342

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; SEQ ID NO 11583
; LENGTH: 621
; TYPE: PRF
; ORGANISM: Klebsiella pneumoniae
US-09-489-039A-11583

Query Match      25.3%; Score 333; DB 4; Length 621;
Best Local Similarity 38.1%; Pred. No. 3e-22;
Matches 85; Conservative 35; Mismatches 83; Indels 20; Gaps 6;

QY 7 DIALLDVAPLSGLETAGGVTALIKRNSIPTKQIPTTYSNDQPGVLIQVVEGRAM 66
Db 390 ELLLDVPLSLGLETGGVLEKVPINPTTIPVARAQKFTFKDGGTAMSHVMQGEREL 449
QY 67 TKDNNLLGRFELSGIPAPRGVPIEFTDANGILNVTATDKSTGKANKITITNDKGR 126
Db 450 VQCRSLARFALGIPALPAGGAHIRTFFQVDADGLLSVTAMEKSTGVEASIQKPSYG- 508
QY 127 LSKEIERMVQEAKEYKAEDVQ-----RERVSAKNALESYAFNMK-----SAVEDGL 175
Db 509 LTDGEIATMIKDSMSY-AEQDIQARMLAEQKVEARVLESLSALAADAALLSAAERQAI 567
QY 176 KG---KISEADKKVLDKQCEVISWLDANTLAEKDFEHKKE 215
Db 568 DAAAEQVRAAAGDDADAIEAKITNDTQ-----QEFARMD 606

RESULT 77
US-09-543-681A-7673
; Sequence 7673, Application US/09543681A
; Patent No. 6605709
; GENERAL INFORMATION:
; APPLICANT: GARY BRETON
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABILIS
; FILE REFERENCE: 2709.1002-001
; CURRENT APPLICATION NUMBER: US/09/543,681A
; PRIOR FILING DATE: 2000-04-05
; PRIOR APPLICATION NUMBER: US 60/128,706
; PRIOR FILING DATE: 1999-04-09
; NUMBER OF SEQ ID NOS: 8344
; SEQ ID NO 7673
; LENGTH: 623
; TYPE: PRF
; ORGANISM: Proteus mirabilis
US-09-543-681A-7673

Query Match      25.0%; Score 328; DB 4; Length 623;
Best Local Similarity 36.5%; Pred. No. 8.7e-22;
Matches 81; Conservative 39; Mismatches 76; Indels 26; Gaps 6;

QY 7 DIALLDVAPLSGLETAGGVTALIKRNSIPTKQIPTTYSNDQPGVLIQVVEGRAM 66
Db 392 EMLLDVPLSLGLETGGVLEKVPINPTTIPVARAQKFTFKDGGTAMSHVMQGEREM 451
QY 67 TKDNNLLGRFELSGIPAPRGVPIEFTDANGILNVTATDKSTGKANKITITNDKGR 126
Db 452 VSDCRSLARTFLAGIPPPAGGAHIRTFFQVDADGLLSVSAMEKSTGVEASVQVKPSYG- 510
QY 127 LSKEIERMVQEAKEYKAED-----EVORERVSAKNALESYAFNMKSAVEDGLKGISEA 182
Db 511 LSDTEIANITQSSMENAKEDLQARRLAEQKVEARVLES-----LTAALQED---AHLLTE 563
QY 183 DKKKVLDKQCEVISWLDANTLAEKDE-----FEHKKELEQ 218
Db 564 DEXTAIDNV-----VDTLIESVGTDPVAIENAIKQLDK 597

RESULT 78
US-09-328-352-7730
; Sequence 7730, Application US/09328352
; Patent No. 6562958
; GENERAL INFORMATION:
; APPLICANT: Gary L. Breton et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
; FILE REFERENCE: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS
; CURRENT APPLICATION NUMBER: US/09/328,352
; CURRENT FILING DATE: 1999-06-04
; SEQ ID NO 7730
; LENGTH: 620
; TYPE: PRF
; ORGANISM: Acinetobacter baumannii
US-09-328-352-7730

Query Match      24.3%; Score 319.5; DB 4; Length 620;
Best Local Similarity 37.7%; Pred. No. 5.3e-21;
Matches 81; Conservative 37; Mismatches 78; Indels 19; Gaps 4;

QY 4 NVQD-LLLLDVAPLSGLETAGGVTALIKRNSIPTKQIPTTYSNDQPGVLIQVVEG 62
Db 381 NSQDGLLLDVTPLSLGLETGGVLEKVPINPTTIPVARAQKFTFKDGGTAMSHVMQ 440
QY 63 ERMTKXNNLLGRFELSGIPAPRGVPIEFTDANGILNVTATDKSTGKANKITITN 122
Db 441 ERDLVEHCRSLGRFVLHGIPPTAGQARIEVTPQVDADGLLTVSAREATSGVQAHIDIKP 500
QY 123 DKGRLSKEIERMVQEAKEYKAED-----VORERVSAKNALESYAFNMKSAVE----- 171
Db 501 SYG-LSEADTERLLISGFQHAEDKNLRLHETKVEARELEALEQALKVDADLLDEKQL 559
QY 172 -----DEGLKGIKISADKKVLDKQCEVISWLD 200
Db 560 EALNSAKESLKAQLEGSDIQAIEQAVQQLKVHSDA 594

RESULT 79
US-09-207-388-12
; Sequence 12, Application US/09207388
; Patent No. 6497880
; GENERAL INFORMATION:
; APPLICANT: Wisniewski, Jan
; TITLE OF INVENTION: HEAT SHOCK GENES AND PROTEINS FROM
; TITLE OF INVENTION: NEISSERIA MENINGITIDIS, CANDIDA GLABRATA AND ASPERGILLUS
; FILE REFERENCE: 870109.411
; CURRENT APPLICATION NUMBER: US/09/207,388
; CURRENT FILING DATE: 1998-12-08
; NUMBER OF SEQ ID NOS: 102
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 12
; LENGTH: 415
; TYPE: PRF
; ORGANISM: Neisseria meningitidis
US-09-207-388-12

Query Match      21.7%; Score 285; DB 4; Length 415;
Best Local Similarity 62.9%; Pred. No. 4.7e-18;
Matches 56; Conservative 11; Mismatches 22; Indels 0; Gaps 0;

QY 7 DIALLDVAPLSGLETAGGVTALIKRNSIPTKQIPTTYSNDQPGVLIQVVEGRAM 66
Db 327 DVLLLDVPLSLGLETGGVMTKLQKNTIPTKASQVFSTAEADNQSATVTHVQGER 386
QY 67 TKDNNLLGRFELSGIPAPRGVPIEFTF 95
Db 387 ASANKSLGQFNLDIAPAPRGMPQIEVTF 415

RESULT 80
US-09-556-877-301
; Sequence 301, Application US/09556877
; Patent No. 6432916
; GENERAL INFORMATION:
; APPLICANT: Probst, Peter
```

APPLICANT: Bhatia, Ajay
APPLICANT: Skeiky, Yasir
APPLICANT: Fling, Steve
APPLICANT: Maisonneuve, Jeff
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT AND
TITLE OF INVENTION: DIAGNOSIS OF CHLAMYDIAL INFECTION
FILE REFERENCE: 210121.469C5
CURRENT APPLICATION NUMBER: US/09/556,877
CURRENT FILING DATE: 2000-04-19
NUMBER OF SEQ ID NOS: 305
SOFTWARE: FastSeq for Windows Version 3.0/4.0
SEQ ID NO 301
LENGTH: 183
TYPE: PR
ORGANISM: Chlamydia
US-09-556-877-301

Query Match 19.3%; Score 254; DB 4; Length 183;
Best Local Similarity 36.6%; Pred. No. 1.1e-15;
Matches 68; Conservative 32; Mismatches 64; Indels 22; Gaps 7;

QY 81 IPPAPRGVPOIEVTFDIDANGILNVATDKSTGKANKITITNDKGRLSKEEIERMVQAE 140
DB 1 IPPAPRGHPQIEVTFDIDANGILHVSADKASGREGQKIRIEASSG-LKEDEIQOIMIRDAE 59

QY 141 KYKAEDVQRRVSNAKNALESYAFNMKSAVEDGLKGKISEADKKV---LDRKQEVISW 197
DB 60 LHKEEDQKREASDVKNEDGMIFRAEKAVKD--YHDKIPAEVLKTEIEHIEKVRQAIAK- 116

QY 198 LDANTLAEK---DEFEHKREL-----EQVCNPIISGLYQAGGPG-----PGGFGAQ 242
DB 117 EDASTTAIKAAASDELSTRMOKIGEAMQASASAAASANAQGGPNINSEDLKKHSFSTR 176

QY 243 GPKGGS 248
DB 177 PPAGGS 182

RESULT 81
US-09-620-412C-301
Sequence 301, Application US/09620412C
Patent No. 6448234
GENERAL INFORMATION:
APPLICANT: Steven P. Fling
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT AND
TITLE OF INVENTION: DIAGNOSIS OF CHLAMYDIAL INFECTION
FILE REFERENCE: 210121.469C7
CURRENT APPLICATION NUMBER: US/09/620,412C
CURRENT FILING DATE: 2000-07-20
NUMBER OF SEQ ID NOS: 363
SOFTWARE: FastSeq for Windows Version 3.0/4.0
SEQ ID NO 301
LENGTH: 183
TYPE: PR
ORGANISM: Chlamydia
US-09-620-412C-301

Query Match 19.3%; Score 254; DB 4; Length 183;
Best Local Similarity 36.6%; Pred. No. 1.1e-15;
Matches 68; Conservative 32; Mismatches 64; Indels 22; Gaps 7;

QY 81 IPPAPRGVPOIEVTFDIDANGILNVATDKSTGKANKITITNDKGRLSKEEIERMVQAE 140
DB 1 IPPAPRGHPQIEVTFDIDANGILHVSADKASGREGQKIRIEASSG-LKEDEIQOIMIRDAE 59

QY 141 KYKAEDVQRRVSNAKNALESYAFNMKSAVEDGLKGKISEADKKV---LDRKQEVISW 197
DB 60 LHKEEDQKREASDVKNEDGMIFRAEKAVKD--YHDKIPAEVLKTEIEHIEKVRQAIAK- 116

QY 198 LDANTLAEK---DEFEHKREL-----EQVCNPIISGLYQAGGPG-----PGGFGAQ 242
DB 117 EDASTTAIKAAASDELSTRMOKIGEAMQASASAAASANAQGGPNINSEDLKKHSFSTR 176

QY 243 GPKGGS 248
DB 177 PPAGGS 182

RESULT 82
US-09-598-419-301
Sequence 301, Application US/09598419
Patent No. 6565856
GENERAL INFORMATION:
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Scholler, John
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR TREATMENT AND
TITLE OF INVENTION: DIAGNOSIS OF CHLAMYDIAL INFECTION
FILE REFERENCE: 210121.469C6
CURRENT APPLICATION NUMBER: US/09/598,419
CURRENT FILING DATE: 2000-06-20
NUMBER OF SEQ ID NOS: 357
SOFTWARE: FastSeq for Windows Version 3.0/4.0
SEQ ID NO 301
LENGTH: 183
TYPE: PR
ORGANISM: Chlamydia
US-09-598-419-301

Query Match 19.3%; Score 254; DB 4; Length 183;
Best Local Similarity 36.6%; Pred. No. 1.1e-15;
Matches 68; Conservative 32; Mismatches 64; Indels 22; Gaps 7;

QY 81 IPPAPRGVPOIEVTFDIDANGILNVATDKSTGKANKITITNDKGRLSKEEIERMVQAE 140
DB 1 IPPAPRGHPQIEVTFDIDANGILHVSADKASGREGQKIRIEASSG-LKEDEIQOIMIRDAE 59

QY 141 KYKAEDVQRRVSNAKNALESYAFNMKSAVEDGLKGKISEADKKV---LDRKQEVISW 197
DB 60 LHKEEDQKREASDVKNEDGMIFRAEKAVKD--YHDKIPAEVLKTEIEHIEKVRQAIAK- 116

QY 198 LDANTLAEK---DEFEHKREL-----EQVCNPIISGLYQAGGPG-----PGGFGAQ 242
DB 117 EDASTTAIKAAASDELSTRMOKIGEAMQASASAAASANAQGGPNINSEDLKKHSFSTR 176

QY 243 GPKGGS 248
DB 177 PPAGGS 182

RESULT 83
US-09-183-861-49
Sequence 49, Application US/09183861
Patent No. 6365165
GENERAL INFORMATION:
APPLICANT: Reed, Steven G.
APPLICANT: Campos-Neto, Antonio
APPLICANT: Webb, John R.
APPLICANT: Dillon, Davin C.
APPLICANT: Skeiky, Yasir A.W.
TITLE OF INVENTION: LEISHMANIA ANTIGENS FOR USE IN THE THERAPY AND
NUMBER OF SEQUENCES: 87
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
STATE: Washington
COUNTRY: USA
ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/183,861
FILING DATE:

```
/
/ CLASSIFICATION:
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 09/022,765
/ FILING DATE: 12-FEB-1998
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Maki, David J.
/ REGISTRATION NUMBER: 31,392
/ REFERENCE/DOCKET NUMBER: 210121.420C3
/ TELEPHONE: (206) 622-4900
/ TELEFAX: (206) 682-6031
/ INFORMATION FOR SEQ ID NO: 49:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 136 amino acids
/ TYPE: amino acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: peptide
/ ORIGINAL SOURCE:
/ ORGANISM: Leishmania chagasi
/
/ US-09-183-861-49
/
/ Query Match 18.9%; Score 248.5; DB 3; Length 136;
/ Best Local Similarity 44.6%; Pred. No. 2.3e-15;
/ Matches 50; Conservative 28; Mismatches 33; Indels 1; Gaps 1;
/
/ QY 125 GRLSKEIERMVQEAQKAEDEVQRRVSAKNALSYAFNMKSAYVEDEGLKG-KISEAD 183
/ Db 1 GRLSKEIERMVQEAQKAEDEVQRRVSAKNALSYAFNMKSAYVEDEGLKG-KISEAD 60
/
/ QY 184 KKKVLDKQCEVISWLDANTLAEKDEFEHKKRKELEQVCNPIISGLYQAGGPG 235
/ Db 61 KKAIEBAVKDALDFVHENPNADREFEAARTKLSQVNTNPIIQKYQGAAGSG 112
/
/ RESULT 84
/ US-09-022-765-49
/ Sequence 49, Application US/09022765
/ Patent No. 6375955
/ GENERAL INFORMATION:
/ APPLICANT: Reed, Steven G.
/ APPLICANT: Campos-Neto, Antonio
/ APPLICANT: Webb, John R.
/ APPLICANT: Dillon, Davin C.
/ APPLICANT: Skeiky, Yasir A.W.
/ TITLE OF INVENTION: LEISHMANIA ANTIGENS FOR USE IN THE THERAPY AND
/ NUMBER OF SEQUENCES: 87
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: SEED AND BERRY LLP
/ STREET: 6300 Columbia Center, 701 Fifth Avenue
/ CITY: Seattle
/ STATE: Washington
/ COUNTRY: USA
/ ZIP: 98104-7092
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: PatentIn Release #1.0, Version #1.30
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/09/022,765
/ FILING DATE: 12-FEB-1998
/ CLASSIFICATION:
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Maki, David J.
/ REGISTRATION NUMBER: 31,392
/ REFERENCE/DOCKET NUMBER: 210121.420C3
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (206) 622-4900
/ TELEFAX: (206) 682-6031
/ INFORMATION FOR SEQ ID NO: 49:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 136 amino acids
/ TYPE: amino acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: peptide
/ ORIGINAL SOURCE:
/ ORGANISM: Leishmania chagasi
/
/ US-09-183-861-49
/
/ Query Match 18.9%; Score 248.5; DB 3; Length 136;
/ Best Local Similarity 44.6%; Pred. No. 2.3e-15;
/ Matches 50; Conservative 28; Mismatches 33; Indels 1; Gaps 1;
/
/ QY 125 GRLSKEIERMVQEAQKAEDEVQRRVSAKNALSYAFNMKSAYVEDEGLKG-KISEAD 183
/ Db 1 GRLSKEIERMVQEAQKAEDEVQRRVSAKNALSYAFNMKSAYVEDEGLKG-KISEAD 60
/
/ QY 184 KKKVLDKQCEVISWLDANTLAEKDEFEHKKRKELEQVCNPIISGLYQAGGPG 235
/ Db 61 KKAIEBAVKDALDFVHENPNADREFEAARTKLSQVNTNPIIQKYQGAAGSG 112
/
/ RESULT 85
/ US-09-551-974A-49
/ Sequence 49, Application US/09551974A
/ Patent No. 6500437
/ GENERAL INFORMATION:
/ APPLICANT: Reed, Steven G.
/ APPLICANT: Campos-Neto, Antonio
/ APPLICANT: Webb, John R.
/ APPLICANT: Dillon, Davin C.
/ APPLICANT: Skeiky, Yasir A.W.
/ TITLE OF INVENTION: LEISHMANIA ANTIGENS FOR USE IN THE
/ TITLE OF INVENTION: THERAPY AND DIAGNOSIS OF LEISHMANIASIS
/ FILE REFERENCE: 210121.420C5
/ CURRENT APPLICATION NUMBER: US/09/551,974A
/ CURRENT FILING DATE: 2000-04-14
/ NUMBER OF SEQ ID NOS: 101
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 49
/ LENGTH: 136
/ TYPE: PRT
/ ORGANISM: Leishmania chagasi
/
/ US-09-551-974A-49
/
/ Query Match 18.9%; Score 248.5; DB 4; Length 136;
/ Best Local Similarity 44.6%; Pred. No. 2.3e-15;
/ Matches 50; Conservative 28; Mismatches 33; Indels 1; Gaps 1;
/
/ QY 125 GRLSKEIERMVQEAQKAEDEVQRRVSAKNALSYAFNMKSAYVEDEGLKG-KISEAD 183
/ Db 1 GRLSKEIERMVQEAQKAEDEVQRRVSAKNALSYAFNMKSAYVEDEGLKG-KISEAD 60
/
/ QY 184 KKKVLDKQCEVISWLDANTLAEKDEFEHKKRKELEQVCNPIISGLYQAGGPG 235
/ Db 61 KKAIEBAVKDALDFVHENPNADREFEAARTKLSQVNTNPIIQKYQGAAGSG 112
/
/ RESULT 86
/ US-09-565-501A-49
/ Sequence 49, Application US/09565501A
/ Patent No. 6607731
/ GENERAL INFORMATION:
/ APPLICANT: Reed, Steven G.
/ APPLICANT: Campos-Neto, Antonio
/ APPLICANT: Webb, John R.
/ APPLICANT: Dillon, Davin C.
/ APPLICANT: Skeiky, Yasir A.W.
/ APPLICANT: Bhatia, Ajay
/ APPLICANT: Coler, Rhea
/ APPLICANT: Peter, Probst
/ TITLE OF INVENTION: LEISHMANIA ANTIGENS FOR USE IN THE
/ TITLE OF INVENTION: THERAPY AND DIAGNOSIS OF LEISHMANIASIS
/ FILE REFERENCE: 210121.420C6
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/
/ TYPE: amino acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: peptide
/ ORIGINAL SOURCE:
/ ORGANISM: Leishmania chagasi
/
/ US-09-022-765-49
/
/ Query Match 18.9%; Score 248.5; DB 3; Length 136;
/ Best Local Similarity 44.6%; Pred. No. 2.3e-15;
/ Matches 50; Conservative 28; Mismatches 33; Indels 1; Gaps 1;
/
/ QY 125 GRLSKEIERMVQEAQKAEDEVQRRVSAKNALSYAFNMKSAYVEDEGLKG-KISEAD 183
/ Db 1 GRLSKEIERMVQEAQKAEDEVQRRVSAKNALSYAFNMKSAYVEDEGLKG-KISEAD 60
/
/ QY 184 KKKVLDKQCEVISWLDANTLAEKDEFEHKKRKELEQVCNPIISGLYQAGGPG 235
/ Db 61 KKAIEBAVKDALDFVHENPNADREFEAARTKLSQVNTNPIIQKYQGAAGSG 112
/
/ RESULT 85
/ US-09-551-974A-49
/ Sequence 49, Application US/09551974A
/ Patent No. 6500437
/ GENERAL INFORMATION:
/ APPLICANT: Reed, Steven G.
/ APPLICANT: Campos-Neto, Antonio
/ APPLICANT: Webb, John R.
/ APPLICANT: Dillon, Davin C.
/ APPLICANT: Skeiky, Yasir A.W.
/ TITLE OF INVENTION: LEISHMANIA ANTIGENS FOR USE IN THE
/ TITLE OF INVENTION: THERAPY AND DIAGNOSIS OF LEISHMANIASIS
/ FILE REFERENCE: 210121.420C5
/ CURRENT APPLICATION NUMBER: US/09/551,974A
/ CURRENT FILING DATE: 2000-04-14
/ NUMBER OF SEQ ID NOS: 101
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 49
/ LENGTH: 136
/ TYPE: PRT
/ ORGANISM: Leishmania chagasi
/
/ US-09-551-974A-49
/
/ Query Match 18.9%; Score 248.5; DB 4; Length 136;
/ Best Local Similarity 44.6%; Pred. No. 2.3e-15;
/ Matches 50; Conservative 28; Mismatches 33; Indels 1; Gaps 1;
/
/ QY 125 GRLSKEIERMVQEAQKAEDEVQRRVSAKNALSYAFNMKSAYVEDEGLKG-KISEAD 183
/ Db 1 GRLSKEIERMVQEAQKAEDEVQRRVSAKNALSYAFNMKSAYVEDEGLKG-KISEAD 60
/
/ QY 184 KKKVLDKQCEVISWLDANTLAEKDEFEHKKRKELEQVCNPIISGLYQAGGPG 235
/ Db 61 KKAIEBAVKDALDFVHENPNADREFEAARTKLSQVNTNPIIQKYQGAAGSG 112
/
/ RESULT 86
/ US-09-565-501A-49
/ Sequence 49, Application US/09565501A
/ Patent No. 6607731
/ GENERAL INFORMATION:
/ APPLICANT: Reed, Steven G.
/ APPLICANT: Campos-Neto, Antonio
/ APPLICANT: Webb, John R.
/ APPLICANT: Dillon, Davin C.
/ APPLICANT: Skeiky, Yasir A.W.
/ APPLICANT: Bhatia, Ajay
/ APPLICANT: Coler, Rhea
/ APPLICANT: Peter, Probst
/ TITLE OF INVENTION: LEISHMANIA ANTIGENS FOR USE IN THE
/ TITLE OF INVENTION: THERAPY AND DIAGNOSIS OF LEISHMANIASIS
/ FILE REFERENCE: 210121.420C6
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; CURRENT APPLICATION NUMBER: US/09/565,501A
; CURRENT FILING DATE: 2000-05-05
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 49
; LENGTH: 136
; TYPE: PR1
; ORGANISM: Leishmania chagasi
US-09-565-501A-49

Query Match 18.9%; Score 248.5; DB 4; Length 136;
Best Local Similarity 44.6%; Pred. No. 2.3e-15;
Matches 50; Conservative 28; Mismatches 33; Indels 1; Gaps 1;

Qy 125 GRLSKEEIERMVQEAERKKAEDVQERVSANNALESYAFNMKSAVEDEGLKG-KISEAD 183
Db 1 GRLSKEEIERMVREAAEFEDDKRVREVEAKNSLESIAYSLRNQINDKDKLGDKLAADD 60

Qy 184 KKKVLDKQCEVSWLDANTLAKEDEPHKREKLEQVNCNPIISGLYQAGAGPG 235
Db 61 KKAIEAVKDALDFVHENPNADREFEAARTKLSQVTPNPIIQKVYQGAAGSG 112

RESULT 87
US-09-639-206A-49
; Sequence 49, Application US/09639206A
; Patent No. 661337
; GENERAL INFORMATION:
; APPLICANT: Reed, Steven G.
; APPLICANT: Campos-Neto, Antonio
; APPLICANT: Webb, John R.
; APPLICANT: Dillion, Davin C.
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Bhatia, Ajay
; APPLICANT: Coler, Rhea
; APPLICANT: Probst, Peter
; TITLE OF INVENTION: LEISHMANIA ANTIGENS FOR USE IN THE
; TITLE OF INVENTION: THERAPY AND DIAGNOSIS OF LEISHMANIASIS
; FILE REFERENCE: 210121.420C7
; CURRENT APPLICATION NUMBER: US/09/639,206A
; CURRENT FILING DATE: 2000-08-14
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 49
; LENGTH: 136
; TYPE: PR1
; ORGANISM: Leishmania chagasi
US-09-639-206A-49

Query Match 18.9%; Score 248.5; DB 4; Length 136;
Best Local Similarity 44.6%; Pred. No. 2.3e-15;
Matches 50; Conservative 28; Mismatches 33; Indels 1; Gaps 1;

Qy 125 GRLSKEEIERMVQEAERKKAEDVQERVSANNALESYAFNMKSAVEDEGLKG-KISEAD 183
Db 1 GRLSKEEIERMVREAAEFEDDKRVREVEAKNSLESIAYSLRNQINDKDKLGDKLAADD 60

Qy 184 KKKVLDKQCEVSWLDANTLAKEDEPHKREKLEQVNCNPIISGLYQAGAGPG 235
Db 61 KKAIEAVKDALDFVHENPNADREFEAARTKLSQVTPNPIIQKVYQGAAGSG 112

RESULT 88
US-09-874-923-49
; Sequence 49, Application US/09874923
; Patent No. 6638517
; GENERAL INFORMATION:
; APPLICANT: Reed, Steven G.
; APPLICANT: Campos-Neto, Antonio
; APPLICANT: Webb, John R.
; APPLICANT: Dillion, Davin C.
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Bhatia, Ajay
US-09-874-923-49

Query Match 18.9%; Score 248.5; DB 4; Length 136;
Best Local Similarity 44.6%; Pred. No. 2.3e-15;
Matches 50; Conservative 28; Mismatches 33; Indels 1; Gaps 1;

Qy 125 GRLSKEEIERMVQEAERKKAEDVQERVSANNALESYAFNMKSAVEDEGLKG-KISEAD 183
Db 1 GRLSKEEIERMVREAAEFEDDKRVREVEAKNSLESIAYSLRNQINDKDKLGDKLAADD 60

Qy 184 KKKVLDKQCEVSWLDANTLAKEDEPHKREKLEQVNCNPIISGLYQAGAGPG 235
Db 61 KKAIEAVKDALDFVHENPNADREFEAARTKLSQVTPNPIIQKVYQGAAGSG 112

RESULT 89
US-09-902-540-15138
; Sequence 15138, Application US/09902540
; Patent No. 6833447
; GENERAL INFORMATION:
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Wiegand, Roger C.
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
; FILE REFERENCE: 38-10(15849)B
; CURRENT APPLICATION NUMBER: US/09/902,540
; CURRENT FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 60/217,883
; PRIOR FILING DATE: 2000-07-10
; NUMBER OF SEQ ID NOS: 16825
; SEQ ID NO 15138
; LENGTH: 535
; TYPE: PR1
; ORGANISM: Myxococcus xanthus
US-09-902-540-15138

Query Match 17.8%; Score 234.5; DB 4; Length 535;
Best Local Similarity 38.3%; Pred. No. 3.1e-13;
Matches 49; Conservative 31; Mismatches 47; Indels 1; Gaps 1;

Qy 10 LLDVAPLSLGLTAGGVTALIKRNSTIPTKQTQIFTYSNQPGVLIQVYEGEAMTKD 69
Db 389 LVDVTPLSLRIGTVGGYTEKIIDKNTPTPIDRSKFTTTSRDQEKVKIRVYOGESNRAD 448

Qy 70 NNLLGAFELSGIPPPAPRGVPQIEVTFDIDANGILNVTATDKSTGKANKITTTNDKGRLSK 129
Db 449 CEMLGFEFAGFRIGYRGEVKIEVTFEINTDGLVHVSACDTATGQKTSITSLSSG-MSE 507

RESULT 90
US-09-902-540-14235
; Sequence 14235, Application US/09902540
; Patent No. 6833447
; GENERAL INFORMATION:

```

```

; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Wiegand, Roger C.
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
; FILE REFERENCE: 38-10(15849)B
; CURRENT APPLICATION NUMBER: US/09/902,540
; CURRENT FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 60/217,883
; PRIOR FILING DATE: 2000-07-10
; NUMBER OF SEQ ID NOS: 16825
; SEQ ID NO 14235
; LENGTH: 506
; TYPE: PRT
; ORGANISM: Myxococcus xanthus
US-09-540-14235

Query Match      17.2%; Score 226.5; DB 4; Length 506;
Best Local Similarity 35.5%; Pred. No. 1.6e-12;
Matches 44; Conservative 29; Mismatches 46; Indels 5; Gaps 1;

QY 2 SENVQD-----LLLDVAPLSGLGTAGVMTALIKRNSTIPTKOTQIFTTYSNQPGLV 56
Db 378 AHSLODNTNRIQLLDVIPAIGLEKAGAFHVFPRNASIPNAKQLLATISMDNQTELA 437

QY 57 IQVYGERAMTKNNLLGRFELSGLPAPRGVPGQIEVTFDIDANGILNVTATDKSTGKAN 116
Db 438 VRIFQGNELVARNDMLGETFSGIQPRAGPALVEITFDANVEGILTWEARDPVSGREM 497

QY 117 KITI 120
Db 498 KTVV 501

RESULT 91
US-09-581-001B-6
; Sequence 6, Application US/09581001B
; Patent No. 6472142
; GENERAL INFORMATION:
; APPLICANT: Danan-Van Oorschot, Astrid
; APPLICANT: Danan-Van Oorschot, Astrid
; TITLE OF INVENTION: METHODS AND MEANS FOR INDUCING APOPTOSIS BY INTERFERING WITH
; FILE REFERENCE: 2906-4940US
; CURRENT APPLICATION NUMBER: US/09/581.001B
; CURRENT FILING DATE: 2000-07-24
; PRIOR APPLICATION NUMBER: PCT/NL98/00688
; PRIOR FILING DATE: 1998-12-03
; PRIOR APPLICATION NUMBER: EP 97203783.2
; PRIOR FILING DATE: 1997-12-03
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 6
; LENGTH: 69
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-581-001B-6

Query Match      17.0%; Score 223; DB 4; Length 69;
Best Local Similarity 78.2%; Pred. No. 2e-13;
Matches 43; Conservative 5; Mismatches 7; Indels 0; Gaps 0;

QY 49 SDNQPGVLIQVYGERAMTKNNLLGRFELSGLPAPRGVPGQIEVTFDIDANGIL 103
Db 12 SDNQPTVIKVGGERPLTKDNLHLLGTFTVTGTPPAPRGVPGQIEVTFIDVNGIL 66

RESULT 92
US-09-540-10349
; Sequence 10349, Application US/09902540
; Patent No. 6833447
; GENERAL INFORMATION:
; APPLICANT: Goldman, Barry S.

```

```

; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Wiegand, Roger C.
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
; FILE REFERENCE: 38-10(15849)B
; CURRENT APPLICATION NUMBER: US/09/902,540
; CURRENT FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 60/217,883
; PRIOR FILING DATE: 2000-07-10
; NUMBER OF SEQ ID NOS: 16825
; SEQ ID NO 10349
; LENGTH: 690
; TYPE: PRT
; ORGANISM: Myxococcus xanthus
US-09-902-540-10349

Query Match      16.5%; Score 217; DB 4; Length 690;
Best Local Similarity 31.9%; Pred. No. 1.8e-11;
Matches 43; Conservative 35; Mismatches 51; Indels 6; Gaps 1;

QY 5 VQDLLLDVAPLSGLGTAGVMTALIKRNSTIPTKOTQIFTTYSNQPGLVLIQVYGER 64
Db 474 LEGVLDVLPMAIGVGLPGREFKAVMERTSLPSTKSYTLATHRDGQTELELTVFGDS 533

QY 65 AMTKNNLLGRFELSGLPAPRGVPGQIEVTFDIDANGILNVTATDKSTGKANKITIND- 123
Db 534 DKAADNEYLGTLLKLEGLPKLPRGAVQVNTFEVSNESLLKVTAREASSGREVTSTFTTRD 593

QY 124 -----KGRLSKEIE 133
Db 594 TPEAVKARLAQLESE 608

RESULT 93
US-09-902-540-11750
; Sequence 11750, Application US/09902540
; Patent No. 6833447
; GENERAL INFORMATION:
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Wiegand, Roger C.
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
; FILE REFERENCE: 38-10(15849)B
; CURRENT APPLICATION NUMBER: US/09/902,540
; CURRENT FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 60/217,883
; PRIOR FILING DATE: 2000-07-10
; NUMBER OF SEQ ID NOS: 16825
; SEQ ID NO 11750
; LENGTH: 1027
; TYPE: PRT
; ORGANISM: Myxococcus xanthus
US-09-902-540-11750

Query Match      16.4%; Score 216; DB 4; Length 1027;
Best Local Similarity 30.8%; Pred. No. 4e-11;
Matches 45; Conservative 37; Mismatches 60; Indels 4; Gaps 2;

QY 3 ENVQDLLLDVAPLSGLGTAGVMTALIKRNSTIPTKOTQIFTTYSNQPGLVLIQVYEG 62
Db 861 DKVSSVVLIDVLPMTGVAMPGGAFKRVIERNSPLPAQRSAINTTKDNEVFLSIFQG 920

QY 63 ERAMTKNNLLGRFELSGLPAPRGVPGQIEVTFDIDANGILNVTATDKSTGKANKITIN 122
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RESULT 94

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Matches 62; Conservative 32; Mismatches 95; Indels 19; Gaps 4;
QY 9 LLLDVAPLSIGLETAGGVTALIKRNSTIPTKQTIQFTTYSNDQPGVLIQVYGERAMTK 68
Db 389 LLLDVAAQSLGVMGRVKRLIPKNTGVPVARDIFYPGSSGQEARIPVYQGESEFQD 448
QY 69 DNNLLGRFELSGIPAPRGPVQIETVDFDANGILNVTATDKSTGKANKITINDKGRLS 128
Db 449 ENYKLGEEVLKRLHVAARGEVPLEVPFELSSEALSYKATDLTSGNMEAVRLEARAG-LP 507
QY 129 KERIERMVOEAEYKAEDEVQERVSAAKNALESY-----AFNMKSAVEDSGLKG 177
Db 508 QGEAEKLGAEQAHYASQGV----VDAKRAEELFRKLLERGEKARLLQKSAQENSPEA 563
QY 178 KISEADKKYKLDKQCEVISWLDANTLAE 205
Db 564 QATLGTVQRLLDGGR---SALDSGNAQ 588

RESULT 97
5196523-12
; Patent No. 5196523
; APPLICANT: LEE, AMY S.
; TITLE OF INVENTION: CONTROL OF GENE EXPRESSION BY GLUCOSE,
; CALCIUM AND TEMPERATURE
; NUMBER OF SEQUENCES: 28
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/354,988
; FILING DATE: 19-MAY-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 282,880
; FILING DATE: 05-DEC-1988
; APPLICATION NUMBER: 690,951
; FILING DATE: 01-JAN-1985
; SEQ ID NO:12:
; LENGTH: 56
5196523-12

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Matches 36; Conservative 8; Mismatches 11; Indels 0; Gaps 0;
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Db 2 DLVLLHVCPLTLGIETVGGVMTKLIPSNVTVPVTKNSQIFSTASDNOPTVTIKVYE 56

RESULT 98
5196523-12
; Patent No. 5196523
; APPLICANT: LEE, AMY S.
; TITLE OF INVENTION: CONTROL OF GENE EXPRESSION BY GLUCOSE,
; CALCIUM AND TEMPERATURE
; NUMBER OF SEQUENCES: 28
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/354,988
; FILING DATE: 19-MAY-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 282,880
; FILING DATE: 05-DEC-1988
; APPLICATION NUMBER: 690,951
; FILING DATE: 01-JAN-1985
; SEQ ID NO:12:
; LENGTH: 56
5196523-12

Query Match 14.0%; Score 184; DB 6; Length 56;
Best Local Similarity 65.5%; Pred. No. 6.1e-10;
Matches 36; Conservative 8; Mismatches 11; Indels 0; Gaps 0;
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Db 2 DLVLLHVCPLTLGIETVGGVMTKLIPSNVTVPVTKNSQIFSTASDNOPTVTIKVYE 56
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RESULT 99
US-09-710-279-1876
; Sequence 1876, Application US/09710279
; Patent No. 6703492
; GENERAL INFORMATION:
; APPLICANT: KIMMERLY, WILLIAM JOHN
; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
; FILE REFERENCE: PU3480US
; CURRENT APPLICATION NUMBER: US/09/710,279
; CURRENT FILING DATE: 2000-11-09
; PRIOR APPLICATION NUMBER: 60/164,258
; PRIOR FILING DATE: 1999-11-09
; NUMBER OF SEQ ID NOS: 4472
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1876
; LENGTH: 337
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: amino acid sequence
US-09-710-279-1876
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Query Match 12.6%; Score 165; DB 4; Length 337;
Best Local Similarity 56.6%; Pred. No. 4.4e-07;
Matches 30; Conservative 14; Mismatches 9; Indels 0; Gaps 0;
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Db 285 DVKQVLLDVTPLSLGIEIMGGRMNTLIERTTTIPTSQVYSTAADNQPAVV 337
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RESULT 100
US-09-513-783A-172
; Sequence 172, Application US/09513783A
; Patent No. 6416959
; GENERAL INFORMATION:
; APPLICANT: Giuliano, Kenneth A.
; APPLICANT: Kapur, Ravi
; TITLE OF INVENTION: A System for Cell Based Screening
; FILE REFERENCE: 97-022-L1
; CURRENT APPLICATION NUMBER: US/09/513,783A
; CURRENT FILING DATE: 2000-02-25
; NUMBER OF SEQ ID NOS: 180
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 172
; LENGTH: 941
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: GFP-HSP70
US-09-513-783A-172
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Best Local Similarity 16.9%; Pred. No. 0.033;
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QY 60 YEGERAMTKDNNLLGRFELSGIPAPRGPVQIETVDFDANGILNVT----- 107
Db 687 YSSPQDLPPYDPAIAQFSVQKVTYPSQDSSSKVKVVRVNVHGFVSASSLVVHKSEE 746
QY 108 -----TDKSTGKANKITINDKGR-----SKEIERM----- 135
Db 747 NEBPMETDQNAKEEKQVDPBPHVEEQOQTPAENKAEESEMETSQAGSKDKMDQPP 806
QY 136 -----VQEAKEYKAEDVQERVSAAKNALESYA 163
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Db 807 QCQEGKSEDQYCGPANRESAIWQIDREMLNLYIENECKIMQDKLEKERNDKNAVEEYV 866
Qy 164 FNMKSAVEDEGLKGKISEADKKVLDKQOVISWL-DANTLAEKDBEFHKKRKELEQVCNP 222
Db 867 YEMRDKLSGHEYK-FVSEDDRNSTLKLEDTENWLYEDGEDQPKQVYVDKLAELKNLGQP 925
Qy 223 I 223
Db 926 I 926

Search completed: April 6, 2005, 17:25:45
Job time : 49 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: April 6, 2005, 17:24:24 ; Search time 146 Seconds
(without alignments)

586.680 Million cell updates/sec

Title: US-09-646-835-1_COPY_384_641

Perfect score: 1314

Sequence: 1 KSENVODLLLDVAPLSLGL.....FGAGPKGSGSGPTIEVD 258

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Gapop 10.0 , Gapext 0.5

Searched: 1418010 seqs, 331997259 residues

Total number of hits satisfying chosen parameters: 1418010

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database :

Published Applications AA:*
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2: /cgn2_6/prodata/1/pubpaa/PCT_NEW_PUB.pep:*
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6: /cgn2_6/prodata/1/pubpaa/PCTUS_PUBCOMB.pep:*
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8: /cgn2_6/prodata/1/pubpaa/US09_PUBCOMB.pep:*
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10: /cgn2_6/prodata/1/pubpaa/US09B_PUBCOMB.pep:*
11: /cgn2_6/prodata/1/pubpaa/US09C_PUBCOMB.pep:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	1314	100.0	641	9	US-09-759-010-3
2	1314	100.0	641	10	US-09-935-642-1
3	1314	100.0	641	10	US-09-919-039-146
4	1314	100.0	641	15	US-10-380-408A-5
5	1314	100.0	641	17	US-10-792-571-14
6	1309	99.6	476	15	US-10-108-260A-3466
7	1298.5	98.8	640	16	US-10-408-765A-255
8	1258	95.7	641	14	US-10-316-253-28
9	1258	95.7	641	14	US-10-316-253-97
10	1228.5	93.5	642	9	US-09-761-534A-10
11	1228.5	93.5	642	17	US-10-885-523-10
12	1223	93.1	622	14	US-10-132-556A-2
13	1103	83.9	641	16	US-10-408-765A-1675

646	15	US-10-205-331-106	Sequence 106, App
646	17	US-10-841-207-2	Sequence 2, Appli
641	15	US-10-380-408A-7	Sequence 7, Appli
586	16	US-10-408-765A-1753	Sequence 1753, Ap
646	9	US-09-759-010-4	Sequence 4, Appli
646	9	US-09-870-759-43	Sequence 43, Appli
646	10	US-09-935-642-16	Sequence 16, Appli
646	21	US-09-919-039-11	Sequence 11, Appli
646	10	US-09-751-708A-43	Sequence 43, Appli
646	15	US-10-126-103-147	Sequence 147, App
646	15	US-10-431-096-147	Sequence 147, App
646	16	US-10-408-765A-703	Sequence 703, App
646	16	US-10-737-350-1	Sequence 1, Appli
646	17	US-10-841-207-4	Sequence 4, Appli
890	14	US-10-100-957A-174	Sequence 174, App
250	15	US-10-108-260A-4141	Sequence 4141, Ap
641	10	US-09-919-039-73	Sequence 73, Appli
650	15	US-10-380-408A-6	Sequence 6, Appli
621	15	US-10-108-260A-3524	Sequence 3524, Ap
413	15	US-10-108-260A-4616	Sequence 4616, Ap
639	16	US-10-408-765A-1693	Sequence 1693, Ap
639	16	US-10-408-765A-1723	Sequence 1723, Ap
640	15	US-10-369-493-6233	Sequence 6233, Ap
651	13	US-10-108-605-75	Sequence 75, Appli
643	10	US-09-733-179A-11	Sequence 11, Appli
643	10	US-09-919-039-204	Sequence 204, App
643	16	US-10-755-889-396	Sequence 396, App
665	9	US-09-925-302-724	Sequence 724, App
665	10	US-09-925-302-724	Sequence 724, App
655	15	US-10-424-599-234323	Sequence 234323
653	16	US-10-437-963-186650	Sequence 186650,
646	16	US-10-437-963-203543	Sequence 203543,
365	15	US-10-425-114-43012	Sequence 43012, A
648	15	US-10-424-599-156571	Sequence 156571,
649	16	US-10-767-701-46962	Sequence 46962, A
651	15	US-10-425-114-438284	Sequence 438284, A
282	15	US-10-425-114-43851	Sequence 43851, A
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649	15	US-10-424-599-156572	Sequence 156572,
651	15	US-10-425-114-43825	Sequence 43825, A
651	15	US-10-425-114-55946	Sequence 55946, A
444	15	US-10-424-599-195814	Sequence 195814,
649	15	US-10-424-599-197829	Sequence 197829,
648	16	US-10-437-963-102982	Sequence 102982,
662	15	US-10-425-114-62493	Sequence 62493, A
662	15	US-10-425-114-62493	Sequence 62493, A
337	14	US-10-259-165-98	Sequence 98, Appli
337	14	US-10-259-165-98	Sequence 426, App
649	14	US-10-259-165-214	Sequence 214, App
649	14	US-10-259-165-350	Sequence 350, App
669	16	US-10-437-963-196148	Sequence 196148,
486	16	US-10-767-701-47021	Sequence 47021, A
282	15	US-10-424-599-156570	Sequence 156570,
282	15	US-10-425-114-45699	Sequence 45699, A
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572	15	US-10-425-114-57696	Sequence 57696, A
648	15	US-10-425-114-70238	Sequence 70238, A
653	15	US-10-425-114-56213	Sequence 56213, A
653	15	US-10-425-114-58627	Sequence 58627, A
653	15	US-10-425-114-58888	Sequence 58888, A
653	15	US-10-425-114-59160	Sequence 59160, A
653	15	US-10-425-114-60382	Sequence 60382, A
653	15	US-10-425-114-62531	Sequence 62531, A
653	15	US-10-425-114-62531	Sequence 62532, A
653	15	US-10-425-114-62656	Sequence 62656, A
653	15	US-10-425-114-67148	Sequence 67148, A
653	15	US-10-425-114-68232	Sequence 68232, A
653	15	US-10-425-114-69239	Sequence 69239, A
653	15	US-10-425-114-70649	Sequence 70649, A
653	15	US-10-425-114-72128	Sequence 72128, A
653	15	US-10-425-114-72427	Sequence 72427, A
653	15	US-10-425-114-72533	Sequence 72533, A

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89 938 71.4 652 15 US-10-425-114-59328 Sequence 59328, A
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91 938 71.4 652 15 US-10-425-114-62560 Sequence 62560, A
92 938 71.4 652 15 US-10-425-114-63240 Sequence 63240, A
93 938 71.4 652 15 US-10-425-114-63457 Sequence 63457, A
94 938 71.4 652 15 US-10-425-114-63505 Sequence 63505, A
95 938 71.4 652 15 US-10-425-114-65274 Sequence 65274, A
96 928.5 70.7 649 16 US-10-437-963-193938 Sequence 193938, A
97 920.5 70.1 461 15 US-10-425-114-54413 Sequence 54413, A
98 918.5 69.9 658 15 US-10-425-114-57892 Sequence 57892, A
99 912.5 69.4 653 15 US-10-425-114-65502 Sequence 65502, A
100 911 69.3 656 16 US-10-451-467A-536 Sequence 536, App

ALIGNMENTS

RESULT 1

US-09-759-010-3
; Sequence 3, Application US/09759010
; Patent No. US20010034042A1
; GENERAL INFORMATION:
; APPLICANT: Strivastava, Pramod K.
; TITLE OF INVENTION: COMPLEXES OF PEPTIDE BINDING FRAGMENTS OF HEAT-SHOCK
; TITLE OF INVENTION: PROTEINS AND THEIR USE AS IMMUNOTHERAPEUTIC AGENTS
; FILE REFERENCE: 8449-135
; CURRENT APPLICATION NUMBER: US/09/759,010
; CURRENT FILING DATE: 2001-01-12
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 641
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-759-010-3

Query Match 100.0%; Score 1314; DB 9; Length 641;
Best Local Similarity 100.0%; Pred. No. 2.8e-95;
Matches 258; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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DB 384 KSENVQDLLLDVAPLSGLGLETAGGVTALIKENSTIPTKQTQIFTTYSNQPGLVLIQVY 443
QY 61 EGERAMTKONLLGRFELSGIPAPRGVPOIEVTFDIDANGILNVTATDKSTGKANKITI 120
DB 444 EGERAMTKONLLGRFELSGIPAPRGVPOIEVTFDIDANGILNVTATDKSTGKANKITI 503
QY 121 TNDKGRLSKEEIERMVQEAKEYKAEDVQERVSAKNALESYAFNMKSAVEDSLGKGIS 180
DB 504 TNDKGRLSKEEIERMVQEAKEYKAEDVQERVSAKNALESYAFNMKSAVEDSLGKGIS 563
QY 181 EADKKVKLDKQCVISWLDANTLAEDFEHKKLEQVNCNPIISGLYQAGGPGGFG 240
DB 564 EADKKVKLDKQCVISWLDANTLAEDFEHKKLEQVNCNPIISGLYQAGGPGGFG 623
QY 241 AQGPKGSGSGPTIEVD 258
DB 624 AQGPKGSGSGPTIEVD 641

RESULT 2

US-09-935-642-1
; Sequence 1, Application US/09935642
; Publication No. US20030044795A1
; GENERAL INFORMATION:
; APPLICANT: BYRJALSEN, Inger
; APPLICANT: LARSEN, Peter
; APPLICANT: STEPHEN, John
; TITLE OF INVENTION: Biochemical Markers for the Human
; TITLE OF INVENTION: Endometrium

; FILE REFERENCE: 8969-014
; CURRENT APPLICATION NUMBER: US/09/935,642
; CURRENT FILING DATE: 2001-08-24
; PRIOR APPLICATION NUMBER: PCT/GB97/02394
; PRIOR FILING DATE: 1997-09-05
; PRIOR APPLICATION NUMBER: PCT/GB9707132.8
; PRIOR FILING DATE: 1997-04-08
; PRIOR APPLICATION NUMBER: PCT/GB9618600.2
; PRIOR FILING DATE: 1996-09-06
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 641
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-935-642-1

Query Match 100.0%; Score 1314; DB 10; Length 641;
Best Local Similarity 100.0%; Pred. No. 2.8e-95;
Matches 258; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KSENVQDLLLDVAPLSGLGLETAGGVTALIKENSTIPTKQTQIFTTYSNQPGLVLIQVY 60
DB 384 KSENVQDLLLDVAPLSGLGLETAGGVTALIKENSTIPTKQTQIFTTYSNQPGLVLIQVY 443
QY 61 EGERAMTKONLLGRFELSGIPAPRGVPOIEVTFDIDANGILNVTATDKSTGKANKITI 120
DB 444 EGERAMTKONLLGRFELSGIPAPRGVPOIEVTFDIDANGILNVTATDKSTGKANKITI 503
QY 121 TNDKGRLSKEEIERMVQEAKEYKAEDVQERVSAKNALESYAFNMKSAVEDSLGKGIS 180
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DB 564 EADKKVKLDKQCVISWLDANTLAEDFEHKKLEQVNCNPIISGLYQAGGPGGFG 623
QY 241 AQGPKGSGSGPTIEVD 258
DB 624 AQGPKGSGSGPTIEVD 641

RESULT 3

US-09-919-039-146
; Sequence 146, Application US/09919039
; Publication No. US20030108871A1
; GENERAL INFORMATION:
; APPLICANT: Kaefer, Matthew R.
; TITLE OF INVENTION: GENES EXPRESSED IN TREATED HUMAN C3A LIVER CELL CULTURES
; FILE REFERENCE: PA-0035 US
; CURRENT APPLICATION NUMBER: US/09/919,039
; CURRENT FILING DATE: 2002-09-09
; PRIOR APPLICATION NUMBER: 60/222,113
; PRIOR FILING DATE: 2000-07-28
; NUMBER OF SEQ ID NOS: 401
; SOFTWARE: PERL Program
; SEQ ID NO 146
; LENGTH: 641
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. US20030108871A1 1678695CD1
US-09-919-039-146

Query Match 100.0%; Score 1314; DB 10; Length 641;
Best Local Similarity 100.0%; Pred. No. 2.8e-95;
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DB 384 KSENVQDLLLDVAPLSGLGLETAGGVTALIKENSTIPTKQTQIFTTYSNQPGLVLIQVY 443

QY 61 EGERAMTKNNLLGRFELSGIPAPRGVPOIEVTFDIDANGILNVATDSTGKANKITI 120
DB 444 EGERAMTKNNLLGRFELSGIPAPRGVPOIEVTFDIDANGILNVATDSTGKANKITI 503
QY 121 TNDKGRLSKEEIERMVOEAEKYKAEDVQERVSAAKNALESYAFNMKSAVEDEGLKGKIS 180
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DB 564 EADKKVLDKQCEVISWLDANTLAEKDEFEHKKRKELEQVNCNPIISGLYQAGGPGPGFG 623
QY 241 AQPKGSGSGPTIEVD 258
DB 624 AQPKGSGSGPTIEVD 641

RESULT 4

US-10-380-408A-5
; Sequence 5, Application US/10380408A
; Publication No. US20040063173A1
; GENERAL INFORMATION:
; APPLICANT: MUTHOFF, Gabriele
; TITLE OF INVENTION: An Hsp70 peptide stimulating Natural Killer (NK) cell activity
; FILE REFERENCE: E 2022 PCT
; CURRENT APPLICATION NUMBER: US/10/380,408A
; PRIOR FILING DATE: 2003-08-25
; PRIOR APPLICATION NUMBER: EP 00119933.0
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 5
; LENGTH: 641
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-380-408A-5

Query Match 100.0%; Score 1314; DB 15; Length 641;
Best Local Similarity 100.0%; Pred. No. 2.8e-95;
Matches 258; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KSENVQDLLLDVAPLSGLGTAGGVMTALIKRNSTIPTKTQITFTTYSNQPGVLIQVY 60
DB 384 KSENVQDLLLDVAPLSGLGTAGGVMTALIKRNSTIPTKTQITFTTYSNQPGVLIQVY 443
QY 61 EGERAMTKNNLLGRFELSGIPAPRGVPOIEVTFDIDANGILNVATDSTGKANKITI 120
DB 444 EGERAMTKNNLLGRFELSGIPAPRGVPOIEVTFDIDANGILNVATDSTGKANKITI 503
QY 121 TNDKGRLSKEEIERMVOEAEKYKAEDVQERVSAAKNALESYAFNMKSAVEDEGLKGKIS 180
DB 504 TNDKGRLSKEEIERMVOEAEKYKAEDVQERVSAAKNALESYAFNMKSAVEDEGLKGKIS 563
QY 181 EADKKVLDKQCEVISWLDANTLAEKDEFEHKKRKELEQVNCNPIISGLYQAGGPGPGFG 240
DB 564 EADKKVLDKQCEVISWLDANTLAEKDEFEHKKRKELEQVNCNPIISGLYQAGGPGPGFG 623
QY 241 AQPKGSGSGPTIEVD 258
DB 624 AQPKGSGSGPTIEVD 641

RESULT 5

US-10-792-571-14
; Sequence 14, Application US/10792571
; Publication No. US20050048608A1
; GENERAL INFORMATION:
; APPLICANT: Chan, Sham-Yuen
; APPLICANT: Tang, Hsin-yi
; APPLICANT: Tao, Yiwen
; APPLICANT: Wu, Yongjian
; APPLICANT: Kelly, Ruth

; TITLE OF INVENTION: Use of Molecular Chaperones for the Enhanced Production of
; FILE REFERENCE: 03-302-A
; CURRENT APPLICATION NUMBER: US/10/792,571
; PRIOR FILING DATE: 2004-03-03
; PRIOR APPLICATION NUMBER: 60/483,505
; PRIOR FILING DATE: 2003-06-27
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 14
; LENGTH: 641
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-792-571-14

Query Match 100.0%; Score 1314; DB 17; Length 641;
Best Local Similarity 100.0%; Pred. No. 2.8e-95;
Matches 258; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KSENVQDLLLDVAPLSGLGTAGGVMTALIKRNSTIPTKTQITFTTYSNQPGVLIQVY 60
DB 384 KSENVQDLLLDVAPLSGLGTAGGVMTALIKRNSTIPTKTQITFTTYSNQPGVLIQVY 443
QY 61 EGERAMTKNNLLGRFELSGIPAPRGVPOIEVTFDIDANGILNVATDSTGKANKITI 120
DB 444 EGERAMTKNNLLGRFELSGIPAPRGVPOIEVTFDIDANGILNVATDSTGKANKITI 503
QY 121 TNDKGRLSKEEIERMVOEAEKYKAEDVQERVSAAKNALESYAFNMKSAVEDEGLKGKIS 180
DB 504 TNDKGRLSKEEIERMVOEAEKYKAEDVQERVSAAKNALESYAFNMKSAVEDEGLKGKIS 563
QY 181 EADKKVLDKQCEVISWLDANTLAEKDEFEHKKRKELEQVNCNPIISGLYQAGGPGPGFG 240
DB 564 EADKKVLDKQCEVISWLDANTLAEKDEFEHKKRKELEQVNCNPIISGLYQAGGPGPGFG 623
QY 241 AQPKGSGSGPTIEVD 258
DB 624 AQPKGSGSGPTIEVD 641

RESULT 6

US-10-108-260A-3466
; Sequence 3466, Application US/10108260A
; Publication No. US20040005560A1
; GENERAL INFORMATION:
; APPLICANT: HELIX RESEARCH INSTITUTE
; TITLE OF INVENTION: No. US20040005560A1e1 full length cDNA
; FILE REFERENCE: HI-A0106
; CURRENT APPLICATION NUMBER: US/10/108,260A
; CURRENT FILING DATE: 2002-03-27
; NUMBER OF SEQ ID NOS: 5458
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3466
; LENGTH: 476
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-108-260A-3466

Query Match 99.6%; Score 1309; DB 15; Length 476;
Best Local Similarity 99.6%; Pred. No. 4.7e-95;
Matches 257; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KSENVQDLLLDVAPLSGLGTAGGVMTALIKRNSTIPTKTQITFTTYSNQPGVLIQVY 60
DB 219 KSENVQDLLLDVAPLSGLGTAGGVMTALIKRNSTIPTKTQITFTTYSNQPGVLIQVY 278
QY 61 EGERAMTKNNLLGRFELSGIPAPRGVPOIEVTFDIDANGILNVATDSTGKANKITI 120
DB 279 EGERAMTKNNLLGRFELSGIPAPRGVPOIEVTFDIDANGILNVATDSTGKANKITI 338
QY 121 TNDKGRLSKEEIERMVOEAEKYKAEDVQERVSAAKNALESYAFNMKSAVEDEGLKGKIS 180
DB 339 TNDKGRLSKEEIERMVOEAEKYKAEDVQERVSAAKNALESYAFNMKSAVEDEGLKGKIS 398

	Query Match	95.7%	Score 1258;	DB 14;	Length 641;
	Best Local Similarity	95.3%;	Pred. No. 7.5e-91;		
	Matches 246;	Conservative 7;	Mismatches 5;	Indels 0;	Gaps 0;
Qy	1	KSENVQDLILLDVAPISLGLETAGGVTWTAIIKKNSTIPKQTQITFTTYSNQEGVLIQVY	60		
Db	384	KSENVQDLILLDVAPISLGLETAGGVTWTAIIKKNSTIPKQTQITFTTYSNQEGVLIQVY	443		
Qy	61	EGERAMTKNNLLGREFELSGIIPAPRGVPQIEVTFDIDANGILNVATATDKSTGKANKITI	120		
Db	444	EGERAMTRDNNLLGREFELSGIIPAPRGVPQIEVTFDIDANGILNVATATDKSTGKANKITI	503		
Qy	121	TNDKGRLSKEETIRMVOEABKYKAEDEVORERSAKNALESYAFNMKSAVEDEGLKGKIS	180		


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Db 504 TNDKGRLSKEEIERMVOEAEYKAEDVQVRAAKNALESYAFNMKSAVEDGLGKIS 563
Qy 181 EADKKVLDKCQEVISWLDANTLAEDKDFEHKKELEOVNCNPIISGLYQAGAGPGPGFG 240
Db 564 EADKKVLDKCQEVISWLDANTLAEDKDFEHKKELEOVNCNPIISGLYQAGAGPGPGFG 623
Qy 241 AQPKGGSGSGPTIEVD 258
Db 624 AQPKGGSGSGPTIEVD 641

RESULT 10
US-09-761-534A-10
; Sequence 10, Application US/09761534A
; Patent No. US20020146426A1
; GENERAL INFORMATION:
; APPLICANT: Huang, Qian
; APPLICANT: Richmond, Joan F.L.
; APPLICANT: Cho, Bryan K.
; APPLICANT: Palliser, Deborah
; APPLICANT: Chen, Jianzhu
; APPLICANT: Eisen, Herman N.
; APPLICANT: Young, Richard A.
; TITLE OF INVENTION: In Vivo CTL Elicitation By Heat Shock
; TITLE OF INVENTION: Protein Fusion Proteins Maps To A Discrete Domain and is
; FILE REFERENCE: 0399.2006-003
; CURRENT APPLICATION NUMBER: US/09/761,534A
; CURRENT FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: PCT/US00/32831
; PRIOR FILING DATE: 2000-12-01
; PRIOR APPLICATION NUMBER: US 60/176,143
; PRIOR FILING DATE: 2000-01-14
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 642
; TYPE: PRT
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Murine hsp70
US-09-761-534A-10

Query Match 93.5%; Score 1228.5; DB 9; Length 642;
Best Local Similarity 93.1%; Pred. No. 1.6e-88;
Matches 241; Conservative 11; Mismatches 6; Indels 1; Gaps 1;

Qy 1 KSENVODLLLDVAPLSGLGLETAGGVMTALIKNSTIPTKTQITFTTYSNQPGLVQY 60
Db 384 KSENVODLLLDVAPLSGLGLETAGGVMTALIKNSTIPTKTQITFTTYSNQPGLVQY 443
Qy 61 EGERAMTKDNNLGRFELSGIPAPRGVQIETFTDANGILNVTATDKSTGKANKITI 120
Db 444 EGERAMTRDNNLGRFELSGIPAPRGVQIETFTDANGILNVTATDKSTGKANKITI 503
Qy 121 TNDKGRLSKEEIERMVOEAEYKAEDVQVRAAKNALESYAFNMKSAVEDGLGKIS 180
Db 504 TNDKGRLSKEEIERMVOEAEYKAEDVQVRAAKNALESYAFNMKSAVEDGLGKIS 563
Qy 181 EADKKVLDKCQEVISWLDANTLAEDKDFEHKKELEOVNCNPIISGLYQAGAGPGPGFG 240
Db 564 EADKKVLDKCQEVISWLDANTLAEDKDFEHKKELEOVNCNPIISGLYQAGAGPGPGFG 623
Qy 241 AQPKGGSGSGPTIEVD 258
Db 624 AQPKGGSGSGPTIEVD 642

RESULT 11
US-10-885-523-10
; Sequence 10, Application US/10885523
; Publication No. US20050048079A1

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; GENERAL INFORMATION:
; APPLICANT: Huang, Qian
; APPLICANT: Richmond, Joan F.L.
; APPLICANT: Cho, Bryan K.
; APPLICANT: Palliser, Deborah
; APPLICANT: Chen, Jianzhu
; APPLICANT: Eisen, Herman N.
; APPLICANT: Young, Richard A.
; TITLE OF INVENTION: In Vivo CTL Elicitation By Heat Shock
; TITLE OF INVENTION: Protein Fusion Proteins Maps To A Discrete Domain and is
; FILE REFERENCE: 0399.2006-003
; CURRENT APPLICATION NUMBER: US/10/885,523
; CURRENT FILING DATE: 2004-07-01
; PRIOR APPLICATION NUMBER: US/09/761,534
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: PCT/US00/32831
; PRIOR FILING DATE: 2000-12-01
; PRIOR APPLICATION NUMBER: US 60/176,143
; PRIOR FILING DATE: 2000-01-14
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 642
; TYPE: PRT
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Murine hsp70
US-10-885-523-10

Query Match 93.5%; Score 1228.5; DB 17; Length 642;
Best Local Similarity 93.1%; Pred. No. 1.6e-88;
Matches 241; Conservative 11; Mismatches 6; Indels 1; Gaps 1;

Qy 1 KSENVODLLLDVAPLSGLGLETAGGVMTALIKNSTIPTKTQITFTTYSNQPGLVQY 60
Db 384 KSENVODLLLDVAPLSGLGLETAGGVMTALIKNSTIPTKTQITFTTYSNQPGLVQY 443
Qy 61 EGERAMTKDNNLGRFELSGIPAPRGVQIETFTDANGILNVTATDKSTGKANKITI 120
Db 444 EGERAMTRDNNLGRFELSGIPAPRGVQIETFTDANGILNVTATDKSTGKANKITI 503
Qy 121 TNDKGRLSKEEIERMVOEAEYKAEDVQVRAAKNALESYAFNMKSAVEDGLGKIS 180
Db 504 TNDKGRLSKEEIERMVOEAEYKAEDVQVRAAKNALESYAFNMKSAVEDGLGKIS 563
Qy 181 EADKKVLDKCQEVISWLDANTLAEDKDFEHKKELEOVNCNPIISGLYQAGAGPGPGFG 240
Db 564 EADKKVLDKCQEVISWLDANTLAEDKDFEHKKELEOVNCNPIISGLYQAGAGPGPGFG 623
Qy 241 AQPKGGSGSGPTIEVD 258
Db 624 AQPKGGSGSGPTIEVD 642

RESULT 12
US-10-132-556A-2
; Sequence 2, Application US/10132556A
; Publication No. US20030082629A1
; GENERAL INFORMATION:
; APPLICANT: Volloch, Vladimir
; APPLICANT: Sherman, Michael
; TITLE OF INVENTION: SCREENING METHODS FOR COMPOUNDS USEFUL
; TITLE OF INVENTION: IN THE REGULATION OF CELL PROLIFERATION
; FILE REFERENCE: A32367-PCT-USA-A 066290.0106
; CURRENT APPLICATION NUMBER: US/10/132,556A
; CURRENT FILING DATE: 2002-04-25
; PRIOR APPLICATION NUMBER: 09/936,879
; PRIOR FILING DATE: 2001-09-18
; PRIOR APPLICATION NUMBER: PCT/US00/07350
; PRIOR FILING DATE: 2000-03-17
; PRIOR APPLICATION NUMBER: 60/125,046
; PRIOR FILING DATE: 1999-03-18

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; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: Fast-SEQ for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 622
; TYPE: PRT
; ORGANISM: Homo sapien
US-10-132-556A-2

Query Match      93.1%; Score 1223; DB 14; Length 622;
Best Local Similarity 100.0%; Pred. No. 4.2e-88;
Matches 241; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KSENVQDLLLLDVAPLSLGLETAGGVTALIKENSTIPTKTQITFTTYSNQPGLVLIQVY 60
DB 382 KSENVQDLLLLDVAPLSLGLETAGGVTALIKENSTIPTKTQITFTTYSNQPGLVLIQVY 441
QY 61 EGERAMTKDNLLGRFELSGIPAPRGVQPIEVTFDIDANGILNVATDSTGKANKITI 120
DB 442 EGERAMTKDNLLGRFELSGIPAPRGVQPIEVTFDIDANGILNVATDSTGKANKITI 501
QY 121 TNDKGRLSKEIEIRMVQEAKEYKAEDVQERVSAKNALESYAFNMKSAVEDGLGKGIS 180
DB 502 TNDKGRLSKEIEIRMVQEAKEYKAEDVQERVSAKNALESYAFNMKSAVEDGLGKGIS 561
QY 181 EADKKVLDKQCEVISWLDANTLAEKDEFEHKKRKELEQVNCNPIISGLYQAGGPGPGFG 240
DB 562 EADKKVLDKQCEVISWLDANTLAEKDEFEHKKRKELEQVNCNPIISGLYQAGGPGPGFG 621
QY 241 A 241
DB 622 A 622

RESULT 13
US-10-408-765A-1675
; Sequence 1675, Application US/10408765A
; Publication No. US20040101874A1
; GENERAL INFORMATION:
; APPLICANT: Ghosh, Soumitra S.
; APPLICANT: Fahy, Eoin D.
; APPLICANT: Zhang, Bing
; APPLICANT: Gibson, Bradford W.
; APPLICANT: Taylor, Steven W.
; APPLICANT: Glenn, Gary M.
; APPLICANT: Warnock, Dale E.
; TITLE OF INVENTION: TARGETS FOR THERAPEUTIC INTERVENTION
; TITLE OF INVENTION: IDENTIFIED IN THE MITOCHONDRIAL PROTEOME
; FILE REFERENCES: 660088.465
; CURRENT APPLICATION NUMBER: US/10/408, 765A
; CURRENT FILING DATE: 2003-04-04
; NUMBER OF SEQ ID NOS: 3077
; SOFTWARE: Fast-SEQ for Windows Version 4.0
; SEQ ID NO 1675
; LENGTH: 641
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-408-765A-1675

Query Match      83.9%; Score 1103; DB 16; Length 641;
Best Local Similarity 82.3%; Pred. No. 1.4e-78;
Matches 218; Conservative 16; Mismatches 15; Indels 16; Gaps 2;

QY 1 KSENVQDLLLLDVAPLSLGLETAGGVTALIKENSTIPTKTQITFTTYSNQPGLVLIQVY 60
DB 386 KSENVQDLLLLDVAPLSLGLETAGGVTALIKENSTIPTKTQITFTTYSNQPGLVLIQVY 445
QY 61 EGERAMTKDNLLGRFELSGIPAPRGVQPIEVTFDIDANGILNVATDSTGKANKITI 120
DB 446 EGERAMTKDNLLGRFELSGIPAPRGVQPIEVTFDIDANGILNVATDSTGKANKITI 505
QY 121 TNDKGRLSKEIEIRMVQEAKEYKAEDVQERVSAKNALESYAFNMKSAVEDGLGKGIS 180
DB 506 TNDKGRLSKEIEIRMVQEAKEYKAEDVQERVSAKNALESYAFNMKSAVEDGLGKGIS 565
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QY 181 EADKKVLDKQCEVISWLDANTLAEKDEFEHKKRKELEQVNCNPIISGLYQAGGPGPGFG 240
DB 566 ESDKNKILDKCNELLSWLVNQLAEKDFDHRKKELEQVNCNPIITKLYQG-----G 616
QY 241 AOGPKGGSG-----SGPTIEVD 258
DB 617 CTGPACGTGYVPRPATGTPTIEVD 641

RESULT 14
US-10-205-331-106
; Sequence 106, Application US/10205331
; Publication No. US20040058326A1
; GENERAL INFORMATION:
; APPLICANT: Warner-Lambert Company
; APPLICANT: Lee, Kevin
; APPLICANT: Dixon, Alistair
; APPLICANT: Brooksbank, Robert
; APPLICANT: Finnock, Robert
; TITLE OF INVENTION: Identification and Use of Molecules Implicated in Pain
; FILE REFERENCE: WL-A-018199
; CURRENT APPLICATION NUMBER: US/10/205,331
; CURRENT FILING DATE: 2002-07-24
; PRIOR APPLICATION NUMBER: GB 0118354.0
; PRIOR FILING DATE: 2001-07-27
; NUMBER OF SEQ ID NOS: 117
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 106
; LENGTH: 646
; TYPE: PRT
; ORGANISM: Rattus norvegicus
; FEATURE:
; OTHER INFORMATION: Heat shock cognate protein 70
US-10-205-331-106

Query Match      83.8%; Score 1100.5; DB 15; Length 646;
Best Local Similarity 81.7%; Pred. No. 2.2e-78;
Matches 215; Conservative 23; Mismatches 20; Indels 5; Gaps 3;

QY 1 KSENVQDLLLLDVAPLSLGLETAGGVTALIKENSTIPTKTQITFTTYSNQPGLVLIQVY 60
DB 384 KSENVQDLLLLDVAPLSLGLETAGGVTALIKENSTIPTKTQITFTTYSNQPGLVLIQVY 443
QY 61 EGERAMTKDNLLGRFELSGIPAPRGVQPIEVTFDIDANGILNVATDSTGKANKITI 120
DB 444 EGERAMTKDNLLGRFELSGIPAPRGVQPIEVTFDIDANGILNVATDSTGKANKITI 503
QY 121 TNDKGRLSKEIEIRMVQEAKEYKAEDVQERVSAKNALESYAFNMKSAVEDGLGKGIS 180
DB 504 TNDKGRLSKEIEIRMVQEAKEYKAEDVQERVSAKNALESYAFNMKSAVEDGLGKGIS 563
QY 181 EADKKVLDKQCEVISWLDANTLAEKDEFEHKKRKELEQVNCNPIISGLYQAGGPG--PG 237
DB 564 DEDKQKILDKCNELLSWLVNQLAEKDFDHRKKELEQVNCNPIITKLYQAGGPGMPG 623
QY 238 GF--GAQGPKGSGSGPTIEVD 258
DB 624 GFPGGGAPPGSGSGPTIEVD 646

RESULT 15
US-10-841-207-2
; Sequence 2, Application US/10841207
; Publication No. US20050009772A1
; GENERAL INFORMATION:
; APPLICANT: Caprioli, Joseph
; TITLE OF INVENTION: Methods and Compositions for the Treatment of Glaucoma and Other
; TITLE OF INVENTION: Retinal Diseases
; FILE REFERENCE: A-72263/TAL/MWR (468290-00515)
; CURRENT APPLICATION NUMBER: US/10/841,207
; CURRENT FILING DATE: 2004-05-06
; PRIOR APPLICATION NUMBER: US 60/468,554
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; PRIOR FILING DATE: 2003-05-06
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2
; LENGTH: 646
; TYPE: PRT
; ORGANISM: Rattus norvegicus
US-10-841-207-2

Query Match      83.8%; Score 1100.5; DB 17; Length 646;
Best Local Similarity 81.7%; Pred. No. 2.2e-78;
Matches 215; Conservative 23; Mismatches 20; Indels 5; Gaps 3;

QY 1 KSENVQDLLLDVAPLSGLGLETAGGVTALIKRNTSTPTKQTQIFTTYSNQPGVLIQVY 60
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 384 KSENVQDLLLDVTPLSGLGLETAGGVTALIKRNTTPTKQTQIFTTYSNQPGVLIQVY 443

QY 61 EGERAMTKNNLGRFELSGIPAPRGVPOIETFDIDANGILNVATDSTGKANKITI 120
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 444 EGERAMTKNNLGRFELSGIPAPRGVPOIETFDIDANGILNVSAVDKSTGKANKITI 503

QY 121 TNDKGRLSKEEIERMWQAEKYKAEDVQREVRSYAKNALESYAFNMKSASVEDGLGKGIS 180
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 504 TNDKGRLSKEDIERMWQAEKYKAEDKQDKVSSKNLSLEYAFNMKATVEDEKLQKIN 563

QY 181 EADKKVKLDKQEVISWLDANTLAEDFEHKKRKELEQVNCNPIISGLYQAGG-PG--PG 237
    :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 564 DEDKQKILDKCNEIISWLDKNTAEKEFEHQQKELEKVCNPIITKLYQSAGGMPGMPG 623

QY 238 GF--GAQPKGGSGSGPTIEVD 258
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 624 GPFPGGAPPSGGSGSGPTIEVD 646

RESULT 16
US-10-380-408A-7
; Sequence 7, Application US/10380408A
; Publication No. US20040063173A1
; GENERAL INFORMATION:
; APPLICANT: MUTHOFF, Gabriele
; TITLE OF INVENTION: An Hep70 peptide stimulating Natural Killer (NK) cell activity
; TITLE OF INVENTION: and uses thereof
; FILE REFERENCE: E 2022 PCT
; CURRENT APPLICATION NUMBER: US/10/380,408A
; PRIOR FILING DATE: 2003-08-25
; PRIOR APPLICATION NUMBER: EP 00119933.0
; PRIOR FILING DATE: 2000-09-13
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 7
; LENGTH: 641
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-380-408A-7

Query Match      83.6%; Score 1099; DB 15; Length 641;
Best Local Similarity 81.9%; Pred. No. 2.8e-78;
Matches 217; Conservative 16; Mismatches 16; Indels 16; Gaps 2;

QY 1 KSENVQDLLLDVAPLSGLGLETAGGVTALIKRNTSTPTKQTQIFTTYSNQPGVLIQVY 60
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 386 KSENVQDLLLDVAPLSGLGLETAGGVTALIKRNTTTPPKQTQIFTTYSNQPGVLIQVY 445

QY 61 EGERAMTKNNLGRFELSGIPAPRGVPOIETFDIDANGILNVATDSTGKANKITI 120
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 446 EGERAMTKNNLGRFELSGIPAPRGVPOIETFDIDANGILNVATDSTGKANKITI 505

QY 121 TNDKGRLSKEEIERMWQAEKYKAEDVQREVRSYAKNALESYAFNMKSASVEDGLGKGIS 180
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 506 TNDKGRLSKEEIERMWLDKAEKYKAEDVQREKIAAKNALESYAFNMKSVDSEGLGKGIS 565

QY 181 EADKKVKLDKQEVISWLDANTLAEDFEHKKRKELEQVNCNPIISGLYQAGGPGPGG 240
    :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
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Db 566 ESDKNKILDKCNELLSWLVNQLAEKDFDHRKKELEQMCNPIITKLYQG-----G 616
QY 241 AQGPKGGSG-----SGPTIEVD 258
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 617 CTGACGTGYVGRPATGPTIEVD 641

RESULT 17
US-10-408-765A-1753
; Sequence 1753, Application US/10408765A
; Publication No. US20040101874A1
; GENERAL INFORMATION:
; APPLICANT: Ghosh, Soumitra S.
; APPLICANT: Fahy, Eoin D.
; APPLICANT: Zhang, Bing
; APPLICANT: Gibson, Bradford W.
; APPLICANT: Taylor, Steven W.
; APPLICANT: Glenn, Gary M.
; APPLICANT: Warnock, Dale E.
; TITLE OF INVENTION: TARGETS FOR THERAPEUTIC INTERVENTION
; TITLE OF INVENTION: IDENTIFIED IN THE MITOCHONDRIAL PROTEOME
; FILE REFERENCE: 660088.465
; CURRENT APPLICATION NUMBER: US/10/408,765A
; CURRENT FILING DATE: 2003-04-04
; NUMBER OF SEQ ID NOS: 3077
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1753
; LENGTH: 586
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-408-765A-1753

Query Match      83.5%; Score 1097.5; DB 16; Length 586;
Best Local Similarity 81.4%; Pred. No. 3.3e-78;
Matches 214; Conservative 24; Mismatches 20; Indels 5; Gaps 3;

QY 1 KSENVQDLLLDVAPLSGLGLETAGGVTALIKRNTSTPTKQTQIFTTYSNQPGVLIQVY 60
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 324 KSENVQDLLLDVTPLSGLGLETAGGVTALIKRNTTPTKQTQIFTTYSNQPGVLIQVY 383

QY 61 EGERAMTKNNLGRFELSGIPAPRGVPOIETFDIDANGILNVATDSTGKANKITI 120
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 384 EGERAMTKNNLGRFELSGIPAPRGVPOIETFDIDANGILNVSAVDKSTGKANKITI 443

QY 121 TNDKGRLSKEEIERMWQAEKYKAEDVQREVRSYAKNALESYAFNMKSASVEDGLGKGIS 180
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 444 TNDKGRLSKEDIERMWQAEKYKAEDKQDKVSSKNLSLEYAFNMKATVEDEKLQKIN 503

QY 181 EADKKVKLDKQEVISWLDANTLAEDFEHKKRKELEQVNCNPIISGLYQAGG-PG--PG 237
    :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 504 DEDKQKILDKCNEIISWLDKNTAEKEFEHQQKELEKVCNPIITKLYQSAGGMPGMPG 563

QY 238 GF--GAQPKGGSGSGPTIEVD 258
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 564 GPFPGGAPPSGGSGSGPTIEVD 586

RESULT 18
US-09-759-010-4
; Sequence 4, Application US/09759010
; Patent No. US20010034042A1
; GENERAL INFORMATION:
; APPLICANT: Srivastava, Pramod K.
; TITLE OF INVENTION: COMPLEXES OF PEPTIDE BINDING FRAGMENTS OF HEAT-SHOCK
; TITLE OF INVENTION: PROTEINS AND THEIR USE AS IMMUNOTHERAPEUTIC AGENTS
; FILE REFERENCE: 8449-135
; CURRENT APPLICATION NUMBER: US/09/759,010
; CURRENT FILING DATE: 2001-01-12
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 646
; TYPE: PRT
```

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; ORGANISM: Homo sapiens
US-09-759-010-4

Query Match      83.5%; Score 1097.5; DB 9; Length 646;
Best Local Similarity 81.4%; Pred. No. 3.7e-78;
Matches 214; Conservative 24; Mismatches 20; Indels 5; Gaps 3;

QY 1 KSENVQDLLLLDVAPLSGLGLETAGGVTALIKRNTSTPTKQTQITFTTYSNQPGLVLIQVY 60
DB 384 KSENVQDLLLLDVTPLSGLGLETAGGVTALIKRNTTPTKQTQITFTTYSNQPGLVLIQVY 443

QY 61 EGERAMTKDNNLLGRFELSGIPPPAPRGVPOIEVTFDIDANGILNVATDSTGKANKITI 120
DB 444 EGERAMTKDNNLLGKFLTGIPPPAPRGVPOIEVTFDIDANGILNVSAVDKSTGKANKITI 503

QY 121 TNDKGRLSKEEIERMWQAEKYKAEDVQREVRSNAKNALESYAFNMKSASVEDGLKKGKIS 180
DB 504 TNDKGRLSKEDIERMVQAEKYKAEDQKQKRDVSSKNLSLESYAFNMKATVEDEKLQKIN 563

QY 181 EADKKVKLDKQEVISWLDANTLAEKDFEHEKKELEQVNCNPIISGLYQAGG-PG--PG 237
DB 564 DEDQKILDKCNEIINWLDKNQTAKEEFHQQKELEKVCNPIITKLYQSAGGMPGMPG 623

QY 238 GF--GAQGPKGSGSGPTIEVD 258
DB 624 GPPGGAGPPSGGASSGPTIEVD 646

RESULT 19
US-09-870-759-43
; Sequence 43, Application US/09870759
; Patent No. US20020177551A1
; GENERAL INFORMATION:
; APPLICANT: TERMAN, David S
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT OF NEOPLASTIC DISEASE
; FILE REFERENCE: 870759
; CURRENT APPLICATION NUMBER: US/09/870,759
; PRIOR FILING DATE: 2002-01-14
; PRIOR APPLICATION NUMBER: US 60/208,128
; PRIOR FILING DATE: 2000-05-30
; NUMBER OF SEQ ID NOS: 166
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 43
; LENGTH: 646
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-870-759-43

```

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Query Match      83.5%; Score 1097.5; DB 9; Length 646;
Best Local Similarity 81.4%; Pred. No. 3.7e-78;
Matches 214; Conservative 24; Mismatches 20; Indels 5; Gaps 3;

QY 1 KSENVQDLLLLDVAPLSGLGLETAGGVTALIKRNTSTPTKQTQITFTTYSNQPGLVLIQVY 60
DB 384 KSENVQDLLLLDVTPLSGLGLETAGGVTALIKRNTTPTKQTQITFTTYSNQPGLVLIQVY 443

QY 61 EGERAMTKDNNLLGRFELSGIPPPAPRGVPOIEVTFDIDANGILNVATDSTGKANKITI 120
DB 444 EGERAMTKDNNLLGKFLTGIPPPAPRGVPOIEVTFDIDANGILNVSAVDKSTGKANKITI 503

QY 121 TNDKGRLSKEEIERMWQAEKYKAEDVQREVRSNAKNALESYAFNMKSASVEDGLKKGKIS 180
DB 504 TNDKGRLSKEDIERMVQAEKYKAEDQKQKRDVSSKNLSLESYAFNMKATVEDEKLQKIN 563

QY 181 EADKKVKLDKQEVISWLDANTLAEKDFEHEKKELEQVNCNPIISGLYQAGG-PG--PG 237
DB 564 DEDQKILDKCNEIINWLDKNQTAKEEFHQQKELEKVCNPIITKLYQSAGGMPGMPG 623

QY 238 GF--GAQGPKGSGSGPTIEVD 258
DB 624 GPPGGAGPPSGGASSGPTIEVD 646

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RESULT 20
US-09-935-642-16
; Sequence 16, Application US/09935642
; Publication No. US20030044795A1
; GENERAL INFORMATION:
; APPLICANT: BYRJALSEN, Inger
; APPLICANT: LARSEN, Peter
; APPLICANT: STEPHEN, John
; TITLE OF INVENTION: Biochemical Markers for the Human
; TITLE OF INVENTION: Endometrium
; FILE REFERENCE: 8969-014
; CURRENT APPLICATION NUMBER: US/09/935,642
; CURRENT FILING DATE: 2001-08-24
; PRIOR APPLICATION NUMBER: PCT/GB97/02394
; PRIOR FILING DATE: 1997-09-05
; PRIOR APPLICATION NUMBER: PCT/GB9707132.8
; PRIOR FILING DATE: 1997-04-08
; PRIOR APPLICATION NUMBER: PCT/GB9618600.2
; PRIOR FILING DATE: 1996-09-06
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 16
; LENGTH: 646
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-935-642-16

Query Match      83.5%; Score 1097.5; DB 10; Length 646;
Best Local Similarity 81.4%; Pred. No. 3.7e-78;
Matches 214; Conservative 24; Mismatches 20; Indels 5; Gaps 3;

QY 1 KSENVQDLLLLDVAPLSGLGLETAGGVTALIKRNTSTPTKQTQITFTTYSNQPGLVLIQVY 60
DB 384 KSENVQDLLLLDVTPLSGLGLETAGGVTALIKRNTTPTKQTQITFTTYSNQPGLVLIQVY 443

QY 61 EGERAMTKDNNLLGRFELSGIPPPAPRGVPOIEVTFDIDANGILNVATDSTGKANKITI 120
DB 444 EGERAMTKDNNLLGKFLTGIPPPAPRGVPOIEVTFDIDANGILNVSAVDKSTGKANKITI 503

QY 121 TNDKGRLSKEEIERMWQAEKYKAEDVQREVRSNAKNALESYAFNMKSASVEDGLKKGKIS 180
DB 504 TNDKGRLSKEDIERMVQAEKYKAEDQKQKRDVSSKNLSLESYAFNMKATVEDEKLQKIN 563

QY 181 EADKKVKLDKQEVISWLDANTLAEKDFEHEKKELEQVNCNPIISGLYQAGG-PG--PG 237
DB 564 DEDQKILDKCNEIINWLDKNQTAKEEFHQQKELEKVCNPIITKLYQSAGGMPGMPG 623

QY 238 GF--GAQGPKGSGSGPTIEVD 258
DB 624 GPPGGAGPPSGGASSGPTIEVD 646

RESULT 21
US-09-919-039-11
; Sequence 11, Application US/09919039
; Publication No. US20030108871A1
; GENERAL INFORMATION:
; APPLICANT: Kaser, Matthew R.
; TITLE OF INVENTION: GENES EXPRESSED IN TREATED HUMAN C3A LIVER CELL CULTURES
; FILE REFERENCE: PA-0035 US
; CURRENT APPLICATION NUMBER: US/09/919,039
; CURRENT FILING DATE: 2002-09-09
; PRIOR APPLICATION NUMBER: 60/222,113
; PRIOR FILING DATE: 2000-07-28
; NUMBER OF SEQ ID NOS: 401
; SOFTWARE: PERL Program
; SEQ ID NO 11
; LENGTH: 646
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No. US20030108871A1 1545176CD1

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US-09-919-039-11

Query Match 83.5%; Score 1097.5; DB 10; Length 646;
 Best Local Similarity 81.4%; Pred. No. 3.7e-78;
 Matches 214; Conservative 24; Mismatches 20; Indels 5; Gaps 3;
 QY 1 KSENVQDLLLLDVAPLSGLGLETAGGVTALIKRNTSTPTKQTQITFTTYSNQPGLVQVY 60
 DB 384 KSENVQDLLLLDVTPLSGLGLETAGGVTALIKRNTTPTKQTQITFTTYSNQPGLVQVY 443
 QY 61 EGERAMTKNNLLGRFELSGIPPPAPRGVPOIEVTFDIDANGILNVTATDSTGKANKITI 120
 DB 444 EGERAMTKNNLLGKFLTGIPPPAPRGVPOIEVTFDIDANGILNVSADVSTGKANKITI 503
 QY 121 TNDKGRLSKEIEIERMVQEAKEYKAEDVQVRERVSNAKNALESYAFNMKSAVEDGLKGIS 180
 DB 504 TNDKGRLSKEDIERMVQEAKEYKAEDKQDRKVSNNLSLESYAFNMKATVEDEKLGKIN 563
 QY 181 EADKKVLDKQCVISWLDANTLAEDKDEFEHKEKELEQVNCNPIITKLYQSAGGMPGMPG 237
 DB 564 DEDKQKILDKCNELIINWLDKNTAEKEFEHQKELEKVCNPIITKLYQSAGGMPGMPG 623
 QY 238 GF-GAQQPKGGSGSGPTIEVD 258
 DB 624 GPPGGAPPSSGSGPTIEVD 646
 RESULT 22
 US-09-751-708A-43
 ; Sequence 43, Application US/09751708A
 ; Publication No. US2003015713A1
 ; GENERAL INFORMATION:
 ; APPLICANT: TERMAN, David S
 ; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT OF NEOPLASTIC DISEASE
 ; FILE REFERENCE: 751708
 ; CURRENT APPLICATION NUMBER: US/09/751.708A
 ; PRIOR FILING DATE: 2002-10-15
 ; PRIOR APPLICATION NUMBER: US 60/173,371
 ; NUMBER OF SEQ ID NOS: 166
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 43
 ; LENGTH: 646
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-09-751-708A-43

Query Match 83.5%; Score 1097.5; DB 10; Length 646;
 Best Local Similarity 81.4%; Pred. No. 3.7e-78;
 Matches 214; Conservative 24; Mismatches 20; Indels 5; Gaps 3;
 QY 1 KSENVQDLLLLDVAPLSGLGLETAGGVTALIKRNTSTPTKQTQITFTTYSNQPGLVQVY 60
 DB 384 KSENVQDLLLLDVTPLSGLGLETAGGVTALIKRNTTPTKQTQITFTTYSNQPGLVQVY 443
 QY 61 EGERAMTKNNLLGRFELSGIPPPAPRGVPOIEVTFDIDANGILNVTATDSTGKANKITI 120
 DB 444 EGERAMTKNNLLGKFLTGIPPPAPRGVPOIEVTFDIDANGILNVSADVSTGKANKITI 503
 QY 121 TNDKGRLSKEIEIERMVQEAKEYKAEDVQVRERVSNAKNALESYAFNMKSAVEDGLKGIS 180
 DB 504 TNDKGRLSKEDIERMVQEAKEYKAEDKQDRKVSNNLSLESYAFNMKATVEDEKLGKIN 563
 QY 181 EADKKVLDKQCVISWLDANTLAEDKDEFEHKEKELEQVNCNPIITKLYQSAGGMPGMPG 237
 DB 564 DEDKQKILDKCNELIINWLDKNTAEKEFEHQKELEKVCNPIITKLYQSAGGMPGMPG 623
 QY 238 GF-GAQQPKGGSGSGPTIEVD 258
 DB 624 GPPGGAPPSSGSGPTIEVD 646

RESULT 23

US-10-126-103-147

; Sequence 147, Application US/10126103
 ; Publication No. US20030224486A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Bristol-Myers Squibb Company
 ; TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES ASSOCIATED WITH THE NF-KB PATHWAY
 ; FILE REFERENCE: D0108.np
 ; CURRENT APPLICATION NUMBER: US/10/126.103
 ; CURRENT FILING DATE: 2002-04-19
 ; PRIOR APPLICATION NUMBER: US 60/284,962
 ; PRIOR FILING DATE: 2001-04-19
 ; PRIOR APPLICATION NUMBER: US 60/286,645
 ; PRIOR FILING DATE: 2001-04-26
 ; PRIOR APPLICATION NUMBER: US 60/346,986
 ; PRIOR FILING DATE: 2002-01-09
 ; NUMBER OF SEQ ID NOS: 284
 ; SOFTWARE: PatentIn version 3.0
 ; SEQ ID NO 147
 ; LENGTH: 646
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-10-126-103-147

Query Match 83.5%; Score 1097.5; DB 15; Length 646;
 Best Local Similarity 81.4%; Pred. No. 3.7e-78;
 Matches 214; Conservative 24; Mismatches 20; Indels 5; Gaps 3;
 QY 1 KSENVQDLLLLDVAPLSGLGLETAGGVTALIKRNTSTPTKQTQITFTTYSNQPGLVQVY 60
 DB 384 KSENVQDLLLLDVTPLSGLGLETAGGVTALIKRNTTPTKQTQITFTTYSNQPGLVQVY 443
 QY 61 EGERAMTKNNLLGRFELSGIPPPAPRGVPOIEVTFDIDANGILNVTATDSTGKANKITI 120
 DB 444 EGERAMTKNNLLGKFLTGIPPPAPRGVPOIEVTFDIDANGILNVSADVSTGKANKITI 503
 QY 121 TNDKGRLSKEIEIERMVQEAKEYKAEDVQVRERVSNAKNALESYAFNMKSAVEDGLKGIS 180
 DB 504 TNDKGRLSKEDIERMVQEAKEYKAEDKQDRKVSNNLSLESYAFNMKATVEDEKLGKIN 563
 QY 181 EADKKVLDKQCVISWLDANTLAEDKDEFEHKEKELEQVNCNPIITKLYQSAGGMPGMPG 237
 DB 564 DEDKQKILDKCNELIINWLDKNTAEKEFEHQKELEKVCNPIITKLYQSAGGMPGMPG 623
 QY 238 GF-GAQQPKGGSGSGPTIEVD 258
 DB 624 GPPGGAPPSSGSGPTIEVD 646

RESULT 24

US-10-431-096-147
 ; Sequence 147, Application US/10431096
 ; Publication No. US2004008696A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Bristol-Myers Squibb Company
 ; TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES ASSOCIATED WITH THE NF-KB
 ; FILE REFERENCE: D0108A CIP
 ; CURRENT APPLICATION NUMBER: US/10/431.096
 ; CURRENT FILING DATE: 2003-05-07
 ; PRIOR APPLICATION NUMBER: US 60/284,962
 ; PRIOR FILING DATE: 2001-04-19
 ; PRIOR APPLICATION NUMBER: US 10/126,103
 ; PRIOR FILING DATE: 2002-04-19
 ; PRIOR APPLICATION NUMBER: US 60/286,645
 ; PRIOR FILING DATE: 2001-04-26
 ; PRIOR APPLICATION NUMBER: US 60/346,986
 ; PRIOR FILING DATE: 2002-01-09
 ; NUMBER OF SEQ ID NOS: 307
 ; SOFTWARE: PatentIn version 3.2
 ; SEQ ID NO 147
 ; LENGTH: 646
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens

US-10-431-096-147

Query Match 83.5%; Score 1097.5; DB 15; Length 646;
Best Local Similarity 81.4%; Pred. No. 3.7e-78;
Matches 214; Conservative 24; Mismatches 20; Indels 5; Gaps 3;

QY 1 KSENVQDLLLLDVAPLSGLGLETAGGVTALIKRNSTIPTKTQITFTTYSNQPGLVLIQVY 60
DB 384 KSENVQDLLLLDVTPLSGLGLETAGGVTALIKRNSTIPTKTQITFTTYSNQPGLVLIQVY 443

QY 61 EGERAMTKONNLLGRFELSGIPAPRGVPOIEVTFDIDANGILNVATDKSTGKANKITI 120
DB 444 EGERAMTKONNLLGKFLGTGIPAPRGVPOIEVTFDIDANGILNVSAVDKSTGKANKITI 503

QY 121 TNDKGRLSKEEIERMWQAEKYKAEDVQERVSNAKNALESYAFNMKSVADEGLKKGKIS 180
DB 504 TNDKGRLSKEDIERMWQAEKYKAEDKQDKVSSKNSLESYAFNMKATVEDEKLOGKIN 563

QY 181 EADKKVLDKQCVISWLDANTLAEDFEHFKRKELEQVNCNPIISGLYQAGG-PG--PG 237
DB 564 DEDKQKILDKCNEIINWLDKNQTAKEEFHQKELEKVCNPIITKLYQSAGGMPGMPG 623

QY 238 GF--GAQGPKGSGSGPTIEVD 258
DB 624 GFPGGAPPSSGSGPTIEVD 646

RESULT 25

US-10-408-765A-703

; Sequence 703, Application US/10408765A
; Publication No. US20040101874A1

; GENERAL INFORMATION:

; APPLICANT: Ghosh, Soumitra S.

; APPLICANT: Fahy, Eoin D.

; APPLICANT: Zhang, Bing

; APPLICANT: Gibson, Bradford W.

; APPLICANT: Taylor, Steven W.

; APPLICANT: Warnock, Dale E.

; TITLE OF INVENTION: TARGETS FOR THERAPEUTIC INTERVENTION
; IDENTIFIED IN THE MITOCHONDRIAL PROTEOME

; FILE REFERENCE: 660088.465

; CURRENT APPLICATION NUMBER: US/10/408, 765A

; CURRENT FILING DATE: 2003-04-04

; NUMBER OF SEQ ID NOS: 3077

; SOFTWARE: Fast-Seq for Windows Version 4.0

; SEQ ID NO 703

; LENGTH: 646

; TYPE: PRT

; ORGANISM: Homo sapiens

US-10-408-765A-703

Query Match 83.5%; Score 1097.5; DB 16; Length 646;
Best Local Similarity 81.4%; Pred. No. 3.7e-78;
Matches 214; Conservative 24; Mismatches 20; Indels 5; Gaps 3;

QY 1 KSENVQDLLLLDVAPLSGLGLETAGGVTALIKRNSTIPTKTQITFTTYSNQPGLVLIQVY 60
DB 384 KSENVQDLLLLDVTPLSGLGLETAGGVTALIKRNSTIPTKTQITFTTYSNQPGLVLIQVY 443

QY 61 EGERAMTKONNLLGRFELSGIPAPRGVPOIEVTFDIDANGILNVATDKSTGKANKITI 120
DB 444 EGERAMTKONNLLGKFLGTGIPAPRGVPOIEVTFDIDANGILNVSAVDKSTGKANKITI 503

QY 121 TNDKGRLSKEEIERMWQAEKYKAEDVQERVSNAKNALESYAFNMKSVADEGLKKGKIS 180
DB 504 TNDKGRLSKEDIERMWQAEKYKAEDKQDKVSSKNSLESYAFNMKATVEDEKLOGKIN 563

QY 181 EADKKVLDKQCVISWLDANTLAEDFEHFKRKELEQVNCNPIISGLYQAGG-PG--PG 237
DB 564 DEDKQKILDKCNEIINWLDKNQTAKEEFHQKELEKVCNPIITKLYQSAGGMPGMPG 623

QY 238 GF--GAQGPKGSGSGPTIEVD 258

Db 624 GFPGGAPPSSGSGPTIEVD 646

RESULT 26

US-10-737-350-1

; Sequence 1, Application US/10737350

; Publication No. US20040185511A1

; GENERAL INFORMATION:

; APPLICANT: GEORGES, ELIAS

; TITLE OF INVENTION: HSC70 DIRECTED DIAGNOSTICS AND THERAPEUTICS FOR
; MULTIDRUG RESISTANT NEOPLASTIC DISEASE

; FILE REFERENCE: 112418.149US (AUR-011US)

; CURRENT APPLICATION NUMBER: US/10/737,350

; CURRENT FILING DATE: 2003-12-15

; PRIOR APPLICATION NUMBER: 60/438,012

; PRIOR FILING DATE: 2003-01-03

; NUMBER OF SEQ ID NOS: 27

; SOFTWARE: PatentIn Ver. 3.2

; SEQ ID NO 1

; LENGTH: 646

; TYPE: PRT

; ORGANISM: Homo sapiens

US-10-737-350-1

Query Match 83.5%; Score 1097.5; DB 16; Length 646;
Best Local Similarity 81.4%; Pred. No. 3.7e-78;
Matches 214; Conservative 24; Mismatches 20; Indels 5; Gaps 3;

QY 1 KSENVQDLLLLDVAPLSGLGLETAGGVTALIKRNSTIPTKTQITFTTYSNQPGLVLIQVY 60
DB 384 KSENVQDLLLLDVTPLSGLGLETAGGVTALIKRNSTIPTKTQITFTTYSNQPGLVLIQVY 443

QY 61 EGERAMTKONNLLGRFELSGIPAPRGVPOIEVTFDIDANGILNVATDKSTGKANKITI 120
DB 444 EGERAMTKONNLLGKFLGTGIPAPRGVPOIEVTFDIDANGILNVSAVDKSTGKANKITI 503

QY 121 TNDKGRLSKEEIERMWQAEKYKAEDVQERVSNAKNALESYAFNMKSVADEGLKKGKIS 180
DB 504 TNDKGRLSKEDIERMWQAEKYKAEDKQDKVSSKNSLESYAFNMKATVEDEKLOGKIN 563

QY 181 EADKKVLDKQCVISWLDANTLAEDFEHFKRKELEQVNCNPIISGLYQAGG-PG--PG 237
DB 564 DEDKQKILDKCNEIINWLDKNQTAKEEFHQKELEKVCNPIITKLYQSAGGMPGMPG 623

QY 238 GF--GAQGPKGSGSGPTIEVD 258
DB 624 GFPGGAPPSSGSGPTIEVD 646

RESULT 27

US-10-841-207-4

; Sequence 4, Application US/10841207

; Publication No. US20050009772A1

; GENERAL INFORMATION:

; APPLICANT: Caprioli, Joseph

; TITLE OF INVENTION: Methods and Compositions for the Treatment of Glaucoma and Other
; Retinal Diseases

; FILE REFERENCE: A-72263/TAL/MWR (468290-00515)

; CURRENT APPLICATION NUMBER: US/10/841,207

; CURRENT FILING DATE: 2004-05-06

; PRIOR APPLICATION NUMBER: US 60/468,554

; PRIOR FILING DATE: 2003-05-06

; NUMBER OF SEQ ID NOS: 4

; SOFTWARE: PatentIn version 3.2

; SEQ ID NO 4

; LENGTH: 646

; TYPE: PRT

; ORGANISM: Homo sapiens

US-10-841-207-4

Query Match 83.5%; Score 1097.5; DB 17; Length 646;
Best Local Similarity 81.4%; Pred. No. 3.7e-78;

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Matches 214; Conservative 24; Mismatches 20; Indels 5; Gaps 3;
Qy 1 KSENVQDLLLDVAPLSGLTAGVMTALIKRNTIPTKTQTQITFTTYSNQPGLIQVY 60
Db 384 KSENVQDLLLDVAPLSGLTAGVMTALIKRNTIPTKTQTQITFTTYSNQPGLIQVY 443
Qy 61 EGERAMTKNNLLGRFELSGIPPPAPRGVPOIEVTFDIDANGILNVATDSTGKANKITI 120
Db 444 EGERAMTKNNLLGRFELSGIPPPAPRGVPOIEVTFDIDANGILNVATDSTGKANKITI 503
Qy 121 TNDKGRLSKEIEIRMWQAEKYKAEDVQERVSNAKNALESYAFNMKSAVEDGLKGKIS 180
Db 504 TNDKGRLSKEIEIRMWQAEKYKAEDVQERVSNAKNALESYAFNMKSAVEDGLKGKIN 563
Qy 181 EADKKVLDKQCVISWLDANTLAEDKFEHKKRKELEQVNCNPIISGLYQAGG--PG 237
Db 564 DEDQKILDKCNEIINWLDKNQTAKEEFHKKRKELEQVNCNPIITKLYQSAGGMPGMPG 623
Qy 238 GF--GAQPGKGGSGGPTIEVD 258
Db 624 GFPGGAPPSSGASSGPTIEVD 646

RESULT 28
US-10-100-957A-174
; Sequence 174, Application US/10100957A
; Publication No. US20030096322A1
; GENERAL INFORMATION:
; APPLICANT: Giuliano, Kenneth A.
; TITLE OF INVENTION: A System for Cell Based Screening
; FILE REFERENCE: 97-022-LIA
; CURRENT APPLICATION NUMBER: US/10/100,957A
; PRIOR FILING DATE: 2002-03-19
; NUMBER OF SEQ ID NOS: 180
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 174
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: GFP-HSC70
US-10-100-957A-174

Query Match 83.5%; Score 1097.5; DB 14; Length 890;
Best Local Similarity 81.4%; Pred. No. 5.7e-78;
Matches 214; Conservative 24; Mismatches 20; Indels 5; Gaps 3;
Qy 1 KSENVQDLLLDVAPLSGLTAGVMTALIKRNTIPTKTQTQITFTTYSNQPGLIQVY 60
Db 628 KSENVQDLLLDVAPLSGLTAGVMTALIKRNTIPTKTQTQITFTTYSNQPGLIQVY 687
Qy 61 EGERAMTKNNLLGRFELSGIPPPAPRGVPOIEVTFDIDANGILNVATDSTGKANKITI 120
Db 688 EGERAMTKNNLLGRFELSGIPPPAPRGVPOIEVTFDIDANGILNVATDSTGKANKITI 747
Qy 121 TNDKGRLSKEIEIRMWQAEKYKAEDVQERVSNAKNALESYAFNMKSAVEDGLKGKIS 180
Db 748 TNDKGRLSKEIEIRMWQAEKYKAEDVQERVSNAKNALESYAFNMKSAVEDGLKGKIN 807
Qy 181 EADKKVLDKQCVISWLDANTLAEDKFEHKKRKELEQVNCNPIISGLYQAGG--PG 237
Db 808 DEDQKILDKCNEIINWLDKNQTAKEEFHKKRKELEQVNCNPIITKLYQSAGGMPGMPG 867
Qy 238 GF--GAQPGKGGSGGPTIEVD 258
Db 868 GFPGGAPPSSGASSGPTIEVD 890

RESULT 29
US-10-108-260A-4141
; Sequence 4141, Application US/10108260A
; Publication No. US20040005560A1
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; GENERAL INFORMATION:
; APPLICANT: HELIX RESEARCH INSTITUTE
; TITLE OF INVENTION: No. US20040005560A1e1 full length cDNA
; FILE REFERENCE: H1-A0106
; CURRENT APPLICATION NUMBER: US/10/108,260A
; CURRENT FILING DATE: 2002-03-27
; NUMBER OF SEQ ID NOS: 5458
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4141
; LENGTH: 250
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-108-260A-4141

Query Match 83.5%; Score 1097; DB 15; Length 250;
Best Local Similarity 100.0%; Pred. No. 1.2e-78;
Matches 213; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 46 TTYSDNQPGLIQVYEGERAMTKNNLLGRFELSGIPPPAPRGVPOIEVTFDIDANGILNV 105
Db 38 TTYSDNQPGLIQVYEGERAMTKNNLLGRFELSGIPPPAPRGVPOIEVTFDIDANGILNV 97
Qy 106 TATDKSTGKANKITITNDKGRLSKEIEIRMWQAEKYKAEDVQERVSNAKNALESYAFN 165
Db 98 TATDKSTGKANKITITNDKGRLSKEIEIRMWQAEKYKAEDVQERVSNAKNALESYAFN 157
Qy 166 MKSAVEDGLKGKISEADKKVLDKQCVISWLDANTLAEDKFEHKKRKELEQVNCNPIIS 225
Db 158 MKSAVEDGLKGKISEADKKVLDKQCVISWLDANTLAEDKFEHKKRKELEQVNCNPIIS 217
Qy 226 GLYQAGGPGPGFGAGQPKGSGSGPTIEVD 258
Db 218 GLYQAGGPGPGFGAGQPKGSGSGPTIEVD 250

RESULT 30
US-09-919-039-73
; Sequence 73, Application US/09919039
; Publication No. US20030108871A1
; GENERAL INFORMATION:
; APPLICANT: Kaser, Matthew R.
; TITLE OF INVENTION: GENES EXPRESSED IN TREATED HUMAN C3A LIVER CELL CULTURES
; FILE REFERENCE: PA-0035 US
; CURRENT APPLICATION NUMBER: US/09/919,039
; CURRENT FILING DATE: 2002-09-09
; PRIOR FILING DATE: 2002-07-28
; NUMBER OF SEQ ID NOS: 401
; SOFTWARE: PERL Program
; SEQ ID NO 73
; LENGTH: 641
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. US20030108871A1 701484CD1
US-09-919-039-73

Query Match 83.2%; Score 1093; DB 10; Length 641;
Best Local Similarity 81.5%; Pred. No. 8.4e-78;
Matches 216; Conservative 16; Mismatches 17; Indels 16; Gaps 2;
Qy 1 KSENVQDLLLDVAPLSGLTAGVMTALIKRNTIPTKTQTQITFTTYSNQPGLIQVY 60
Db 386 KSENVQDLLLDVAPLSGLTAGVMTALIKRNTIPTKTQTQITFTTYSNQPGLIQVY 445
Qy 61 EGERAMTKNNLLGRFELSGIPPPAPRGVPOIEVTFDIDANGILNVATDSTGKANKITI 120
Db 446 EGERAMTKNNLLGRFELSGIPPPAPRGVPOIEVTFDIDANGILNVATDSTGKANKITI 505
Qy 121 TNDKGRLSKEIEIRMWQAEKYKAEDVQERVSNAKNALESYAFNMKSAVEDGLKGKIS 180
Db 506 TNDKGRLSKEIEIRMWQAEKYKAEDVQERVSNAKNALESYAFNMKSAVEDGLKGKIS 565
```


Matches	204;	Conservative	24;	Mismatches	25;	Indels	5;	Gaps	1
Qy	1	KSENV	DLLLDLVAPLSGLGETAGGVMTALIKRNSTIPTKTQTFTTYSDDNQPGVLIQVY	60					
Db	387	KSENV	DLLLDLVDTPFLSLGIETAGGVTPLIKRNTTIPTKQTQTFTTYSDDNQSSVLVQVY	446					
Qy	61	EGERAMTKNNILGRFELSGIPPA	RGPVPQIEVTFDIDANGILNVTATDKSTGKANKITI	120					
Db	447	EGERAMTKNNILGKFOLDITP	PAPRGVPQIEVTFDIDANGILNVTAAADKSTGKENKITI	506					
Qy	121	TNDKGRLSKEEIERMVQEAEKYKAEDVEQRERVS	AKNALBSYAFNMKSASVEDGLKGKIS	180					
Db	507	TNDKGRLSKDDIDRMVQEAREYKSDENARDRV	AKNALESYTNKOTVDEKLKGKIS	566					
Qy	181	EADKKKVLDKCQEVISWLDANTLAEKDEFEHKR	KLEBQCVCNPPIISGLYGAGGGPPGGFG	240					
Db	567	EODKNKILDKCQEVINLDRNMAEKDEYEHKQ	ELERVNCNPIISKLYQGCGGGSGGG	626					
Qy	241	AQGP	KGGSGGTIEEVD 258						
Db	627	S-----	GASGPTIEEVD 639						
RESULT 36									
US-10-369-493-6233									
; Sequence 6233, Application US/10369493									
; Publication No. US20030233675A1									
; GENERAL INFORMATION:									
; APPLICANT: Cao, Yongwei									
; APPLICANT: Hinkle, Gregory J.									
; APPLICANT: Slater, Steven C.									
; APPLICANT: Goldman, Barry S.									
; APPLICANT: Chen, Xianfeng									
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION									
; FILE REFERENCE: 38-10(52052)/B									
; CURRENT APPLICATION NUMBER: US/10/369,493									
; CURRENT FILING DATE: 2003-02-28									
; PRIOR APPLICATION NUMBER: US 60/360,039									
; PRIOR FILING DATE: 2002-02-21									
; NUMBER OF SEQ ID NOS: 47374									
; SEQ ID NO 6233									
; LENGTH: 640									
; TYPE: PRT									
; ORGANISM: Caenorhabditis elegans									
US-10-369-493-6233									
Query Match 78.7%; Score 1034; DB 15; Length 640;									
Best Local Similarity 77.9%; Pred. No. 3.9e-73;									
Matches 201; Conservative 21; Mismatches 34; Indels 2; Gaps 1									
Qy	1	KSENV	DLLLDLVAPLSGLGETAGGVMTALIKRNSTIPTKTQTFTTYSDDNQPGVLIQVY	60					
Db	385	KSEAV	DLLLDLVAPLSGLGETAGGVMTALIKRNTTIPTKTAQTFTTYSDDNQPGVLIQVY	444					
Qy	61	EGERAMTKNNILGRFELSGIPPA	RGPVPQIEVTFDIDANGILNVTATDKSTGKANKITI	120					
Db	445	EGERAMTKNNILGKFELSGIP	PAPRGVPQIEVTFDIDANGILNVSATDKSTGQNKITI	504					
Qy	121	TNDKGRLSKEEIERMVQEAEKYKAEDVEQRERVS	AKNALBSYAFNMKSASVEDGLKGKIS	180					
Db	505	TNDKGRLSKDDIERMWNNEABKYKADDAEQADR	IGAKNGLESYAFNLKQTIETDEKLKOKIS	564					
Qy	181	EADKKKVLDKCQEVISWLDANTLAEKDEFEHKR	KLEBOVCNPIISGLYGAGGGPPGGFG	240					
Db	565	PEDKCKTEDKCDIELLKWLDSNQTAEKEFEHQ	KDLGLELANPIISKLYQSAGGAPP--A	622					
Qy	241	AQGP	KGGSGGTIEEVD 258						
Db	623	APGA	GAGGTTIEEVD 640						
RESULT 37									

US-10-108-605-75
; Sequence 75, Application US/10108605
; Publication No. US20020160934A1
; GENERAL INFORMATION:
; APPLICANT: Broadus, Julie
; APPLICANT: Stam, Lynn
; APPLICANT: Bachmann, Jane
; APPLICANT: Kamdar, Kim
; TITLE OF INVENTION: NUCLEIC ACID SEQUENCES FROM DROSOPHILA MELANOGASTER THAT ENCODE
; FILE REFERENCE: 31133B
; CURRENT APPLICATION NUMBER: US/10/108,605
; CURRENT FILING DATE: 2002-03-27
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 09/761,142
; PRIOR FILING DATE: 2000-01-14
; PRIOR APPLICATION NUMBER: US 60/176,418
; NUMBER OF SEQ ID NOS: 361
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 75
; LENGTH: 651
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
US-10-108-605-75

Query Match 78.4%; Score 1030; DB 13; Length 651;
Best Local Similarity 74.3%; Pred. No. 8.2e-73;
Matches 199; Conservative 28; Mismatches 31; Indels 10; Gaps 2;

QY 1 KSENVODLLLDVAPLSGLGLETAGGVTALIKRNSIPTKQTIPTTYSNQGVLQIYV 60
DB 384 KSENVODLLLDVAPLSGLGLETAGGVTALIKRNSIPTKQTIPTTYSNQGVLQIYV 443

QY 61 EGERAMTKNNLLGRFELSGIPAPRGVPOIEVTFDANGILNVATDKSTGKANKITI 120
DB 444 EGERAMTKNNLLGRFELSGIPAPRGVPOIEVTFDANGILNVATDKSTGKANKITI 503

QY 121 TNDKGRLSKEEIERMVQEAKEYKAEDVQREVRSKNALESYAFNMKSADVEGLKGKIS 180
DB 504 TNDKGRLSKEEIERMVQEAKEYKAEDVQREVRSKNALESYAFNMKSADVEGLKGKIS 563

QY 181 EADKKVLDKQCOVISWLDANTLAEDKDEFEHKKRKELEQVNCNPIISGLYQAGGPGGFG 232
DB 564 DSDRTTLLDKCNETIKWLDANLADKEEYEHQKRELEQICRPIFSLRSLYGGPGVPGGSSCG 623

QY 233 GPG--PGGFGAAGPGKGGSGGPTIEVD 258
DB 624 GPGGMPGAGAGAGAGAGGAGPTIEVD 651

RESULT 38
US-09-733-179A-11
; Sequence 11, Application US/09733179A
; Publication No. US20030073160A1
; GENERAL INFORMATION:
; APPLICANT: Boux, Heather A.
; APPLICANT: Rodriguez, Henry
; APPLICANT: Wong, Geraldine S.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DETECTING STRESS-INDUCIBLE PROTEINS
; FILE REFERENCE: 12071-006001
; CURRENT APPLICATION NUMBER: US/09/733,179A
; CURRENT FILING DATE: 2000-12-07
; PRIOR FILING DATE: 2000-12-07
; PRIOR APPLICATION NUMBER: WO 00/33341
; PRIOR FILING DATE: 2000-12-07
; PRIOR APPLICATION NUMBER: US 60/169,535
; PRIOR FILING DATE: 1999-12-07
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11
; LENGTH: 643
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-733-179A-11

Query Match 77.0%; Score 1012; DB 10; Length 643;
Best Local Similarity 74.4%; Pred. No. 2.1e-71;
Matches 192; Conservative 33; Mismatches 33; Indels 0; Gaps 0;

QY 1 KSENVODLLLDVAPLSGLGLETAGGVTALIKRNSIPTKQTIPTTYSNQGVLQIYV 60
DB 386 KCEKVQDLLLLDVAPLSLGLETAGGVTALIQRNATIPKTQTFTTYSNQGVLQIYV 445

QY 61 EGERAMTKNNLLGRFELSGIPAPRGVPOIEVTFDANGILNVATDKSTGKANKITI 120
DB 446 EGERAMTKNNLLGRFELSGIPAPRGVPOIEVTFDANGILNVATDKSTGKANKITI 505

QY 121 TNDKGRLSKEEIERMVQEAKEYKAEDVQREVRSKNALESYAFNMKSADVEGLKGKIS 180
DB 506 TNDKGRLSKEEIERMVQEAKEYKAEDVQREVRSKNALESYAFNMKSADVEGLKGKIS 565

QY 181 EADKKVLDKQCOVISWLDANTLAEDKDEFEHKKRKELEQVNCNPIISGLYQAGGPGGFG 240
DB 566 EEDRRKQDKCREVLAWLEHNLQAEKEEYEHQKRELEQICRPIFSLRSLYGGPGVPGGSSCG 625

QY 241 AOGPKGGSGGPTIEVD 258
DB 626 TQARQGDPTGTPIIEVD 643

RESULT 39
US-09-919-039-204
; Sequence 204, Application US/09919039
; Publication No. US20030108871A1
; GENERAL INFORMATION:
; APPLICANT: Kaser, Matthew R.
; TITLE OF INVENTION: GENES EXPRESSED IN TREATED HUMAN C3A LIVER CELL CULTURES
; FILE REFERENCE: PA-0035 US
; CURRENT APPLICATION NUMBER: US/09/919,039
; CURRENT FILING DATE: 2002-09-09
; PRIOR APPLICATION NUMBER: 60/222,113
; PRIOR FILING DATE: 2000-07-28
; NUMBER OF SEQ ID NOS: 401
; SOFTWARE: PERL Program
; SEQ ID NO 204
; LENGTH: 643
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. US20030108871A1 1440032CD1
US-09-919-039-204

Query Match 77.0%; Score 1012; DB 10; Length 643;
Best Local Similarity 74.4%; Pred. No. 2.1e-71;
Matches 192; Conservative 33; Mismatches 33; Indels 0; Gaps 0;

QY 1 KSENVODLLLDVAPLSGLGLETAGGVTALIKRNSIPTKQTIPTTYSNQGVLQIYV 60
DB 386 KCEKVQDLLLLDVAPLSLGLETAGGVTALIQRNATIPKTQTFTTYSNQGVLQIYV 445

QY 61 EGERAMTKNNLLGRFELSGIPAPRGVPOIEVTFDANGILNVATDKSTGKANKITI 120
DB 446 EGERAMTKNNLLGRFELSGIPAPRGVPOIEVTFDANGILNVATDKSTGKANKITI 505

QY 121 TNDKGRLSKEEIERMVQEAKEYKAEDVQREVRSKNALESYAFNMKSADVEGLKGKIS 180
DB 506 TNDKGRLSKEEIERMVQEAKEYKAEDVQREVRSKNALESYAFNMKSADVEGLKGKIS 565

QY 181 EADKKVLDKQCOVISWLDANTLAEDKDEFEHKKRKELEQVNCNPIISGLYQAGGPGGFG 240
DB 566 EEDRRKQDKCREVLAWLEHNLQAEKEEYEHQKRELEQICRPIFSLRSLYGGPGVPGGSSCG 625

QY 241 AOGPKGGSGGPTIEVD 258
DB 626 TQARQGDPTGTPIIEVD 643

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; NAME/KEY: SITE
; LOCATION: (239)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-925-302-724

Query Match 77.0%; Score 1012; DB 9; Length 665;
Best Local Similarity 74.4%; Pred. No. 2.2e-71;
Matches 192; Conservative 33; Mismatches 33; Indels 0; Gaps 0;

Qy 1 KSENVQDLLLDDVAPLSGLGLETAGGVMTALIKNSTIPTKTQTFITYSDNQPGVLIQVY 60
Db 408 KCEKVQDLLLDDVAPLSGLGLETAGGVMTTLIQRNATIPTKTQTFITYSDNQPGVFIQVY 467
Qy 61 EGERAMTKNNLLGRPELSGIPPPAPRGVPOIEVTFDIDANGILNVATDSTGKANKITI 120
Db 468 EGERAMTKNNLLGRPELSGIPPPAPRGVPOIEVTFDIDANGILSVTADRSTGKANKITI 527
Qy 121 TNDKGRLSKKEIERMVOEAEKYKAEDVQERYSAKNALESYAFNMKSAVEDEGLKGKIS 180
Db 528 TNDKGRLSKEEVRMWEAEQYKAEDBAQDRVAKNLSLEAHVHFVWKSLOEBSLRDKIP 587
Qy 181 EADKKVKYLDKCOEIVISWLDANTILAEKDEPEHKRKELEQVCNPIISGLYQAGAGPGPGFG 240
Db 588 EEDRRKQMDKCREVLAWLEHNQLAEKKEVEHQKRELEICRPIFSRLYGGPGVPGGSSCG 647
Qy 241 AQPGKGGSGGPTIEVD 258
Db 648 TQARQGDPTGPTIEVD 665

RESULT 42
US-09-925-302-724
; Sequence 724, Application US/09925302
; Publication No. US20030064072A9
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
; FILE REFERENCE: PA104
; CURRENT APPLICATION NUMBER: US/09/925,302
; CURRENT FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: PCT/US00/05918
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: 60/124,270
; PRIOR FILING DATE: 1999-03-12
; NUMBER OF SEQ ID NOS: 896
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 724
; LENGTH: 665
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (216)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (239)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-925-302-724

Query Match 77.0%; Score 1012; DB 10; Length 665;
Best Local Similarity 74.4%; Pred. No. 2.2e-71;
Matches 192; Conservative 33; Mismatches 33; Indels 0; Gaps 0;

Qy 1 KSENVQDLLLDDVAPLSGLGLETAGGVMTALIKNSTIPTKTQTFITYSDNQPGVLIQVY 60
Db 408 KCEKVQDLLLDDVAPLSGLGLETAGGVMTTLIQRNATIPTKTQTFITYSDNQPGVFIQVY 467
Qy 61 EGERAMTKNNLLGRPELSGIPPPAPRGVPOIEVTFDIDANGILNVATDSTGKANKITI 120
Db 468 EGERAMTKNNLLGRPELSGIPPPAPRGVPOIEVTFDIDANGILSVTADRSTGKANKITI 527
Qy 121 TNDKGRLSKKEIERMVOEAEKYKAEDVQERYSAKNALESYAFNMKSAVEDEGLKGKIS 180

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Db 528 TNDKRLSKKEEVRMVHAEQYKAEDBAQRDRVAAKNSLEAHVHVFKSLQEESLRDKIP 587
Qy 181 EADKKVLDKQCOVISWLDANTLAEKDBFEHKKRKELEQVNCNPIISGLYQAGGPGGCGFG 240
Db 588 EEDRRKQDKCREVLAWLEHNLQAEKYEYHQRKELEQICNPISFSLRYGGPGVPGGSSCG 647
Qy 241 AQGPKGGSGGPTIEEVD 258
Db 648 TQARQGDPTGPTIEEVD 665

RESULT 43
US-10-424-599-234323
; Sequence 234323, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 234323
; LENGTH: 655
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_53620C.1.pap
US-10-424-599-234323

Query Match 73.4%; Score 965; DB 15; Length 655;
Best Local Similarity 70.2%; Pred. No. 1.1e-67;
Matches 186; Conservative 32; Mismatches 39; Indels 8; Gaps 1;

Qy 2 SENVDLLLDVAPLSLGLTAGGVTALIKRNSTIPTKQITFTTYSNDQPGVLIQVYE 61
Db 391 NEKVQDLLLDVTPLSLGLTAGGVTALIPRNTTPTKKEQVFSTYSNDQPGVLIQVFE 450
Qy 62 GERAMTKDNLLGRFELSGIPPRGVPQIEVTFDIDANGILNVATDKSTGKANKITIT 121
Db 451 GERARTKDNLLGKFLSGIPPRGVPQITVCFDIDANGILNVSAEDKTTGQKNKITIT 510
Qy 122 NDKGRLSKEIERMVQAEKYKAEDVQERERSAKNALESYAFNMKSAVEDEGLKGKISE 191
Db 511 NDKGRLSKEDIKRWQAEKYKSEDEHKKKVEAKNALENYAYNMRNTVKDDKIGEKLOP 570
Qy 182 ADKKVLDKQCOVISWLDANTLAEKDBFEHKKRKELEQVNCNPIISGLYQAGGPGGFGA 241
Db 571 ADKKIEDAEIQALWLDNSQLAEADFEDEKMELESICNPIIAKMYQGGAGPDVGAGA 630
Qy 242 QG-----PKGGSGGPTIEEVD 258
Db 631 GAAEDDYAPPPSGSGAGPKIEEVD 655

RESULT 44
US-10-437-963-186650
; Sequence 186650, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 203543
; LENGTH: 646
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_98717C.1.pap
US-10-437-963-186650

Query Match 73.3%; Score 963; DB 16; Length 646;
Best Local Similarity 72.0%; Pred. No. 1.6e-67;
Matches 185; Conservative 28; Mismatches 44; Indels 0; Gaps 0;

Qy 2 SENVDLLLDVAPLSLGLTAGGVTALIKRNSTIPTKQITFTTYSNDQPGVLIQVYE 61
Db 390 NEKVQDLLLDVTPLSLGLTAGGVTALIPRNTTPTKKEQVFSTYSNDQPGVLIQVFE 449
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; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 186650
; LENGTH: 653
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_8342C.1.pap
US-10-437-963-186650

Query Match 73.3%; Score 963.5; DB 16; Length 653;
Best Local Similarity 71.9%; Pred. No. 1.5e-67;
Matches 189; Conservative 25; Mismatches 42; Indels 7; Gaps 2;

Qy 2 SENVDLLLDVAPLSLGLTAGGVTALIKRNSTIPTKQITFTTYSNDQPGVLIQVYE 61
Db 392 NORVQDLLLDVTPLSLGLTAGGVTALIPRNTTPTKKEQVFSTYSNDQPGVLIQVFE 451
Qy 62 GERAMTKDNLLGRFELSGIPPRGVPQIEVTFDIDANGILNVATDKSTGKANKITIT 121
Db 452 GERTRTKDNLLGKFLSGIPPRGVPQINVTFDIDANGILNVSAEDKTTGKKNKITIT 511
Qy 122 NDKGRLSKEIERMVQAEKYKAEDVQERERSAKNALESYAFNMKSAVEDEGLKGKISE 181
Db 512 NDKGRLSKEIERMVQAEKYKAEDVQERERSAKNALENYAYNMRNTVDEKIASLPA 571
Qy 182 ADKKVLDKQCOVISWLDANTLAEKDBFEHKKRKELEQVNCNPIISGLYQAGGPGGFG-- 239
Db 572 DDKKTEDAIEDAIKWLDGNQLAEADFEDEKMELESICNPIISKMYQGGAG-GPAGMDE 630
Qy 240 ----GAQGGSGSGGPTIEEVD 258
Db 631 DAPNGSAGTGGSGGAGPKIEEVD 653

RESULT 45
US-10-437-963-203543
; Sequence 203543, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 203543
; LENGTH: 646
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_98717C.1.pap
US-10-437-963-203543

Query Match 73.3%; Score 963; DB 16; Length 646;
Best Local Similarity 72.0%; Pred. No. 1.6e-67;
Matches 185; Conservative 28; Mismatches 44; Indels 0; Gaps 0;

Qy 2 SENVDLLLDVAPLSLGLTAGGVTALIKRNSTIPTKQITFTTYSNDQPGVLIQVYE 61
Db 390 NEKVQDLLLDVTPLSLGLTAGGVTALIPRNTTPTKKEQVFSTYSNDQPGVLIQVFE 449
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QY 62 GERAMTKNNLLGRFELSGIPAPRGVPOIEVTFDIDANGILNVATDKSTGKANKITIT 121
Db 450 GERARTKNNLLGKFLSGIPAPRGVPOINVCDFIDANGILNVSAEDKTTGQKNKITIT 509
QY 122 NDGRSLKSEIERMVQAEKYKAEDVORERVSNAKNALESYAFNMKSAVEDGLKGKISE 181
Db 510 NDGRSLKSEIERMVQAEKYKAEDBEHKKKVDKNALENYAYNMRNTIKDKIASKLSA 569
QY 182 ADKKKVLDCQEVISWLDANTLAEKDFEHRKKELEQVNCNPIISGLYQAGGPGPGFGA 241
Db 570 DDKKRIEDALEQAIQWLDGNQLAEADFEFDMKELEGICNPITAKMTYQGPADWAGGMD 629
QY 242 QGPKGGSGSGPTIEVD 258
Db 630 DAPAGSGGAGPKIEVD 646

RESULT 46
US-10-425-114-43012
; Sequence 43012, Application US/10425114
; Publication No. US20040034889A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaka, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 43012
; LENGTH: 365
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: 700567610_FLI.pep
US-10-425-114-43012

Query Match 72.8%; Score 957; DB 15; Length 365;
Best Local Similarity 71.0%; Pred. No. 2.3e-67;
Matches 184; Conservative 29; Mismatches 44; Indels 2; Gaps 1;
QY 2 SENVDLLLDVAPLSIGLETAGVMTALIKRNSTIPTKTQOIFTTYSNDQPGVLIQVYE 61
Db 107 NEKVQDLLLDVTPLSIGLETAGVMTVLPRTTIPTRKEQVFSTYSNDQPGVLIQVYE 166
QY 62 GERAMTKNNLLGRFELSGIPAPRGVPOIEVTFDIDANGILNVATDKSTGKANKITIT 121
Db 167 GERTRDNNLLGKFLSGIPAPRGVPOITVCDFIDANGILNVSAEDKTTGQKNKITIT 226
QY 122 NDGRSLKSEIERMVQAEKYKAEDVORERVSNAKNALESYAFNMKSAVEDGLKGKISE 181
Db 227 NDGRSLKSEIERMVQAEKYKAEDBEHKKKVENAKNTLENYAYNMRNTIKDKIASKLSA 286
QY 182 ADKKKVLDCQEVISWLDANTLAEKDFEHRKKELEQVNCNPIISGLYQAGGPGPGFGA 241
Db 287 DDKKRIEDALEQAIQWLDGNQLAEADFEFDMKELEGICNPITAKMTYQGPADWAGGMD 346
QY 242 QGPKGGSGSGSGPTIEVD 258
Db 347 DGPAGSGGAGPKIEVD 365

RESULT 47
US-10-424-599-156571
; Sequence 156571, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J

; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated with
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 156571
; LENGTH: 648
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_112404C.1.pap
US-10-424-599-156571

Query Match 72.8%; Score 957; DB 15; Length 648;
Best Local Similarity 71.0%; Pred. No. 4.8e-67;
Matches 184; Conservative 29; Mismatches 44; Indels 2; Gaps 1;
QY 2 SENVDLLLDVAPLSIGLETAGVMTALIKRNSTIPTKTQOIFTTYSNDQPGVLIQVYE 61
Db 390 NEKVQDLLLDVTPLSIGLETAGVMTVLPRTTIPTRKEQVFSTYSNDQPGVLIQVYE 449
QY 62 GERAMTKNNLLGRFELSGIPAPRGVPOIEVTFDIDANGILNVATDKSTGKANKITIT 121
Db 450 GERTRDNNLLGKFLSGIPAPRGVPOITVCDFIDANGILNVSAEDKTTGQKNKITIT 509
QY 122 NDGRSLKSEIERMVQAEKYKAEDVORERVSNAKNALESYAFNMKSAVEDGLKGKISE 181
Db 510 NDGRSLKSEIERMVQAEKYKAEDBEHKKKVENAKNTLENYAYNMRNTIKDKIASKLSA 569
QY 182 ADKKKVLDCQEVISWLDANTLAEKDFEHRKKELEQVNCNPIISGLYQAGGPGPGFGA 241
Db 570 DDKKRIEDALEQAIQWLDGNQLAEADFEFDMKELEGICNPITAKMTYQGPADWAGGMD 629
QY 242 QGPKGGSGSGSGPTIEVD 258
Db 630 DGPAGSGGAGPKIEVD 648

RESULT 48

US-10-767-701-46962
; Sequence 46962, Application US/10767701
; Publication No. US20040172684A1
; GENERAL INFORMATION:
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53535)B
; CURRENT APPLICATION NUMBER: US/10/767,701
; CURRENT FILING DATE: 2004-01-29
; NUMBER OF SEQ ID NOS: 63128
; SEQ ID NO 46962
; LENGTH: 649
; TYPE: PRT
; ORGANISM: Sorghum bicolor
; FEATURE:
; OTHER INFORMATION: Clone ID: SORBI-28MAY03-C49_296.pap
US-10-767-701-46962

Query Match 72.8%; Score 956; DB 16; Length 649;
Best Local Similarity 71.8%; Pred. No. 5.8e-67;
Matches 186; Conservative 31; Mismatches 40; Indels 2; Gaps 1;
QY 2 SENVDLLLDVAPLSIGLETAGVMTALIKRNSTIPTKTQOIFTTYSNDQPGVLIQVYE 61
Db 391 NEKVQDLLLDVTPLSIGLETAGVMTVLPRTTIPTRKEQVFSTYSNDQPGVLIQVYE 450
QY 62 GERAMTKNNLLGRFELSGIPAPRGVPOIEVTFDIDANGILNVATDKSTGKANKITIT 121

```

; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 43851
; LENGTH: 282
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: 700567825_FLI.pep
; US-10-425-114-43851

Query Match 72.6%; Score 954; DB 15; Length 282;
Best Local Similarity 70.7%; Pred. No. 2.8e-67;
Matches 183; Conservative 30; Mismatches 44; Indels 2; Gaps 1;

QY 2 SENVDLLLDVAPLSGLGTAGVMTALIKRSTIPTKOTQIFTTYSNQPGLIOVYE 61
DB :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
24 NEKVQDLLLDVTPLSGLGTAGVMTVLIPRNTTIPTKKEQVFTSYDNQPGVLIQVYE 83
QY 62 GERAMTKDNNLGRFELSGIPPPAPRGVPOIETVFDIDANGILNVATDKSTGKANKITIT 121
DB :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
84 GERTRDNNLKGKFLSGIPPPAPRGVPOITVCFDIDANGILNVSAEDKTTGQKNKITTIT 143
QY 122 NDKGRLSKEEIERMVQAEKYKAEDVQREVRSKNALESYAFNMKSAAVEDGLKGKISE 181
DB :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
144 NDKGRLSKEEIERMVQAEKYKAEDVQREVRSKNALESYAFNMKSAAVEDGLKGKISE 203
QY 182 ADKKKVLDDKQEVISWLDANTLAEDFEHKKRKELEOVCPNPIISGLYQAGGPGGFGA 241
DB :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
204 DDKKKIEDAIEQAQLDGNQLAEDFEHKKRKELEOVCPNPIISGLYQAGGPGGFGA 263
QY 242 QGPKGGSGS--GPTIEVD 258
DB :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
264 DGPAGSGSGAGPKIEVD 282

RESULT 51
US-10-424-599-156568
; Sequence 156568, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 156568
; LENGTH: 323
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(323)
; OTHER INFORMATION: unsure at all Xaa locations
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_112401C.1.pep
; US-10-424-599-156568

Query Match 72.6%; Score 954; DB 15; Length 323;
Best Local Similarity 70.7%; Pred. No. 3.3e-67;
Matches 183; Conservative 30; Mismatches 44; Indels 2; Gaps 1;

; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 62894
; LENGTH: 651
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: LIB143-053-G1_FLI.pep
; US-10-425-114-62894

Query Match 72.7%; Score 955; DB 15; Length 651;
Best Local Similarity 72.2%; Pred. No. 7e-67;
Matches 187; Conservative 28; Mismatches 42; Indels 2; Gaps 2;

QY 2 SENVDLLLDVAPLSGLGTAGVMTALIKRSTIPTKOTQIFTTYSNQPGLIOVYE 61
DB :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
393 NEKVQDLLLDVTPLSGLGTAGVMTVLIPRNTTIPTKKEQVFTSYDNQPGVLIQVYE 452
QY 62 GERAMTKDNNLGRFELSGIPPPAPRGVPOIETVFDIDANGILNVATDKSTGKANKITIT 121
DB :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
453 GERATKDNLLGKFLSGIPPPAPRGVPOITVTFDIDANGILNVSAEDKTTGQKNKITTIT 512
QY 122 NDKGRLSKEEIERMVQAEKYKAEDVQREVRSKNALESYAFNMKSAAVEDGLKGKISE 181
DB :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
513 NDKGRLSKEEIERMVQAEKYKAEDVQREVRSKNALESYAFNMKSAAVEDGLKGKISE 572
QY 182 ADKKKVLDDKQEVISWLDANTLAEDFEHKKRKELEOVCPNPIISGLYQAGGPGGFGA 239
DB :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
573 DDKKKIEDAIVDSATSWLDNSQLAEVDFEDKKRKELEOVCPNPIISGLYQAGGPGGFGA 632
QY 240 GAQGPKGSGSGPTIEVD 258
DB :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
633 DEDAPSGSGAGPKIEVD 651

RESULT 50
US-10-425-114-43851
; Sequence 43851, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
```

```

; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 43851
; LENGTH: 282
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: 700567825_FLI.pep
; US-10-425-114-43851

Query Match 72.6%; Score 954; DB 15; Length 282;
Best Local Similarity 70.7%; Pred. No. 2.8e-67;
Matches 183; Conservative 30; Mismatches 44; Indels 2; Gaps 1;

QY 2 SENVDLLLDVAPLSGLGTAGVMTALIKRSTIPTKOTQIFTTYSNQPGLIOVYE 61
DB :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
24 NEKVQDLLLDVTPLSGLGTAGVMTVLIPRNTTIPTKKEQVFTSYDNQPGVLIQVYE 83
QY 62 GERAMTKDNNLGRFELSGIPPPAPRGVPOIETVFDIDANGILNVATDKSTGKANKITIT 121
DB :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
84 GERTRDNNLKGKFLSGIPPPAPRGVPOITVCFDIDANGILNVSAEDKTTGQKNKITTIT 143
QY 122 NDKGRLSKEEIERMVQAEKYKAEDVQREVRSKNALESYAFNMKSAAVEDGLKGKISE 181
DB :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
144 NDKGRLSKEEIERMVQAEKYKAEDVQREVRSKNALESYAFNMKSAAVEDGLKGKISE 203
QY 182 ADKKKVLDDKQEVISWLDANTLAEDFEHKKRKELEOVCPNPIISGLYQAGGPGGFGA 241
DB :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
204 DDKKKIEDAIEQAQLDGNQLAEDFEHKKRKELEOVCPNPIISGLYQAGGPGGFGA 263
QY 242 QGPKGGSGS--GPTIEVD 258
DB :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
264 DGPAGSGSGAGPKIEVD 282

RESULT 51
US-10-424-599-156568
; Sequence 156568, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 156568
; LENGTH: 323
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(323)
; OTHER INFORMATION: unsure at all Xaa locations
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_112401C.1.pep
; US-10-424-599-156568

Query Match 72.6%; Score 954; DB 15; Length 323;
Best Local Similarity 70.7%; Pred. No. 3.3e-67;
Matches 183; Conservative 30; Mismatches 44; Indels 2; Gaps 1;

; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 62894
; LENGTH: 651
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: LIB143-053-G1_FLI.pep
; US-10-425-114-62894

Query Match 72.7%; Score 955; DB 15; Length 651;
Best Local Similarity 72.2%; Pred. No. 7e-67;
Matches 187; Conservative 28; Mismatches 42; Indels 2; Gaps 2;

QY 2 SENVDLLLDVAPLSGLGTAGVMTALIKRSTIPTKOTQIFTTYSNQPGLIOVYE 61
DB :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
393 NEKVQDLLLDVTPLSGLGTAGVMTVLIPRNTTIPTKKEQVFTSYDNQPGVLIQVYE 452
QY 62 GERAMTKDNNLGRFELSGIPPPAPRGVPOIETVFDIDANGILNVATDKSTGKANKITIT 121
DB :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
453 GERATKDNLLGKFLSGIPPPAPRGVPOITVTFDIDANGILNVSAEDKTTGQKNKITTIT 512
QY 122 NDKGRLSKEEIERMVQAEKYKAEDVQREVRSKNALESYAFNMKSAAVEDGLKGKISE 181
DB :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
513 NDKGRLSKEEIERMVQAEKYKAEDVQREVRSKNALESYAFNMKSAAVEDGLKGKISE 572
QY 182 ADKKKVLDDKQEVISWLDANTLAEDFEHKKRKELEOVCPNPIISGLYQAGGPGGFGA 239
DB :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
573 DDKKKIEDAIVDSATSWLDNSQLAEVDFEDKKRKELEOVCPNPIISGLYQAGGPGGFGA 632
QY 240 GAQGPKGSGSGPTIEVD 258
DB :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
633 DEDAPSGSGAGPKIEVD 651

RESULT 50
US-10-425-114-43851
; Sequence 43851, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
```



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; OTHER INFORMATION: unsure at all xaa locations
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_100455C.1.pap
US-10-437-963-102982

Query Match      72.4%; Score 951; DB 16; Length 648;
Best Local Similarity 71.0%; Pred. No. 1.4e-66;
Matches 184; Conservative 29; Mismatches 44; Indels 2; Gaps 1;

QY 2 SENVDLLLDVAPLSGLGTAGVMTALIKRSTPTKOTQIFTTYSNDNPGVLIQVYE 61
DB :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 390 NEKVQDLLLDVTPLSGLGTAGVMTVLIPRNTTPTKKEQVFSTYSNDNPGVLIQVYE 449
DB :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 62 GERAMTKNNLLGRFELSGIPPRGVPQIEVTFDIDANGILNVATDKSTGKANKITIT 121
DB :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 450 GERAMTKNNLLGRFELSGIPPRGVPQITVCDFIDANGILNVSAEDKTTGQKNKITTIT 509
DB :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 122 NDKGRLSKEEIERMVQAEKYKAEDVQRRVSAKNALESYAFNMKSAAVEDEGLKGKISE 181
DB :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 510 NDKGRLSKEEIERMVQAEKYKAEDVQRRVSAKNALESYAFNMKSAAVEDEGLKGKISE 569
DB :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 182 ADKKKVLDDKQEVISWLDANTLAEDVQRRVSAKNALESYAFNMKSAAVEDEGLKGKISE 239
DB :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 570 DDKKKTIEDAVDGAISWLDNSQLAEVEFEDEKMKLESGICNPITAKMYQEGAGMGAAGM 629
DB :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 240 GAQPKGSGSGPTIEVD 258
DB :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 630 DEDAPSGSGAGPKIEVD 648
DB :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 58
US-10-425-114-62493
; Sequence 62493, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E.
; APPLICANT: Tabaska, Jack E.
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 62493
; LENGTH: 662
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: LIB143-057-HI_FLI.pap
US-10-425-114-62884

Query Match      72.2%; Score 949; DB 15; Length 662;
Best Local Similarity 71.4%; Pred. No. 2.1e-66;
Matches 185; Conservative 29; Mismatches 43; Indels 2; Gaps 1;

QY 2 SENVDLLLDVAPLSGLGTAGVMTALIKRSTPTKOTQIFTTYSNDNPGVLIQVYE 61
DB :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 404 NEKVQDLLLDVTPLSGLGTAGVMTVLIPRNTTPTKKEQVFSTYSNDNPGVLIQVYE 463
DB :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 62 GERAMTKNNLLGRFELSGIPPRGVPQIEVTFDIDANGILNVATDKSTGKANKITIT 121
DB :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 464 GERAMTKNNLLGRFELSGIPPRGVPQITVTFDIDANGILNVSAEDKTTGQKNKITTIT 523
DB :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 122 NDKGRLSKEEIERMVQAEKYKAEDVQRRVSAKNALESYAFNMKSAAVEDEGLKGKISE 181
DB :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 524 NDKGRLSKEEIERMVQAEKYKAEDVQRRVSAKNALESYAFNMKSAAVEDEGLKGKISE 583
DB :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 182 ADKKKVLDDKQEVISWLDANTLAEDVQRRVSAKNALESYAFNMKSAAVEDEGLKGKISE 239
DB :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 584 EDKKKTIEDAVDGAISWLDNSQLAEVEFEDEKMKLESGICNPITAKMYQEGAGMGAAGM 643
DB :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 240 GAQPKGSGSGPTIEVD 258
DB :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 644 DEDAPSGSGAGPKIEVD 662
DB :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 60
US-10-259-165-98
; Sequence 98, Application US/10259165
; Publication No. US20030135888A1
; GENERAL INFORMATION:
; APPLICANT: Zhu, Tong
; APPLICANT: Wang, Xun
; APPLICANT: Chang, Hur-song
; APPLICANT: Briggs, Steven P.
; APPLICANT: Cooper, Bret
; APPLICANT: Glazebrook, Jane
; APPLICANT: Goff, Stephen A.
; APPLICANT: Katagiri, Fumiaki
; APPLICANT: Kreps, Joel
; APPLICANT: Moughamer, Todd
; APPLICANT: Provart, Nicholas
```

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; APPLICANT: Ricke, Darrell
; TITLE OF INVENTION: GENES THAT ARE MODULATED BY POSTTRANSCRIPTIONAL GENE SILENCING
; FILE REFERENCE: 70030-NP
; CURRENT APPLICATION NUMBER: US/10/259,165
; CURRENT FILING DATE: 2002-09-26
; PRIOR APPLICATION NUMBER: US 60/370,620
; PRIOR FILING DATE: 2002-04-04
; PRIOR APPLICATION NUMBER: US 60/368,327
; PRIOR FILING DATE: 2002-03-27
; PRIOR APPLICATION NUMBER: US 60/325,277
; PRIOR FILING DATE: 2001-09-26
; NUMBER OF SEQ ID NOS: 782
; SOFTWARE: PatentList.pl version 3.0.4 (C) 2001 Syngenta
; SEQ ID NO 98
; LENGTH: 337
; TYPE: PRT
; ORGANISM: Oryza sativa
US-10-259-165-98

Query Match 72.0%; Score 946; DB 14; Length 337;
Best Local Similarity 70.3%; Pred. No. 1.5e-66;
Matches 182; Conservative 31; Mismatches 44; Indels 2; Gaps 1;

Qy 2 SENVDLLLDVAPLSGLGTAGGVTALIKRSTIPTKQTQFTTYSNQPGLVQVYE 61
Db 79 NEKVQDLLLDVTPLSGLGTAGGVTALIPRNTTIPTKKEQVFSTYSNQPGLVQVYE 138
Qy 62 GERAMTKNNLLGRFELSGIPPPAPRGVPOIETVDFIDANGILNVATDKSTGKANKITIT 121
Db 139 GERTRDNNLLGKFLSGIPPPAPRGVPOITVCFDIDANGILNVSAEDKTTGQKNKIIIT 198
Qy 122 NDKGRLSKEEIERMVQAEKYKAEDVQREVSNAKNALESYAFNMKSASVEDEGLKGKISE 181
Db 199 NDKGRLSKEEIERMVQAEKYKAEDVQREVSNAKNALESYAFNMKNITIKDEKIASKLP 258
Qy 182 ADKKKVLDCQEVISWLDANTLAERKDEFEHKELEQVNCPIISGLYQAGGPGGFGA 241
Db 259 ADKKKIEDAIDQAIQWLDGNQLADEAFDDKMKLEGCINPIIAKMYQAGADMGMD 318
Qy 242 QG--PKGSGSGPTIEVD 258
Db 319 DDAPPAGSGAGPKIEVD 337

RESULT 61
US-10-259-165-426
; Sequence 426, Application US/10259165
; Publication No. US20030135888A1
; GENERAL INFORMATION:
; APPLICANT: Zhu, Tong
; APPLICANT: Wang, Xun
; APPLICANT: Chang, Hur-song
; APPLICANT: Briggs, Steven P.
; APPLICANT: Cooper, Bret
; APPLICANT: Glazebrook, Jane
; APPLICANT: Goff, Stephen A.
; APPLICANT: Katagiri, Fumiaki
; APPLICANT: Kreps, Joel
; APPLICANT: Moughamer, Todd
; APPLICANT: Provart, Nicholas
; APPLICANT: Ricke, Darrell
; TITLE OF INVENTION: GENES THAT ARE MODULATED BY POSTTRANSCRIPTIONAL GENE SILENCING
; FILE REFERENCE: 70030-NP
; CURRENT APPLICATION NUMBER: US/10/259,165
; CURRENT FILING DATE: 2002-09-26
; PRIOR APPLICATION NUMBER: US 60/370,620
; PRIOR FILING DATE: 2002-04-04
; PRIOR APPLICATION NUMBER: US 60/368,327
; PRIOR FILING DATE: 2002-03-27
; PRIOR APPLICATION NUMBER: US 60/325,277
; PRIOR FILING DATE: 2001-09-26
; NUMBER OF SEQ ID NOS: 782
; SOFTWARE: PatentList.pl version 3.0.4 (C) 2001 Syngenta
; SEQ ID NO 99
; LENGTH: 337
; TYPE: PRT
; ORGANISM: Oryza sativa
US-10-259-165-99

Query Match 72.0%; Score 946; DB 14; Length 337;
Best Local Similarity 70.3%; Pred. No. 1.5e-66;
Matches 182; Conservative 31; Mismatches 44; Indels 2; Gaps 1;

Qy 2 SENVDLLLDVAPLSGLGTAGGVTALIKRSTIPTKQTQFTTYSNQPGLVQVYE 61
Db 79 NEKVQDLLLDVTPLSGLGTAGGVTALIPRNTTIPTKKEQVFSTYSNQPGLVQVYE 138
Qy 62 GERAMTKNNLLGRFELSGIPPPAPRGVPOIETVDFIDANGILNVATDKSTGKANKITIT 121
Db 139 GERTRDNNLLGKFLSGIPPPAPRGVPOITVCFDIDANGILNVSAEDKTTGQKNKIIIT 198
Qy 122 NDKGRLSKEEIERMVQAEKYKAEDVQREVSNAKNALESYAFNMKSASVEDEGLKGKISE 181
Db 199 NDKGRLSKEEIERMVQAEKYKAEDVQREVSNAKNALESYAFNMKNITIKDEKIASKLP 258
Qy 182 ADKKKVLDCQEVISWLDANTLAERKDEFEHKELEQVNCPIISGLYQAGGPGGFGA 241
Db 259 ADKKKIEDAIDQAIQWLDGNQLADEAFDDKMKLEGCINPIIAKMYQAGADMGMD 318
Qy 242 QG--PKGSGSGPTIEVD 258
Db 319 DDAPPAGSGAGPKIEVD 337

RESULT 62
US-10-259-165-214
; Sequence 214, Application US/10259165
; Publication No. US20030135888A1
; GENERAL INFORMATION:
; APPLICANT: Zhu, Tong
; APPLICANT: Wang, Xun
; APPLICANT: Chang, Hur-song
; APPLICANT: Briggs, Steven P.
; APPLICANT: Cooper, Bret
; APPLICANT: Glazebrook, Jane
; APPLICANT: Goff, Stephen A.
; APPLICANT: Katagiri, Fumiaki
; APPLICANT: Kreps, Joel
; APPLICANT: Moughamer, Todd
; APPLICANT: Provart, Nicholas
; APPLICANT: Ricke, Darrell
; TITLE OF INVENTION: GENES THAT ARE MODULATED BY POSTTRANSCRIPTIONAL GENE SILENCING
; FILE REFERENCE: 70030-NP
; CURRENT APPLICATION NUMBER: US/10/259,165
; CURRENT FILING DATE: 2002-09-26
; PRIOR APPLICATION NUMBER: US 60/370,620
; PRIOR FILING DATE: 2002-04-04
; PRIOR APPLICATION NUMBER: US 60/368,327
; PRIOR FILING DATE: 2002-03-27
; PRIOR APPLICATION NUMBER: US 60/325,277
; PRIOR FILING DATE: 2001-09-26
; NUMBER OF SEQ ID NOS: 782
; SOFTWARE: PatentList.pl version 3.0.4 (C) 2001 Syngenta
; SEQ ID NO 214
; LENGTH: 649
; TYPE: PRT
; ORGANISM: Oryza sativa
US-10-259-165-214

Query Match 72.0%; Score 946; DB 14; Length 649;
Best Local Similarity 70.3%; Pred. No. 3.6e-66;
Matches 182; Conservative 31; Mismatches 44; Indels 2; Gaps 1;

Qy 2 SENVDLLLDVAPLSGLGTAGGVTALIKRSTIPTKQTQFTTYSNQPGLVQVYE 61
Db 391 NEKVQDLLLDVTPLSGLGTAGGVTALIPRNTTIPTKKEQVFSTYSNQPGLVQVYE 450

```

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; SEQ ID NO 426
; LENGTH: 337
; TYPE: PRT
; ORGANISM: Oryza sativa
US-10-259-165-426

Query Match 72.0%; Score 946; DB 14; Length 337;
Best Local Similarity 70.3%; Pred. No. 1.5e-66;
Matches 182; Conservative 31; Mismatches 44; Indels 2; Gaps 1;

Qy 2 SENVDLLLDVAPLSGLGTAGGVTALIKRSTIPTKQTQFTTYSNQPGLVQVYE 61
Db 79 NEKVQDLLLDVTPLSGLGTAGGVTALIPRNTTIPTKKEQVFSTYSNQPGLVQVYE 138
Qy 62 GERAMTKNNLLGRFELSGIPPPAPRGVPOIETVDFIDANGILNVATDKSTGKANKITIT 121
Db 139 GERTRDNNLLGKFLSGIPPPAPRGVPOITVCFDIDANGILNVSAEDKTTGQKNKIIIT 198
Qy 122 NDKGRLSKEEIERMVQAEKYKAEDVQREVSNAKNALESYAFNMKSASVEDEGLKGKISE 181
Db 199 NDKGRLSKEEIERMVQAEKYKAEDVQREVSNAKNALESYAFNMKNITIKDEKIASKLP 258
Qy 182 ADKKKVLDCQEVISWLDANTLAERKDEFEHKELEQVNCPIISGLYQAGGPGGFGA 241
Db 259 ADKKKIEDAIDQAIQWLDGNQLADEAFDDKMKLEGCINPIIAKMYQAGADMGMD 318
Qy 242 QG--PKGSGSGPTIEVD 258
Db 319 DDAPPAGSGAGPKIEVD 337

RESULT 62
US-10-259-165-214
; Sequence 214, Application US/10259165
; Publication No. US20030135888A1
; GENERAL INFORMATION:
; APPLICANT: Zhu, Tong
; APPLICANT: Wang, Xun
; APPLICANT: Chang, Hur-song
; APPLICANT: Briggs, Steven P.
; APPLICANT: Cooper, Bret
; APPLICANT: Glazebrook, Jane
; APPLICANT: Goff, Stephen A.
; APPLICANT: Katagiri, Fumiaki
; APPLICANT: Kreps, Joel
; APPLICANT: Moughamer, Todd
; APPLICANT: Provart, Nicholas
; APPLICANT: Ricke, Darrell
; TITLE OF INVENTION: GENES THAT ARE MODULATED BY POSTTRANSCRIPTIONAL GENE SILENCING
; FILE REFERENCE: 70030-NP
; CURRENT APPLICATION NUMBER: US/10/259,165
; CURRENT FILING DATE: 2002-09-26
; PRIOR APPLICATION NUMBER: US 60/370,620
; PRIOR FILING DATE: 2002-04-04
; PRIOR APPLICATION NUMBER: US 60/368,327
; PRIOR FILING DATE: 2002-03-27
; PRIOR APPLICATION NUMBER: US 60/325,277
; PRIOR FILING DATE: 2001-09-26
; NUMBER OF SEQ ID NOS: 782
; SOFTWARE: PatentList.pl version 3.0.4 (C) 2001 Syngenta
; SEQ ID NO 214
; LENGTH: 649
; TYPE: PRT
; ORGANISM: Oryza sativa
US-10-259-165-214

Query Match 72.0%; Score 946; DB 14; Length 649;
Best Local Similarity 70.3%; Pred. No. 3.6e-66;
Matches 182; Conservative 31; Mismatches 44; Indels 2; Gaps 1;

Qy 2 SENVDLLLDVAPLSGLGTAGGVTALIKRSTIPTKQTQFTTYSNQPGLVQVYE 61
Db 391 NEKVQDLLLDVTPLSGLGTAGGVTALIPRNTTIPTKKEQVFSTYSNQPGLVQVYE 450

```


; TYPE: PRT
; ORGANISM: Sorghum bicolor
; FEATURE:
; OTHER INFORMATION: Clone ID: SORBI-28WAY03-C49_355.ppe
US-10-767-701-47021

Query Match 71.8%; Score 944; DB 16; Length 486;
Best Local Similarity 70.3%; Pred. No. 3.5e-66;
Matches 182; Conservative 30; Mismatches 45; Indels 2; Gaps 1;

QY 2 SENVODLLLDVAPLSGLGTAGGVTALIKRSTIPTKQTOIFTTSDNPGVLIQVYE 61
Db 228 NEKVODLLLDVTPSLGLETAGGVTMLIPRNTIPTKKEQVFSTSDNPGVLIQVYE 287
QY 62 GERAMTKDNNLLGRFELSGIPPPAPRGVPQIEVTFDIDANGILNVATDKSTGKANKITIT 121
Db 288 GERTRTDNNLLGKFLSGIPPPAPRGVPQITVCFDIDANGILNVSAEDKTTGQNKITIT 347
QY 122 NDKGRLSKEIERMVQAEKYKAEDVQRRVSAKNALESYAFNMKSAVEDGLKGIKISE 181
Db 348 NDKGRLSKEIERMVQAEKYKAEDVQRRVSAKNALESYAFNMKSAVEDGLKGIKISE 181
QY 182 ADKKVLDKQEVISWLDANTLAEDFEHKKRKELEQVCPNIIISGLYQAGGP--GGGF 239
Db 408 DDKKIEDAIDAALSWLDANQLAEAFEDFKMKELESICNPITIAKMYQGAGADMGAGGM 467
QY 240 GAQGPKGSGSGPTIERVD 258
Db 468 DEAPAGSGGPKIEVD 486

RESULT 66
US-10-424-599-156570
; Sequence 156570, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J
; APPLICANT: Kovalic, David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 156570
; LENGTH: 282
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_112403C.1.ppe
US-10-424-599-156570

Query Match 71.7%; Score 942; DB 15; Length 282;
Best Local Similarity 71.3%; Pred. No. 2.5e-66;
Matches 181; Conservative 28; Mismatches 43; Indels 2; Gaps 1;

QY 7 DILLDVPAPLSGLGTAGGVTALIKRSTIPTKQTOIFTTSDNPGVLIQVYGERAM 66
Db 29 DILLDVPAPLSGLGTAGGVTALIPRNTIPTKKEQVFSTSDNPGVLIQVYGERTR 89
QY 67 TKDNNLLGRFELSGIPPPAPRGVPQIEVTFDIDANGILNVATDKSTGKANKITITNDKGR 126
Db 89 TRDNNLLGKFLSGIPPPAPRGVPQITVCFDIDANGILNVSAEDKTTGQNKITITNDKGR 148
QY 127 LSKEIERMVQAEKYKAEDVQRRVSAKNALESYAFNMKSAVEDGLKGIKISEADKKK 186
Db 149 LSKEIERMVQAEKYKAEDVQRRVSAKNALESYAFNMKSAVEDGLKGIKISEADKKK 208
QY 187 VLDKQEVISWLDANTLAEDFEHKKRKELEQVCPNIIISGLYQAGGPFGGAGGPKG 246
Db 209 IEDAIEQAIQWLDGNQLAEAFEDFKMKELESICNPITIAKMYQGAGGADMGADGPAA 268

QY 247 GSGS--GPTIEEVD 258
Db 269 GSGSGAGPKIEVD 282

RESULT 67
US-10-425-114-45699
; Sequence 45699, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E.
; APPLICANT: Tabaska, Jack E.
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 45699
; LENGTH: 282
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: 700839890_FLI.ppe
US-10-425-114-45699

Query Match 71.7%; Score 942; DB 15; Length 282;
Best Local Similarity 71.3%; Pred. No. 2.5e-66;
Matches 181; Conservative 28; Mismatches 43; Indels 2; Gaps 1;

QY 7 DILLDVPAPLSGLGTAGGVTALIKRSTIPTKQTOIFTTSDNPGVLIQVYGERAM 66
Db 29 DILLDVPAPLSGLGTAGGVTALIPRNTIPTKKEQVFSTSDNPGVLIQVYGERTR 88
QY 67 TKDNNLLGRFELSGIPPPAPRGVPQIEVTFDIDANGILNVATDKSTGKANKITITNDKGR 126
Db 89 TRDNNLLGKFLSGIPPPAPRGVPQITVCFDIDANGILNVSAEDKTTGQNKITITNDKGR 148
QY 127 LSKEIERMVQAEKYKAEDVQRRVSAKNALESYAFNMKSAVEDGLKGIKISEADKKK 186
Db 149 LSKEIERMVQAEKYKAEDVQRRVSAKNALESYAFNMKSAVEDGLKGIKISEADKKK 208
QY 187 VLDKQEVISWLDANTLAEDFEHKKRKELEQVCPNIIISGLYQAGGPFGGAGGPKG 246
Db 209 IEDAIEQAIQWLDGNQLAEAFEDFKMKELESICNPITIAKMYQGAGGADMGADGPAA 268

RESULT 68
US-10-437-963-106268
; Sequence 106268, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963

; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 106268
; LENGTH: 650
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_10728C.1.pep
; US-10-437-963-106268

Query Match 71.5%; Score 939.5; DB 16; Length 650;
Best Local Similarity 70.4%; Pred. No. 1.2e-65;
Matches 183; Conservative 29; Mismatches 45; Indels 3; Gaps 1;

QY 2 SENVQDLLLLDVAPLSGLTAGGVTALIKRNSTIPTKTQTOIFTTYSNQPGLIQVYE 61
DB 391 NEKVQDLLLLDVTPLSGLTAGGVTMLPRNTTPTKKEQVFSTYSDNQPGVLIQVYE 450
QY 62 GERAMTKDNNLLGRFELSGIPPPAPRGVPOIEVTFDIDANGILNVATDKSTGKANKITIT 121
DB 451 GERTRDNNLLGKFLSGIPPPAPRGVPOITVCFDIDANGILNVSAEDKTTGQKNKITIT 510
QY 122 NDKGRLSKEEIERMVQAEKYKAEDQVRERSAKNALESYAFNMKSASVEDEGLKGKISE 181
DB 511 NDKGRLSKEEIERMVQAEKYKAEDQVRERSAKNALESYAFNMKSASVEDEGLKGKISE 570
QY 182 ADKKKVLDCQEVISWLDANTLAEDFEHKKRKELEQVNCNPIISGLYQAGGPGVLIQVYE 241
DB 571 ADKKKIEDAIDGALSILDSNQLAEAEFEDEKMKELGVCNPIIAKMYQAGADMGAGMDR 630
QY 242 QGPK---GGSGSGPTIEVD 258
DB 631 DAPAAAGSGSGPGPKIEVD 650

RESULT 69

US-10-425-114-57696
; Sequence 57696, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 57696
; LENGTH: 572
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: UC-ZMFLB73197B03_FLI.pep
; US-10-425-114-57696

Query Match 71.5%; Score 939; DB 15; Length 572;
Best Local Similarity 69.5%; Pred. No. 1.1e-65;
Matches 180; Conservative 32; Mismatches 45; Indels 2; Gaps 1;

QY 2 SENVQDLLLLDVAPLSGLTAGGVTALIKRNSTIPTKTQTOIFTTYSNQPGLIQVYE 61
DB 314 NEKVQDLLLLDVTPLSGLTAGGVTMLPRNTTPTKKEQVFSTYSDNQPGVLIQVYE 373
QY 62 GERAMTKDNNLLGRFELSGIPPPAPRGVPOIEVTFDIDANGILNVATDKSTGKANKITIT 121
DB 374 GERTRDNNLLGKFLSGIPPPAPRGVPOITVCFDIDANGILNVSAEDKTTGQKNKITIT 433
QY 122 NDKGRLSKEEIERMVQAEKYKAEDQVRERSAKNALESYAFNMKSASVEDEGLKGKISE 181

DB 434 NDKGRLSKEEIERMVQAEKYKAEDFEHKKRKELEQVNCNPIISGLYQAGGPGVLIQVYE 493
QY 182 ADKKKVLDCQEVISWLDANTLAEDFEHKKRKELEQVNCNPIISGLYQAGGPGVLIQVYE 239
DB 494 DDKKIEDAIDGALSILDSNQLAEAEFEDEKMKELGVCNPIIAKMYQAGADMGAGMDR 553
QY 240 GAQGPKGSGSGPTIEVD 258
DB 554 DEDAPAGSGSGPGPKIEVD 572

RESULT 70

US-10-425-114-70238
; Sequence 70238, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 70238
; LENGTH: 648
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: UC-ZMFLMO17201H08_FLI.pep
; US-10-425-114-70238

Query Match 71.5%; Score 939; DB 15; Length 648;
Best Local Similarity 69.5%; Pred. No. 1.3e-65;
Matches 180; Conservative 32; Mismatches 45; Indels 2; Gaps 1;

QY 2 SENVQDLLLLDVAPLSGLTAGGVTALIKRNSTIPTKTQTOIFTTYSNQPGLIQVYE 61
DB 390 NEKVQDLLLLDVTPLSGLTAGGVTMLPRNTTPTKKEQVFSTYSDNQPGVLIQVYE 449
QY 62 GERAMTKDNNLLGRFELSGIPPPAPRGVPOIEVTFDIDANGILNVATDKSTGKANKITIT 121
DB 450 GERTRDNNLLGKFLSGIPPPAPRGVPOITVCFDIDANGILNVSAEDKTTGQKNKITIT 509
QY 122 NDKGRLSKEEIERMVQAEKYKAEDQVRERSAKNALESYAFNMKSASVEDEGLKGKISE 181
DB 510 NDKGRLSKEEIERMVQAEKYKAEDQVRERSAKNALESYAFNMKSASVEDEGLKGKISE 569
QY 182 ADKKKVLDCQEVISWLDANTLAEDFEHKKRKELEQVNCNPIISGLYQAGGPGVLIQVYE 239
DB 570 DDKKIEDAIDGALSILDSNQLAEAEFEDEKMKELGVCNPIIAKMYQAGADMGAGMDR 629
QY 240 GAQGPKGSGSGPTIEVD 258
DB 630 DEDAPAGSGSGPGPKIEVD 648

RESULT 71

US-10-425-114-56213
; Sequence 56213, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei


```

: APPLICANT: Kovalic, David K.
: APPLICANT: Screen, Steven E
: APPLICANT: Tabaska, Jack E
: APPLICANT: Cao, Yongwei
: TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
: TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
: FILE REFERENCE: 38-21(53)131B
: CURRENT APPLICATION NUMBER: US/10/425,114
: CURRENT FILING DATE: 2003-04-28
: NUMBER OF SEQ ID NOS: 73128
: SEQ ID NO 59160
: LENGTH: 653
: TYPE: PRT
: ORGANISM: Zea mays
: FEATURE:
: OTHER INFORMATION: Clone ID: LIB3912-003-H10_FLI pep
: US-10-425-114-59160

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[illegible]

```

RESULT 75
US-10-425-114-60382
; Sequence 60382, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kowalic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 60382
; LENGTH: 653
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: LIB3591-002-D10_FLI pep
US-10-425-114-60382

```

Query Match 71.5%; Score 939; DB 15; Length 653;
Best Local Similarity 69.5%; Pred. No. 1.3e-65;
Matches 180; Conservative 32; Mismatches 45; Indels 2; Gaps 1;
QY 2 SENVDLLLLDVAPLSLGLETAGGVMTALIKRNTIPKQIFTTYSNDQPGVLIQWE 61

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395 NEKQDLLLLLDTPLSLGLETAGGVTWLIPRNTIIPYKKGQVFTSYSDNQEVLIQVYE 454
62 GERAMTKDNNLLGRFELSGIPPPARGVPQIEVTFDIDANGILNVTATDKSTGKANKITIT 121
455 GERTRTRDNNLLGKRFELSGIPPPARGVPQITVCFDIDANGILNVAEDKTTTQGNKITT 514
122 NDKRLSKERTERMVQRAEKYKADEVOBERVSKNAVALESYAFNMKSAYEDELGKGKISE 181
515 NDKRLSKERLERKVVQRAEKYSDEEHKKKVSKNLSLENTAYNWRNTIKDKBIASKLAA 574
182 ADKXKVLDKCOEIVSWLDANTLARKDBEPHKRKELEQVCNPIISGLYOGAGGP--GPGGF 239
575 DDKKKIEDATDAAI'SWLDANQLAEADBPDDKKMKELSLCNPIIAKMYQAGAGDMGSGGCM 634
240 GAQPKPGSGSGPTIEVD 258
635 DEDAPAGSGGPGPKIEVD 653

RESULT 76
US-10-425-114-62531
; Sequence 62531, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 62531
; LENGTH: 653
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: 700476808_FLI.dep
US-10-425-114-62531

```

Query Match	71.5%;	Score 939;	DB 15;	Length 653;
Best Local Similarity	69.5%;	Pred. No. 1.3e-65;		
Matches 180;	Conservative 39;	Mismatches 45;	Indels 2;	Gaps 1;

Qy	2	SENVDLLLDVAPLSLGLETAGVMTALIKRNSTTPTKTQTQITFTTYSNQPGVLIQVYE	61
Db	395	NEKVDILLLDVTPLSLGLETAGVMTVLIPRNTTPTKCEQVFSTYSNQPGVLIQVYE	454
Qy	62	GERAMTKDNNLGRFELSGTTPPAPRGVQPLEVTFDIDANGILNVATDKSTGRANKITIT	121
Db	455	GERTRTRDNNLLGKFELSGTTPPAPRGVQPLTVCFDIDANGILNVSAEDKTTGQNKKITIT	514
Qy	122	NDGRLSKSBIEIRMWQBAEKYKAEDVQREVRSAQNALSYAFNMKSAVDEGLKGIKE	181
Db	515	NDGRLSKSBIEIRKWQBAEKYKSEDEHKKKVSQSLNLYANMRNTIIDEKIASKLAA	574
Qy	182	ADKKCVLDKQCVISWLDANTLAEKDSFEHRRKELEQVCNPIISGLYQGAGGP--GPGGF	239
Db	575	DDKKKIEDAIDAALSWLDANQLAEADFDDKMKELSLCNPIIAKMYQAGADMGSSGGM	634
Qy	240	GAQPGKGGSGSGPTIREVD	258
Db	635	DEDAPAGSGGFGPKPIEVD	653

RESULT 77
US-10-425-114-62532
; Sequence 62532, Application US/10425114

Fri Apr 8 12:06:11 2005

[illegible]

RESULT 79

Query M

Query Match 71.5%; Score 939; DB 15; Length 653;


```
; OTHER INFORMATION: Clone ID: UC-ZMFLMOL7203G05_FLI.pep
US-10-425-114-69239

Query Match          71.5%; Score 939; DB 15; Length 653;
Best Local Similarity 69.5%; Pred. No. 1.3e-65;
Matches 180; Conservative 32; Mismatches 45; Indels 2; Gaps 1;

Qy      2 SENVDLLLLLDVAPLSLGLETAGGVMTALIKRNSTIPKQTQIFFTYSDNPGVLIQVYE 61
Db      395 NEKVQDLLLDDVTPLSLGLETAGGVMTVLIPRNTTPTKKEQVFSTYSNDNPGVLIQVYE 454
Qy      62 GERAMTKONLLGRFELSGIPPAPRGVPQIEVTDIDANGILNVTTATDKSTGKANKITIT 121
Db      455 GERTRDRNNLLGKFELSGIPPAPRGVPQIIVCFDIDANGILNVSAEDKTTGQRNKIIT 514
Qy      122 NDKRLSKSEIERMVQAERYKAEDVEQVRVSNAKNALSYAFNMKSABVEDGLKGKISE 181
Db      515 NDKRLSKSEIERKMVQDAEYKSEDEEHKKVKESKNSLENAYNWRNTIKDEKIASKLAA 574
Qy      182 ADKKKVLDDCKQEVISWLDANTLAERKDFEHRKKELEQVCNPFIISGLYOGAGGP--GPGGF 239
Db      575 DDKKKIEDAIDAATSWLDANOLAEBDFDDKMKLESICNPPIIAKMYCAGADMGGSGGM 634
Qy      240 GAQGPKGGSGSGPTIEVD 258
Db      635 DEDAPAGSGGFGPKIEVD 653

RESULT 82
US-10-425-114-69306
; Sequence 69306, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 69306
; LENGTH: 653
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: UC-ZMFLMOL7099C05_FLI.pep
US-10-425-114-69306

Query Match          71.5%; Score 939; DB 15; Length 653;
Best Local Similarity 69.5%; Pred. No. 1.3e-65;
Matches 180; Conservative 32; Mismatches 45; Indels 2; Gaps 1;

Qy      2 SENVDLLLLLDVAPLSLGLETAGGVMTALIKRNSTIPKQTQIFFTYSDNPGVLIQVYE 61
Db      395 NEKVQDLLLDDVTPLSLGLETAGGVMTVLIPRNTTPTKKEQVFSTYSNDNPGVLIQVYE 454
Qy      62 GERAMTKONLLGRFELSGIPPAPRGVPQIEVTDIDANGILNVTTATDKSTGKANKITIT 121
Db      455 GERTRDRNNLLGKFELSGIPPAPRGVPQIIVCFDIDANGILNVSAEDKTTGQRNKIIT 514
Qy      122 NDKRLSKSEIERMVQAERYKAEDVEQVRVSNAKNALSYAFNMKSABVEDGLKGKISE 181
Db      515 NDKRLSKSEIERKMVQDAEYKSEDEEHKKVKESKNSLENAYNWRNTIKDEKIASKLAA 574
Qy      182 ADKKKVLDDCKQEVISWLDANTLAERKDFEHRKKELEQVCNPFIISGLYOGAGGP--GPGGF 239
Db      575 DDKKKIEDAIDAATSWLDANOLAEBDFDDKMKLESICNPPIIAKMYCAGADMGGSGGM 634
```

QY 240 GAQPKGGSGGPTIEVD 258
 Db 635 DEDAPAGSGGPGKIEVD 653

RESULT 83

US-10-425-114-70649
 ; Sequence 70649, Application US/10425114
 ; Publication No. US20040034888A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Liu, Jingdong
 ; APPLICANT: Zhou, Yihua
 ; APPLICANT: Kovalic, David K.
 ; APPLICANT: Screen, Steven E
 ; APPLICANT: Tabaska, Jack E
 ; APPLICANT: Cao, Yongwei
 ; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
 ; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
 ; FILE REFERENCE: 38-21(53313)B
 ; CURRENT APPLICATION NUMBER: US/10/425,114
 ; CURRENT FILING DATE: 2003-04-28
 ; NUMBER OF SEQ ID NOS: 73128
 ; SEQ ID NO 70649
 ; LENGTH: 653
 ; TYPE: PRT
 ; ORGANISM: Zea mays
 ; FEATURE:
 ; OTHER INFORMATION: Clone ID: UC-ZMFLM017042B02_FLI.pep
 US-10-425-114-70649

Query Match 71.5%; Score 939; DB 15; Length 653;
 Best Local Similarity 69.5%; Pred. No. 1.3e-65;
 Matches 180; Conservative 32; Mismatches 45; Indels 2; Gaps 1;

QY 2 SENVODLLLDVAPLSGLGTAGVMTALIKRNSTIPTKTQIFTTYSNQPGLIQVYE 61
 Db 395 NEKVQDLLLDVTPLSGLGTAGVMTVLPRTTIPTKKEQVFSTYSNQPGLIQVYE 454
 QY 62 GERAMTKDNNLLGRFELSGIPPPAPRGVPQIVTFDIDANGILNVATDKSTGKANKITIT 121
 Db 455 GERTRDNNLLGKFLSGIPPPAPRGVPQIVTFDIDANGILNVSAEDKTTGQKNKITT 514
 QY 122 NDKGRLSKEEIERMVQAEKKAEDVORERSAKNALESYAFNMKSAAVEDGLKGKISE 181
 Db 515 NDKGRLSKEEIERMVQAEKKAEDVORERSAKNALESYAFNMKSAAVEDGLKGKISE 574
 QY 182 ADKKKVLDDKQEVISWLDANTLAEDKFEHKKRKELEQVCNPIISGLYQAGGP--GPGGF 239
 Db 575 DDKKKTEDDAIAISWLDANQLAEDFDDKMKELSLCNPITAKMYQAGADMGGSGGM 634

QY 240 GAQPKGGSGGPTIEVD 258
 Db 635 DEDAPAGSGGPGKIEVD 653

RESULT 84

US-10-425-114-72128
 ; Sequence 72128, Application US/10425114
 ; Publication No. US20040034888A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Liu, Jingdong
 ; APPLICANT: Zhou, Yihua
 ; APPLICANT: Kovalic, David K.
 ; APPLICANT: Screen, Steven E
 ; APPLICANT: Tabaska, Jack E
 ; APPLICANT: Cao, Yongwei
 ; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
 ; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
 ; FILE REFERENCE: 38-21(53313)B
 ; CURRENT APPLICATION NUMBER: US/10/425,114
 ; CURRENT FILING DATE: 2003-04-28
 ; NUMBER OF SEQ ID NOS: 73128
 ; SEQ ID NO 72128

; LENGTH: 653
 ; TYPE: PRT
 ; ORGANISM: Zea mays
 ; FEATURE:
 ; OTHER INFORMATION: Clone ID: LIB3591-108-G8_FLI.pep
 US-10-425-114-72128

Query Match 71.5%; Score 939; DB 15; Length 653;
 Best Local Similarity 69.5%; Pred. No. 1.3e-65;
 Matches 180; Conservative 32; Mismatches 45; Indels 2; Gaps 1;

QY 2 SENVODLLLDVAPLSGLGTAGVMTALIKRNSTIPTKTQIFTTYSNQPGLIQVYE 61
 Db 395 NEKVQDLLLDVTPLSGLGTAGVMTVLPRTTIPTKKEQVFSTYSNQPGLIQVYE 454
 QY 62 GERAMTKDNNLLGRFELSGIPPPAPRGVPQIVTFDIDANGILNVATDKSTGKANKITIT 121
 Db 455 GERTRDNNLLGKFLSGIPPPAPRGVPQIVTFDIDANGILNVSAEDKTTGQKNKITT 514
 QY 122 NDKGRLSKEEIERMVQAEKKAEDVORERSAKNALESYAFNMKSAAVEDGLKGKISE 181
 Db 515 NDKGRLSKEEIERMVQAEKKAEDVORERSAKNALESYAFNMKSAAVEDGLKGKISE 574
 QY 182 ADKKKVLDDKQEVISWLDANTLAEDKFEHKKRKELEQVCNPIISGLYQAGGP--GPGGF 239
 Db 575 DDKKKTEDDAIAISWLDANQLAEDFDDKMKELSLCNPITAKMYQAGADMGGSGGM 634
 QY 240 GAQPKGGSGGPTIEVD 258
 Db 635 DEDAPAGSGGPGKIEVD 653

RESULT 85

US-10-425-114-72427
 ; Sequence 72427, Application US/10425114
 ; Publication No. US20040034888A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Liu, Jingdong
 ; APPLICANT: Zhou, Yihua
 ; APPLICANT: Kovalic, David K.
 ; APPLICANT: Screen, Steven E
 ; APPLICANT: Tabaska, Jack E
 ; APPLICANT: Cao, Yongwei
 ; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
 ; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
 ; FILE REFERENCE: 38-21(53313)B
 ; CURRENT APPLICATION NUMBER: US/10/425,114
 ; CURRENT FILING DATE: 2003-04-28
 ; NUMBER OF SEQ ID NOS: 73128
 ; SEQ ID NO 72427
 ; LENGTH: 653
 ; TYPE: PRT
 ; ORGANISM: Zea mays
 ; FEATURE:
 ; OTHER INFORMATION: Clone ID: 700466311_FLI.pep
 US-10-425-114-72427

Query Match 71.5%; Score 939; DB 15; Length 653;
 Best Local Similarity 69.5%; Pred. No. 1.3e-65;
 Matches 180; Conservative 32; Mismatches 45; Indels 2; Gaps 1;

QY 2 SENVODLLLDVAPLSGLGTAGVMTALIKRNSTIPTKTQIFTTYSNQPGLIQVYE 61
 Db 395 NEKVQDLLLDVTPLSGLGTAGVMTVLPRTTIPTKKEQVFSTYSNQPGLIQVYE 454
 QY 62 GERAMTKDNNLLGRFELSGIPPPAPRGVPQIVTFDIDANGILNVATDKSTGKANKITIT 121
 Db 455 GERTRDNNLLGKFLSGIPPPAPRGVPQIVTFDIDANGILNVSAEDKTTGQKNKITT 514
 QY 122 NDKGRLSKEEIERMVQAEKKAEDVORERSAKNALESYAFNMKSAAVEDGLKGKISE 181
 Db 515 NDKGRLSKEEIERMVQAEKKAEDVORERSAKNALESYAFNMKSAAVEDGLKGKISE 574

```
Qy 182 ADKKVLDKQEVISWLDANTLAEDFEBHKKRKELEQVNCNPIISGLYQAGGP--GPGGF 239
Db 575 DDKKKIEDAIDAAISWLDANQLAEADFDKMKELSLCNPITAKMYQAGADWGGSGGM 634
Qy 240 GAQPKGSGSGPTIEVD 258
Db 635 DEDAPAGSGGPGKIEVD 653

RESULT 86
US-10-425-114-72533
; Sequence 72533, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 72533
; LENGTH: 653
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: 700477929_FLI.pap
US-10-425-114-72533

Query Match 71.5%; Score 939; DB 15; Length 653;
Best Local Similarity 69.5%; Pred. No. 1.3e-65;
Matches 180; Conservative 32; Mismatches 45; Indels 2; Gaps 1;

Qy 2 SENVQDLLLLDVAPLSIGLETAGGVTALIKRNSTIPTKTQITFTTYSNDQPGVLIQVYE 61
Db 395 NEKVQDLLLLDVTPLSIGLETAGGVTMLIPRNTTPTTKEQVFSTYSNDQPGVLIQVYE 454
Qy 62 GERAMTKNNLLGRFELSGIPPPAPRGVPQIEVTFDIDANGILNVATDKSTGKANKITIT 121
Db 455 GERTRDNNLLKGFELSGIPPPAPRGVPQITVCDFIDANGILNVSAEDKTTGQKNKITIT 514
Qy 122 NDKGRLSKEIERMVQAEKYKAEDVQREVSNAKNALESYAFNMKSAAVEDGLKGKISE 181
Db 515 NDKGRLSKEIERMVQAEKYKAEDVQREVSNAKNALESYAFNMKSAAVEDGLKGKISE 574
Qy 182 ADKKVLDKQEVISWLDANTLAEDFEBHKKRKELEQVNCNPIISGLYQAGGP--GPGGF 239
Db 575 DDKKKIEDAIDAAISWLDANQLAEADFDKMKELSLCNPITAKMYQAGADWGGSGGM 634
Qy 240 GAQPKGSGSGPTIEVD 258
Db 635 DEDAPAGSGGPGKIEVD 653

RESULT 87
US-10-425-114-38995
; Sequence 38995, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53313)B
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; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 38995
; LENGTH: 652
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: LIB3067-050-E8_FLI.pap
US-10-425-114-38995

Query Match 71.4%; Score 938; DB 15; Length 652;
Best Local Similarity 69.9%; Pred. No. 1.5e-65;
Matches 181; Conservative 30; Mismatches 46; Indels 2; Gaps 1;

Qy 2 SENVQDLLLLDVAPLSIGLETAGGVTALIKRNSTIPTKTQITFTTYSNDQPGVLIQVYE 61
Db 394 NEKVQDLLLLDVTPLSIGLETAGGVTMLIPRNTTPTTKEQVFSTYSNDQPGVLIQVYE 453
Qy 62 GERAMTKNNLLGRFELSGIPPPAPRGVPQIEVTFDIDANGILNVATDKSTGKANKITIT 121
Db 454 GERTRDNNLLKGFELSGIPPPAPRGVPQITVCDFIDANGILNVSAEDKTTGQKNKITIT 513
Qy 122 NDKGRLSKEIERMVQAEKYKAEDVQREVSNAKNALESYAFNMKSAAVEDGLKGKISE 181
Db 514 NDKGRLSKEIERMVQAEKYKAEDVQREVSNAKNALESYAFNMKSAAVEDGLKGKISE 573
Qy 182 ADKKVLDKQEVISWLDANTLAEDFEBHKKRKELEQVNCNPIISGLYQAGGP--GPGGF 239
Db 574 DDKKKIEDAIDAAISWLDANQLAEADFDKMKELSLCNPITAKMYQAGADWGGSGGM 633
Qy 240 GAQPKGSGSGPTIEVD 258
Db 634 DEDAPAGSGGPGKIEVD 652

RESULT 88
US-10-425-114-55225
; Sequence 55225, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 55225
; LENGTH: 652
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: UC-ZMFLM017391H02_FLI.pap
US-10-425-114-55225

Query Match 71.4%; Score 938; DB 15; Length 652;
Best Local Similarity 69.9%; Pred. No. 1.5e-65;
Matches 181; Conservative 30; Mismatches 46; Indels 2; Gaps 1;

Qy 2 SENVQDLLLLDVAPLSIGLETAGGVTALIKRNSTIPTKTQITFTTYSNDQPGVLIQVYE 61
Db 394 NEKVQDLLLLDVTPLSIGLETAGGVTMLIPRNTTPTTKEQVFSTYSNDQPGVLIQVYE 453
Qy 62 GERAMTKNNLLGRFELSGIPPPAPRGVPQIEVTFDIDANGILNVATDKSTGKANKITIT 121
Db 454 GERTRDNNLLKGFELSGIPPPAPRGVPQITVCDFIDANGILNVSAEDKTTGQKNKITIT 513
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QY 122 NDKGRLSKEEIERMVQAEKKADEVRERVSAAKNALESYAFNMKSAVEDGLKGKISE 181
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 514 NDKGRLSKEEIERMVQAEKKADEVRERVSAAKNALESYAFNMKSAVEDGLKGKISE 573
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 182 ADKKKVLDDKQEVISWLDANTLAEKDFEHRKKELEQVNCNPIISGLYQAGGP--GPGGF 239
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 574 DDKKKIEDAIDAAISWLDANQLAEAFEDFKKKELESNCNPIIAKMTYQAGGDMGAGGM 633
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 240 GAQGPKGSGSGPTIEVD 258
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 634 DEDAPAGSGGPGKIEVD 652
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
RESULT 89
US-10-425-114-59328
; Sequence 59328, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E.
; APPLICANT: Tabaska, Jack E.
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
; FILE REFERENCE: 38-21(53313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 59328
; LENGTH: 652
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: LIB3060-040-B9_FLI.pep
; US-10-425-114-59328

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Query Match 71.4%; Score 938; DB 15; Length 652;
Best Local Similarity 69.9%; Pred. No. 1.5e-65;
Matches 181; Conservative 30; Mismatches 46; Indels 2; Gaps 1;

QY 2 SENVDLLLDVAPLSLGLTAGGVTALIKRNSTIPTKTQIFTTYSNDQPGVLIQVYE 61
    :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 394 NEKVQDLLLDVTPLSLGLTAGGVTALIPRNTIPTKKEQVFSTYSNDQPGVLIQVYE 453
    :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 62 GERATKDNLLGRFELSGIPAPRGVPOIETVFDIDANGILNVTATDKSTGKANKITIT 121
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 454 GERTRTRDNNLLGKFELSGIPAPRGVPOITVCFDIDANGILNVSABDKTTGQKNKITT 513
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 122 NDKGRLSKEEIERMVQAEKKADEVRERVSAAKNALESYAFNMKSAVEDGLKGKISE 181
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 514 NDKGRLSKEEIERMVQAEKKADEVRERVSAAKNALESYAFNMKSAVEDGLKGKISE 573
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 182 ADKKKVLDDKQEVISWLDANTLAEKDFEHRKKELEQVNCNPIISGLYQAGGP--GPGGF 239
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 574 DDKKKIEDAIDAAISWLDANQLAEAFEDFKKKELESNCNPIIAKMTYQAGGDMGAGGM 633
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 240 GAQGPKGSGSGPTIEVD 258
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 634 DEDAPAGSGGPGKIEVD 652
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
RESULT 90
US-10-425-114-61345
; Sequence 61345, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E.
; APPLICANT: Tabaska, Jack E.

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; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
; FILE REFERENCE: 38-21(53313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 61345
; LENGTH: 652
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: LIB3062-021-A10_FLI.pep
; US-10-425-114-61345

Query Match 71.4%; Score 938; DB 15; Length 652;
Best Local Similarity 69.9%; Pred. No. 1.5e-65;
Matches 181; Conservative 30; Mismatches 46; Indels 2; Gaps 1;

QY 2 SENVDLLLDVAPLSLGLTAGGVTALIKRNSTIPTKTQIFTTYSNDQPGVLIQVYE 61
    :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 394 NEKVQDLLLDVTPLSLGLTAGGVTALIPRNTIPTKKEQVFSTYSNDQPGVLIQVYE 453
    :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 62 GERATKDNLLGRFELSGIPAPRGVPOIETVFDIDANGILNVTATDKSTGKANKITIT 121
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 454 GERTRTRDNNLLGKFELSGIPAPRGVPOITVCFDIDANGILNVSABDKTTGQKNKITT 513
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 122 NDKGRLSKEEIERMVQAEKKADEVRERVSAAKNALESYAFNMKSAVEDGLKGKISE 181
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 514 NDKGRLSKEEIERMVQAEKKADEVRERVSAAKNALESYAFNMKSAVEDGLKGKISE 573
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 182 ADKKKVLDDKQEVISWLDANTLAEKDFEHRKKELEQVNCNPIISGLYQAGGP--GPGGF 239
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 574 DDKKKIEDAIDAAISWLDANQLAEAFEDFKKKELESNCNPIIAKMTYQAGGDMGAGGM 633
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 240 GAQGPKGSGSGPTIEVD 258
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 634 DEDAPAGSGGPGKIEVD 652
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

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RESULT 91
US-10-425-114-62560
; Sequence 62560, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E.
; APPLICANT: Tabaska, Jack E.
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
; FILE REFERENCE: 38-21(53313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 62560
; LENGTH: 652
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: 700072802_FLI.pep
; US-10-425-114-62560

Query Match 71.4%; Score 938; DB 15; Length 652;
Best Local Similarity 69.9%; Pred. No. 1.5e-65;
Matches 181; Conservative 30; Mismatches 46; Indels 2; Gaps 1;

QY 2 SENVDLLLDVAPLSLGLTAGGVTALIKRNSTIPTKTQIFTTYSNDQPGVLIQVYE 61
    :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 394 NEKVQDLLLDVTPLSLGLTAGGVTALIPRNTIPTKKEQVFSTYSNDQPGVLIQVYE 453
    :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

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QY 62 GERAMTKDNNLLGRFELSGIPPPAPRGVPOIEVTFDIDANGILNVATDKSTGKANKITIT 121
Db 454 GERTTRDNNLLGKFLSGIPPPAPRGVPOITVCFDIDANGILNVASBDDKTGGKNTIT 513
QY 122 NDKGRLSKEIERMVQAEKYKAEDVQRRVSAKNALESYAFNMKSASVEDGLKGKISE 181
Db 514 NDKGRLSKEIERMVQAEKYKAEDVQRRVSAKNALESYAFNMKSASVEDGLKGKISE 573
QY 182 ADKKKVLDKQEVISWLDANTLAEKDFEHRKKELEQVNCNPIISGLYQGAGGP--GPGGF 239
Db 574 DDKKKIEDAIDAAISWLDANQLAEDEFEDKMKELSLCNPPIAKMYQGAGEDMGAGGM 633
QY 240 GAQPKGGSGSGPTIEVD 258
Db 634 DEDAPAGSGGPGKIEVD 652

RESULT 92
US-10-425-114-63240
; Sequence 63240, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 63240
; LENGTH: 652
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: LIB3180-031-A4_FLI.pep
US-10-425-114-63240

Query Match 71.4%; Score 938; DB 15; Length 652;
Best Local Similarity 69.9%; Pred. No. 1.5e-65;
Matches 181; Conservative 30; Mismatches 46; Indels 2; Gaps 1;

QY 2 SENVDLLLDVAPLSLGLETAGGVTALIKRSTIPTKTOTFTTYSNQPGLIOVYE 61
Db 394 NEKVQDLLLDVTPLSLGLETAGGVTMLIPRNTTIPTKKEQVFSTYSNQPGLIOVYE 453
QY 62 GERAMTKDNNLLGRFELSGIPPPAPRGVPOIEVTFDIDANGILNVATDKSTGKANKITIT 121
Db 454 GERTTRDNNLLGKFLSGIPPPAPRGVPOITVCFDIDANGILNVASBDDKTGGKNTIT 513
QY 122 NDKGRLSKEIERMVQAEKYKAEDVQRRVSAKNALESYAFNMKSASVEDGLKGKISE 181
Db 514 NDKGRLSKEIERMVQAEKYKAEDVQRRVSAKNALESYAFNMKSASVEDGLKGKISE 573
QY 182 ADKKKVLDKQEVISWLDANTLAEKDFEHRKKELEQVNCNPIISGLYQGAGGP--GPGGF 239
Db 574 DDKKKIEDAIDAAISWLDANQLAEDEFEDKMKELSLCNPPIAKMYQGAGEDMGAGGM 633
QY 240 GAQPKGGSGSGPTIEVD 258
Db 634 DEDAPAGSGGPGKIEVD 652

US-10-425-114-63505
; Sequence 63505, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 63505
; LENGTH: 652
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: UC-ZMFLB73249A05_FLI.pep
US-10-425-114-63505

Query Match 71.4%; Score 938; DB 15; Length 652;
Best Local Similarity 69.9%; Pred. No. 1.5e-65;
Matches 181; Conservative 30; Mismatches 46; Indels 2; Gaps 1;
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QY 2  SENVDLLLDVAPLSGLTAGGVTALIKRNSTIPTKQIIFTTYSNQPGLIQVYE 61
Db 394  NEKVQDLLLDVTPLSGLTAGGVTMLIPRNTTIPTKKEQVFSTYSNQPGLIQVYE 453
QY 62  GERAMTKDNNLLGFEISGIPAPRGVPOIEVTFDIDANGILNVATDSTGKANKITIT 121
Db 454  GERTRTRDNNLLGFEISGIPAPRGVPOITVCFDIDANGILNVSAEDKTTGQKNKITIT 513
QY 122  NDKGRLSKEEIERMVQAEKYKAEDVORERSAKNALESYAFNMKSAYEDELKKGISE 181
Db 514  NDKGRLSKEEIERMVQAEKYKAEDVORERSAKNALESYAFNMKSAYEDELKKGISE 181
QY 182  ADKKVKLDKQEVISWLDANTLAEKDFEHRKKELEQVCNPIISGLYQAGGPP--GPGGF 239
Db 574  DDKKKIEDAIDAAISWLDANQLAEDEFEDKMKELSLCNPPIIAKMYQAGAGDMGGAGGM 633
QY 240  GAQGPKGSGSGPTIEVD 258
Db 634  DEDAPAGSGGPGPKIEVD 652

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RESULT 95

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US-10-425-114-65274
; Sequence 65274, Application US/10425114
; Publication No. US20040034889A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E.
; APPLICANT: Tabaska, Jack E.
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
; FILE REFERENCE: 38-21(5313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 65274
; LENGTH: 652
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: LIB4748-005-H4_FLI.pep
US-10-425-114-65274

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Query Match 71.4%; Score 938; DB 15; Length 652;
Best Local Similarity 69.9%; Pred. No. 1.5e-65;
Matches 181; Conservative 30; Mismatches 46; Indels 2; Gaps 1;

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QY 2  SENVDLLLDVAPLSGLTAGGVTALIKRNSTIPTKQIIFTTYSNQPGLIQVYE 61
Db 394  NEKVQDLLLDVTPLSGLTAGGVTMLIPRNTTIPTKKEQVFSTYSNQPGLIQVYE 453
QY 62  GERAMTKDNNLLGFEISGIPAPRGVPOIEVTFDIDANGILNVATDSTGKANKITIT 121
Db 454  GERTRTRDNNLLGFEISGIPAPRGVPOITVCFDIDANGILNVSAEDKTTGQKNKITIT 513
QY 122  NDKGRLSKEEIERMVQAEKYKAEDVORERSAKNALESYAFNMKSAYEDELKKGISE 181
Db 514  NDKGRLSKEEIERMVQAEKYKAEDVORERSAKNALESYAFNMKSAYEDELKKGISE 181
QY 182  ADKKVKLDKQEVISWLDANTLAEKDFEHRKKELEQVCNPIISGLYQAGGPP--GPGGF 239
Db 574  DDKKKIEDAIDAAISWLDANQLAEDEFEDKMKELSLCNPPIIAKMYQAGAGDMGGAGGM 633
QY 240  GAQGPKGSGSGPTIEVD 258
Db 634  DEDAPAGSGGPGPKIEVD 652

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RESULT 96

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US-10-437-963-193938

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; Sequence 193938, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated with
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 193938
; LENGTH: 649
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_90028C.1.pep
US-10-437-963-193938

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```

Query Match 70.7%; Score 928.5; DB 16; Length 649;
Best Local Similarity 69.4%; Pred. No. 8.7e-65;
Matches 179; Conservative 33; Mismatches 45; Indels 1; Gaps 1;

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QY 2  SENVDLLLDVAPLSGLTAGGVTALIKRNSTIPTKQIIFTTYSNQPGLIQVYE 61
Db 392  NEKVQDLLLDVTPLSGLTAGGVTMLIPRNTTIPTKKEQVFSTYSNQPGLIQVYE 451
QY 62  GERAMTKDNNLLGFEISGIPAPRGVPOIEVTFDIDANGILNVATDSTGKANKITIT 121
Db 452  GERTRTRDNNLLGFEISGIPAPRGVPOITVCFDIDANGILNVSAEDKTTGQKNKITIT 511
QY 122  NDKGRLSKEEIERMVQAEKYKAEDVORERSAKNALESYAFNMKSAYEDELKKGISE 181
Db 512  NDKGRLSKEEIERMVQAEKYKAEDVORERSAKNALESYAFNMKSAYEDELKKGISE 181
QY 182  ADKKVKLDKQEVISWLDANTLAEKDFEHRKKELEQVCNPIISGLYQAGGPPGFGA 241
Db 572  DDKKKIEDAVEQAIQWLDNNQLAEVEFEEDKMKELSLCNPPIIAKMYQAGAGDMGGGMD 631
QY 242  QGP-KGGSGSGPTIEVD 258
Db 632  DAPAGSGGPGPKIEVD 649

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RESULT 97

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US-10-425-114-54413
; Sequence 54413, Application US/10425114
; Publication No. US20040034889A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E.
; APPLICANT: Tabaska, Jack E.
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
; FILE REFERENCE: 38-21(5313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 54413
; LENGTH: 461
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: UC-ZMFLB73199A09_FLI.pep

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US-10-425-114-54413
Query Match      70.1%; Score 920.5; DB 15; Length 461;
Best Local Similarity 69.2%; Pred. No. 2.4e-64;
Matches 180; Conservative 32; Mismatches 45; Indels 3; Gaps 2;

Qy  2  SENVDLLLDVAPLSLGLETAGGVTALIKRNTIPTKQTQIPTTYSNDQPGVLIQVYE 61
Db  202 NEKVQDLLLLDVTPSLGLETAGGVTALIPRNTIPTKKEQVFTSYSDNQPGVLIQVYE 261

Qy  62  GERAMTKNNLLGRFELSGIPAPRGVPQIEVTFDIDANGILNVTATDKSTGKANKITIT 121
Db  262 GERAMTKNNLLGRFELSGIPAPRGVPQITVCFDIDANGILNVSADKTTGQKNKITIT 321

Qy  122 NDKGRLSKEIERMVQAEKYKAEDVQREVRSNAKNALESYAFNMKSAVEDGLKGKISE 181
Db  322 NDKGRLSKEIERMVQAEKYKAEDBEHKKKVDKNSLENYAYNMRNTIKDDKIASKLGA 381

Qy  182 ADKKVLDKQEVISWLDANTLAEDFEHKKRKELEQVNCNPIISGLYQAGAGP--GGGF 239
Db  382 DDKKRIENAVDGAISWLDNSQLAEVDFEDKMKLEGCNPIIAKMYQAGAGMGAAGM 441

Qy  240 GAQGP-KGGSGSGPTIEVD 258
Db  442 DEDAPAGGSAAGPKIEVD 461

RESULT 98
US-10-425-114-57892
; Sequence 57892, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E.
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 57892
; LENGTH: 658
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: UC-ZMFLMO17117B05_FLI.pep
US-10-425-114-57892
Query Match      69.9%; Score 918.5; DB 15; Length 658;
Best Local Similarity 69.2%; Pred. No. 5.5e-64;
Matches 180; Conservative 31; Mismatches 46; Indels 3; Gaps 2;

Qy  2  SENVDLLLDVAPLSLGLETAGGVTALIKRNTIPTKQTQIPTTYSNDQPGVLIQVYE 61
Db  399 NEKVQDLLLLDVTPSLGLETAGGVTALIPRNTIPTKKEQVFTSYSDNQPGVLIQVYE 458

Qy  62  GERAMTKNNLLGRFELSGIPAPRGVPQIEVTFDIDANGILNVTATDKSTGKANKITIT 121
Db  459 GERAMTKNNLLGRFELSGIPAPRGVPQITVCFDIDANGILNVSADKTTGQKNKITIT 518

Qy  122 NDKGRLSKEIERMVQAEKYKAEDVQREVRSNAKNALESYAFNMKSAVEDGLKGKISE 181
Db  519 NDKGRLSKEIERMVQAEKYKAEDBEHKKKVDKNSLENYAYNMRNTIKDDKIASKLGA 578

Qy  182 ADKKVLDKQEVISWLDANTLAEDFEHKKRKELEQVNCNPIISGLYQAGAGP--GGGF 239
Db  579 DDKKRIENAVDGAISWLDNSQLAEVDFEDKMKLEGCNPIIAKMYQAGAGMGAAGM 638

Qy  240 GAQGP-KGGSGSGPTIEVD 258

US-10-425-114-57892
Query Match      69.9%; Score 918.5; DB 15; Length 658;
Best Local Similarity 69.2%; Pred. No. 5.5e-64;
Matches 180; Conservative 31; Mismatches 46; Indels 3; Gaps 2;

Qy  2  SENVDLLLDVAPLSLGLETAGGVTALIKRNTIPTKQTQIPTTYSNDQPGVLIQVYE 61
Db  399 NEKVQDLLLLDVTPSLGLETAGGVTALIPRNTIPTKKEQVFTSYSDNQPGVLIQVYE 458

Qy  62  GERAMTKNNLLGRFELSGIPAPRGVPQIEVTFDIDANGILNVTATDKSTGKANKITIT 121
Db  459 GERAMTKNNLLGRFELSGIPAPRGVPQITVCFDIDANGILNVSADKTTGQKNKITIT 518

Qy  122 NDKGRLSKEIERMVQAEKYKAEDVQREVRSNAKNALESYAFNMKSAVEDGLKGKISE 181
Db  519 NDKGRLSKEIERMVQAEKYKAEDBEHKKKVDKNSLENYAYNMRNTIKDDKIASKLGA 578

Qy  182 ADKKVLDKQEVISWLDANTLAEDFEHKKRKELEQVNCNPIISGLYQAGAGP--GGGF 239
Db  579 DDKKRIENAVDGAISWLDNSQLAEVDFEDKMKLEGCNPIIAKMYQAGAGMGAAGM 638

Qy  240 GAQGP-KGGSGSGPTIEVD 258

US-10-425-114-65502
; Sequence 65502, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E.
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 65502
; LENGTH: 653
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: LIB4766-015-H12_FLI.pep
US-10-425-114-65502
Query Match      69.4%; Score 912.5; DB 15; Length 653;
Best Local Similarity 68.8%; Pred. No. 1.6e-63;
Matches 179; Conservative 32; Mismatches 46; Indels 3; Gaps 2;

Qy  2  SENVDLLLDVAPLSLGLETAGGVTALIKRNTIPTKQTQIPTTYSNDQPGVLIQVYE 61
Db  394 NEKVQDLLLLDVTPSLGLETAGGVTALIPRNTIPTKKEQVFTSYSDNQPGVLIQVYE 453

Qy  62  GERAMTKNNLLGRFELSGIPAPRGVPQIEVTFDIDANGILNVTATDKSTGKANKITIT 121
Db  454 GERAMTKNNLLGRFELSGIPAPRGVPQITVCFDIDANGILNVSADKTTGQKNKITIT 513

Qy  122 NDKGRLSKEIERMVQAEKYKAEDVQREVRSNAKNALESYAFNMKSAVEDGLKGKISE 181
Db  514 NDKGRLSKEIERMVQAEKYKAEDBEHKKKVDKNSLENYAYNMRNTIKDDKIASKLGA 573

Qy  182 ADKKVLDKQEVISWLDANTLAEDFEHKKRKELEQVNCNPIISGLYQAGAGP--GGGF 239
Db  574 DDKKRIENAVDGAISWLDNSQLAEVDFEDKMKLEGCNPIIAKMYQAGAGMGAAGM 633

Qy  240 GAQGP-KGGSGSGPTIEVD 258
Db  634 DEDAPAGGSAAGPKIEVD 653

RESULT 100
US-10-451-467A-536
; Sequence 536, Application US/10451467A
; Publication No. US20040161840A1
; GENERAL INFORMATION:
; APPLICANT: CONTRERAS, ROLAND HENRI
; APPLICANT: EBERHARDT, INES
; APPLICANT: LUYTEN, WALTER HERMAN MARIA LOUIS
; APPLICANT: REEKMAN, RYEKA JOSEPHINA
; TITLE OF INVENTION: BAX-RESPONSIVE GENES FOR DRUG TARGET IDENTIFICATION IN
; FILE REFERENCE: JAB-1667
; CURRENT APPLICATION NUMBER: US/10/451,467A
; CURRENT FILING DATE: 2003-06-19
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: EP 01870002.1
; PRIOR FILING DATE: 2001-01-04
; PRIOR APPLICATION NUMBER: EP 01870003.9
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Search completed: April 6, 2005, 17:37:18
Job time : 152 secs